

# Cytoscape: A Software Environment for Integrated Mod Networks

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Building with a scaffold: emerging strategies for high- to low-level cellular modeling. Trends in Biotechnology, 2003, 21, 255-262.	4.9	171
2	Systems Biology Is Taking Off. Genome Research, 2003, 13, 2377-2380.	2.4	36
3	The Logic of Life. Genome Research, 2003, 13, 2375-2376.	2.4	0
4	Challenges in the Overall Analysis of Microbial Proteomes. Complexus, 2004, 2, 79-86.	0.7	0
5	Predicting protein-peptide interactions via a network-based motif sampler. Bioinformatics, 2004, 20, i274-i282.	1.8	40
6	T1DBase, a community web-based resource for type 1 diabetes research. Nucleic Acids Research, 2004, 33, D544-D549.	6.5	44
7	Discovery of meaningful associations in genomic data using partial correlation coefficients. Bioinformatics, 2004, 20, 3565-3574.	1.8	476
8	GeneNetwork: an interactive tool for reconstruction of genetic networks using microarray data. Bioinformatics, 2004, 20, 3691-3693.	1.8	57
9	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon Halobacterium NRC-1. Genome Research, 2004, 14, 1025-1035.	2.4	130
10	The Biomolecular Interaction Network Database and related tools 2005 update. Nucleic Acids Research, 2004, 33, D418-D424.	6.5	517
11	Control of Yeast Filamentous-Form Growth by Modules in an Integrated Molecular Network. Genome Research, 2004, 14, 380-390.	2.4	78
12	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. Nucleic Acids Research, 2004, 32, W460-W464.	6.5	57
13	Multi-layered Representation for Cell Signaling Pathways. Molecular and Cellular Proteomics, 2004, 3, 1009-1022.	2.5	7
14	PaVESy: Pathway Visualization and Editing System. Bioinformatics, 2004, 20, 2841-2844.	1.8	39
15	WebInterViewer: visualizing and analyzing molecular interaction networks. Nucleic Acids Research, 2004, 32, W89-W95.	6.5	25
16	Global network analysis of phenotypic effects: Protein networks and toxicity modulation in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18006-18011.	3.3	123
17	Genome sequence of Haloarcula marismortui: A halophilic archaeon from the Dead Sea. Genome Research, 2004, 14, 2221-2234.	2.4	268
18	Understanding the yeast proteome: a bioinformatics perspective. Expert Review of Proteomics, 2004, 1, 193-205.	1.3	4

#	ARTICLE	IF	CITATIONS
19	MOLECULAR NETWORKS IN MODEL SYSTEMS. Annual Review of Genomics and Human Genetics, 2004, 5, 177-187.	2.5	20
20	Back to the biology in systems biology: What can we learn from biomolecular networks?. Briefings in Functional Genomics & Proteomics, 2004, 2, 279-297.	3.8	109
21	PathBLAST: a tool for alignment of protein interaction networks. Nucleic Acids Research, 2004, 32, W83-W88.	6.5	360
22	Exploiting biological complexity for strain improvement through systems biology. Nature Biotechnology, 2004, 22, 1261-1267.	9.4	166
23	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
24	DNA-microarray analysis of brain cancer: molecular classification for therapy. Nature Reviews Neuroscience, 2004, 5, 782-792.	4.9	189
25	Computational resources for metabolomics. Briefings in Functional Genomics & Proteomics, 2004, 3, 84-93.	3.8	21
26	PROTEOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 267-293.	2.5	175
27	Towards a systems biology understanding of human health: Interplay between genotype, environment and nutrition. Biotechnology Annual Review, 2004, 10, 51-84.	2.1	46
28	Integrating phenotypic and expression profiles to map arsenic-response networks. Genome Biology, 2004, 5, R95.	13.9	167
29	Comprehensive de novo structure prediction in a systems-biology context for the archaea Halobacterium sp. NRC-1. Genome Biology, 2004, 5, R52.	13.9	45
30	System-based proteomic analysis of the interferon response in human liver cells. Genome Biology, 2004, 5, R54.	13.9	63
31	Systems Biology and New Technologies Enable Predictive and Preventative Medicine. Science, 2004, 306, 640-643.	6.0	977
32	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. Field Crops Research, 2004, 90, 117-131.	2.3	11
33	Hot Spots for Modulating Toxicity Identified by Genomic Phenotyping and Localization Mapping. Molecular Cell, 2004, 16, 117-125.	4.5	90
34	Toward an integrative systems toxicology. Pharmacogenomics, 2004, 5, 1163-1166.	0.6	4
35	Charting gene regulatory networks: strategies, challenges and perspectives. Biochemical Journal, 2004, 381, 1-12.	1.7	73
36	Systems Biology. , 0, , 491-505.		0

#	ARTICLE	IF	CITATIONS
38	Pathway analysis of coronary atherosclerosis. <i>Physiological Genomics</i> , 2005, 23, 103-118.	1.0	144
39	High-throughput metabolic state analysis: the missing link in integrated functional genomics of yeasts. <i>Biochemical Journal</i> , 2005, 388, 669-677.	1.7	147
40	Systematic interpretation of genetic interactions using protein networks. <i>Nature Biotechnology</i> , 2005, 23, 561-566.	9.4	391
41	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005, 23, 951-959.	9.4	380
42	Bioinformatic methods for integrating whole-genome expression results into cellular networks. <i>Drug Discovery Today</i> , 2005, 10, 727-734.	3.2	42
43	Tools enabling the elucidation of molecular pathways active in human disease: application to Hepatitis C virus infection. <i>BMC Bioinformatics</i> , 2005, 6, 154.	1.2	14
44	Component-based software architecture for biosystem reverse engineering. <i>Biotechnology and Bioprocess Engineering</i> , 2005, 10, 400-407.	1.4	2
45	Phenotype analysis using network motifs derived from changes in regulatory network dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 525-546.	1.5	3
47	Protein interaction databases. , 2005, , .		0
48	Refining Protein Subcellular Localization. <i>PLoS Computational Biology</i> , 2005, 1, e66.	1.5	90
49	Balancing protein similarity and gene co-expression reveals new links between genetic conservation and developmental diversity in invertebrates. <i>Bioinformatics</i> , 2005, 21, 1550-1558.	1.8	15
50	Study of coordinative gene expression at the biological process level. <i>Bioinformatics</i> , 2005, 21, 3651-3657.	1.8	11
51	Dynamic Properties of Network Motifs Contribute to Biological Network Organization. <i>PLoS Biology</i> , 2005, 3, e343.	2.6	319
52	A grid layout algorithm for automatic drawing of biochemical networks. <i>Bioinformatics</i> , 2005, 21, 2036-2042.	1.8	57
53	Retroviruses and yeast retrotransposons use overlapping sets of host genes. <i>Genome Research</i> , 2005, 15, 641-654.	2.4	85
54	Genetical Genomics Analysis of a Yeast Segregant Population for Transcription Network Inference. <i>Genetics</i> , 2005, 170, 533-542.	1.2	90
55	Decomposing protein networks into domain-domain interactions. <i>Bioinformatics</i> , 2005, 21, ii220-ii221.	1.8	19
56	Visualizing Biological Pathways: Requirements Analysis, Systems Evaluation and Research Agenda. <i>Information Visualization</i> , 2005, 4, 191-205.	1.2	81



#	ARTICLE	IF	CITATIONS
57	ProViz: protein interaction visualization and exploration. <i>Bioinformatics</i> , 2005, 21, 272-274.	1.8	123
58	Creating, Modeling, and Visualizing Metabolic Networks. , 2005, , 491-518.		5
59	Medusa: a simple tool for interaction graph analysis. <i>Bioinformatics</i> , 2005, 21, 4432-4433.	1.8	170
61	Divergent mechanisms of cis 9, trans 11 $\omega$ -7 and trans 10, cis 12 $\omega$ -6 conjugated linoleic acid affecting insulin resistance and inflammation in apolipoprotein E knockout mice: a proteomics approach. <i>FASEB Journal</i> , 2005, 19, 1746-1748.	0.2	78
62	Response of apolipoprotein E*3 $\Delta$ Leiden transgenic mice to dietary fatty acids: combining liver proteomics with physiological data. <i>FASEB Journal</i> , 2005, 19, 1-26.	0.2	61
63	<i>Drosophila melanogaster</i> : A case study of a model genomic sequence and its consequences. <i>Genome Research</i> , 2005, 15, 1661-1667.	2.4	69
64	Identifying Regulatory Subnetworks for a Set of Genes. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 683-692.	2.5	61
65	DIZZY: STOCHASTIC SIMULATION OF LARGE-SCALE GENETIC REGULATORY NETWORKS (SUPPLEMENTARY) Tj ETQq1.1 0.784314 rgB / 0.3 24	0.3	24
66	Gene function prediction from congruent synthetic lethal interactions in yeast. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0026.	3.2	118
67	Conserved patterns of protein interaction in multiple species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1974-1979.	3.3	714
68	BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in Biological Networks. <i>Bioinformatics</i> , 2005, 21, 3448-3449.	1.8	3,901
69	Discovering Functional Transcription Factor Binding from Superimposed Gene Networks. , 0, , .		0
70	Systems Biology for the Virtual Plant: Figure 1.. <i>Plant Physiology</i> , 2005, 138, 550-554.	2.3	82
71	Proteomic resources: Integrating biomedical information in humans. <i>Gene</i> , 2005, 364, 13-18.	1.0	14
72	Genetic network interactions among replication, repair and nuclear pore deficiencies in yeast. <i>DNA Repair</i> , 2005, 4, 459-468.	1.3	111
73	From protein networks to biological systems. <i>FEBS Letters</i> , 2005, 579, 1821-1827.	1.3	75
74	An integrated approach for inference and mechanistic modeling for advancing drug development. <i>FEBS Letters</i> , 2005, 579, 1878-1883.	1.3	28
75	Computational representation of developmental genetic regulatory networks. <i>Developmental Biology</i> , 2005, 283, 1-16.	0.9	207

#	ARTICLE	IF	CITATIONS
76	Managing genomic and proteomic knowledge. Drug Discovery Today: Technologies, 2005, 2, 197-204.	4.0	4
77	Chapter 12 Bioinformatics standards and tools in proteomics. Comprehensive Analytical Chemistry, 2005, 46, 501-521.	0.7	0
78	Ontological analysis of gene expression data: current tools, limitations, and open problems. Bioinformatics, 2005, 21, 3587-3595.	1.8	766
79	PIMWalker???. Applied Bioinformatics, 2005, 4, 137-139.	1.7	8
80	BioLayoutJava. Applied Bioinformatics, 2005, 4, 71-74.	1.7	50
81	DIZZY: STOCHASTIC SIMULATION OF LARGE-SCALE GENETIC REGULATORY NETWORKS. Journal of Bioinformatics and Computational Biology, 2005, 03, 415-436.	0.3	195
82	A compendium of Caenorhabditis elegans regulatory transcription factors: a resource for mapping transcription regulatory networks. Genome Biology, 2005, 6, R110.	13.9	175
83	iVici: Interrelational Visualization and Correlation Interface. Genome Biology, 2005, 6, R115.	13.9	10
84	Ulysses - an application for the projection of molecular interactions across species. Genome Biology, 2005, 6, R106.	13.9	22
85	Validation and refinement of gene-regulatory pathways on a network of physical interactions. Genome Biology, 2005, 6, R62.	13.9	76
86	Derivation of genetic interaction networks from quantitative phenotype data. Genome Biology, 2005, 6, R38.	13.9	114
87	Recurrent insertion and duplication generate networks of transposable element sequences in the Drosophila melanogaster genome. Genome Biology, 2006, 7, R112.	13.9	188
88	Systematic screening of polyphosphate (poly P) levels in yeast mutant cells reveals strong interdependence with primary metabolism. Genome Biology, 2006, 7, R109.	13.9	68
89	Inferring transcriptional modules from ChIP-chip, motif and microarray data. Genome Biology, 2006, 7, R37.	13.9	89
90	Comparative analysis of Saccharomyces cerevisiae WW domains and their interacting proteins. Genome Biology, 2006, 7, R30.	13.9	52
91	Gene Lethality Detection and Characterization via Topological Analysis of Regulatory Networks. IEEE Transactions on Circuits and Systems Part 1: Regular Papers, 2006, 53, 2438-2443.	0.1	3
92	Have Green Â¿ A Visual Analytics Framework for Large Semantic Graphs. , 2006, , .		18
93	exploRase: Exploratory Data Analysis of Systems Biology Data. , 0, , .		5

#	ARTICLE	IF	CITATIONS
94	Visualization of complementary systems biology data with parallel heatmaps. IBM Journal of Research and Development, 2006, 50, 575-581.	3.2	6
95	Integrative Data Mining for Assessing International Conflict Events. , 2006, , .		0
96	PathBank: Web-Based Querying and Visualziation of an Integrated Biological Pathway Database. , 0, , .		1
97	Systems biology approaches identify ATF3 as a negative regulator of Toll-like receptor 4. Nature, 2006, 441, 173-178.	13.7	755
98	Graph-based methods for analysing networks in cell biology. Briefings in Bioinformatics, 2006, 7, 243-255.	3.2	368
99	PathSys: integrating molecular interaction graphs for systems biology. BMC Bioinformatics, 2006, 7, 55.	1.2	50
100	Effects of prostratin on Cyclin T1/P-TEFb function and the gene expression profile in primary resting CD4+T cells. Retrovirology, 2006, 3, 66.	0.9	74
101	[22] Visualizing Networks. Methods in Enzymology, 2006, 411, 408-421.	0.4	20
102	A network-based analysis of the late-phase reaction of the skin. Journal of Allergy and Clinical Immunology, 2006, 118, 220-225.	1.5	27
103	Modulation of the TLR-Mediated Inflammatory Response by the Endogenous Human Host Defense Peptide LL-37. Journal of Immunology, 2006, 176, 2455-2464.	0.4	491
104	Motif Search in Graphs: Application to Metabolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 360-368.	1.9	146
105	Act Globally, Think Locally: Systems Biology Addresses the PDZ Domain. ACS Chemical Biology, 2006, 1, 207-210.	1.6	24
106	Pathway analysis using random forests classification and regression. Bioinformatics, 2006, 22, 2028-2036.	1.8	210
107	A DNA Integrity Network in the Yeast Saccharomyces cerevisiae. Cell, 2006, 124, 1069-1081.	13.5	490
108	A Gene-Centered C. elegans Protein-DNA Interaction Network. Cell, 2006, 125, 1193-1205.	13.5	224
109	Integrated analysis of multiple data sources reveals modular structure of biological networks. Biochemical and Biophysical Research Communications, 2006, 345, 302-309.	1.0	33
110	Coevolution, modularity and human disease. Current Opinion in Genetics and Development, 2006, 16, 637-644.	1.5	21
111	Engineering Yeast Transcription Machinery for Improved Ethanol Tolerance and Production. Science, 2006, 314, 1565-1568.	6.0	730

#	ARTICLE	IF	CITATIONS
112	Modularity of the Transcriptional Response of Protein Complexes in Yeast. <i>Journal of Molecular Biology</i> , 2006, 363, 589-610.	2.0	27
113	A Wiring of the Human Nucleolus. <i>Molecular Cell</i> , 2006, 22, 285-295.	4.5	56
114	CFinder: locating cliques and overlapping modules in biological networks. <i>Bioinformatics</i> , 2006, 22, 1021-1023.	1.8	845
115	Working Together to Respond to the Challenges of EU Policy to Replace Animal Testing. <i>ATLA Alternatives To Laboratory Animals</i> , 2006, 34, 11-18.	0.7	4
116	BioPAX - biological pathway data exchange format. , 2006, , .		6
117	Virology in the 21st century: finding function with functional genomics. <i>Future Virology</i> , 2006, 1, 47-53.	0.9	10
118	BN++ – A Biological Information System. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 148-161.	1.0	17
119	Microarray analysis of gene expression: considerations in data mining and statistical treatment. <i>Physiological Genomics</i> , 2006, 25, 355-363.	1.0	67
120	Transcriptional activators in yeast. <i>Nucleic Acids Research</i> , 2006, 34, 955-967.	6.5	84
121	Comprehensive curation and analysis of global interaction networks in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biology</i> , 2006, 5, 11.	2.7	276
122	Reconstructing protein complexes: From proteomics to systems biology. <i>Proteomics</i> , 2006, 6, 4724-4731.	1.3	18
123	Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , 2006, 6, 5059-5075.	1.3	23
124	The pitfalls of proteomics experiments without the correct use of bioinformatics tools. <i>Proteomics</i> , 2006, 6, 5577-5596.	1.3	87
125	Proteome informatics II: Bioinformatics for comparative proteomics. <i>Proteomics</i> , 2006, 6, 5445-5466.	1.3	34
126	A first global analysis of plasmid encoded proteins in the ACLAME database. <i>FEMS Microbiology Reviews</i> , 2006, 30, 980-994.	3.9	48
127	Toward the Systems Biology of Vesicle Transport. <i>Traffic</i> , 2006, 7, 761-768.	1.3	7
128	Global mapping of pharmacological space. <i>Nature Biotechnology</i> , 2006, 24, 805-815.	9.4	776
129	Reverse engineering cellular networks. <i>Nature Protocols</i> , 2006, 1, 662-671.	5.5	345

#	ARTICLE	IF	CITATIONS
130	The model organism as a system: integrating 'omics' data sets. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 198-210.	16.1	678
131	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	13.7	2,681
132	Systems biology as a foundation for genome-scale synthetic biology. <i>Current Opinion in Biotechnology</i> , 2006, 17, 488-492.	3.3	109
133	Aggregation of bioinformatics data using Semantic Web technology. <i>Web Semantics</i> , 2006, 4, 216-221.	2.2	30
134	A semantic web approach to biological pathway data reasoning and integration. <i>Web Semantics</i> , 2006, 4, 207-215.	2.2	9
135	Algorithms for network analysis in systems-ADME/Tox using the MetaCore and MetaDrug platforms. <i>Xenobiotica</i> , 2006, 36, 877-901.	0.5	125
136	Designing Highly Flexible and Usable Cyberinfrastructures for Convergence. <i>Annals of the New York Academy of Sciences</i> , 2006, 1093, 161-179.	1.8	14
137	Modeling network growth with assortative mixing. <i>European Physical Journal B</i> , 2006, 50, 617-630.	0.6	16
138	Analysis of microarray experiments of gene expression profiling. <i>American Journal of Obstetrics and Gynecology</i> , 2006, 195, 373-388.	0.7	263
139	One hundred years of high-throughput <i>Drosophila</i> research. <i>Chromosome Research</i> , 2006, 14, 349-362.	1.0	18
140	Advances in the analysis of dynamic protein complexes by proteomics and data processing. <i>Analytical and Bioanalytical Chemistry</i> , 2006, 386, 482-493.	1.9	10
141	Functional gene analysis of individual response to challenge of SIVmac239 in <i>M. mulatta</i> PBMC culture. <i>Virology</i> , 2006, 348, 242-252.	1.1	8
142	Information integration of protein-protein interactions as essential tools for immunomics. <i>Cellular Immunology</i> , 2006, 244, 84-86.	1.4	4
143	Systems biology of innate immunity. <i>Cellular Immunology</i> , 2006, 244, 105-109.	1.4	35
144	Genomics of TGF- $\beta$ 1 signaling in stem cell commitment and dendritic cell development. <i>Cellular Immunology</i> , 2006, 244, 116-120.	1.4	7
145	Biological microarray interpretation: The rules of engagement. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2006, 1759, 319-327.	2.4	40
146	simBio: A Java package for the development of detailed cell models. <i>Progress in Biophysics and Molecular Biology</i> , 2006, 90, 360-377.	1.4	39
147	VANTED: a system for advanced data analysis and visualization in the context of biological networks. <i>BMC Bioinformatics</i> , 2006, 7, 109.	1.2	438

#	ARTICLE	IF	CITATIONS
148	The Gaggle: an open-source software system for integrating bioinformatics software and data sources. BMC Bioinformatics, 2006, 7, 176.	1.2	135
149	A database and tool, IM Browser, for exploring and integrating emerging gene and protein interaction data for Drosophila. BMC Bioinformatics, 2006, 7, 195.	1.2	27
150	Exploration of biological network centralities with CentiBiN. BMC Bioinformatics, 2006, 7, 219.	1.2	168
151	Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. BMC Bioinformatics, 2006, 7, 280.	1.2	221
152	SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. BMC Bioinformatics, 2006, 7, 286.	1.2	46
153	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. BMC Bioinformatics, 2006, 7, 30.	1.2	188
154	Evaluation of clustering algorithms for protein-protein interaction networks. BMC Bioinformatics, 2006, 7, 488.	1.2	742
155	cPath: open source software for collecting, storing, and querying biological pathways. BMC Bioinformatics, 2006, 7, 497.	1.2	108
156	IntNetDB v1.0: an integrated protein-protein interaction network database generated by a probabilistic model. BMC Bioinformatics, 2006, 7, 508.	1.2	73
157	An evaluation of human protein-protein interaction data in the public domain. BMC Bioinformatics, 2006, 7, S19.	1.2	201
158	Global similarity and local divergence in human and mouse gene co-expression networks. BMC Evolutionary Biology, 2006, 6, 70.	3.2	75
159	A high-throughput screen identifying sequence and promiscuity characteristics of the loxP spacer region in Cre-mediated recombination. BMC Genomics, 2006, 7, 73.	1.2	60
160	Transforming omics data into context: Bioinformatics on genomics and proteomics raw data. Electrophoresis, 2006, 27, 2659-2675.	1.3	33
161	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. Bioinformatics, 2006, 22, 1665-1667.	1.8	13
162	An integrative approach for causal gene identification and gene regulatory pathway inference. Bioinformatics, 2006, 22, e489-e496.	1.8	87
163	Computational modeling of the Plasmodiumfalciparum interactome reveals protein function on a genome-wide scale. Genome Research, 2006, 16, 542-549.	2.4	91
164	Using Web Agents for Data Mining of Fungal Genomes. Applied Mycology and Biotechnology, 2006, 6, 297-309.	0.3	1
165	Hierarchical visualization of metabolic networks using virtual reality. , 2006, , .		10

#	ARTICLE	IF	CITATIONS
166	BioCAD. , 2006, , .		0
167	Identification of the Proliferation/Differentiation Switch in the Cellular Network of Multicellular Organisms. PLoS Computational Biology, 2006, 2, e145.	1.5	91
168	Heterotachy in Mammalian Promoter Evolution. PLoS Genetics, 2006, 2, e30.	1.5	102
169	NetAlign: a web-based tool for comparison of protein interaction networks. Bioinformatics, 2006, 22, 2175-2177.	1.8	67
170	Graph-based analysis and visualization of experimental results with ONDEX. Bioinformatics, 2006, 22, 1383-1390.	1.8	193
171	PIANA: protein interactions and network analysis. Bioinformatics, 2006, 22, 1015-1017.	1.8	55
172	Network Analysis of Human In-Stent Restenosis. Circulation, 2006, 114, 2644-2654.	1.6	66
173	A systematic RNA interference screen reveals a cell migration gene network in <i>C. elegans</i> . Journal of Cell Science, 2006, 119, 4811-4818.	1.2	76
174	Proteome Analysis of Halobacterium sp. NRC-1 Facilitated by the Biomodule Analysis Tool BMSorter. Molecular and Cellular Proteomics, 2006, 5, 987-997.	2.5	14
175	Disentangling information flow in the Ras-cAMP signaling network. Genome Research, 2006, 16, 520-526.	2.4	17
176	SEBINI: Software Environment for Biological Network Inference. Bioinformatics, 2006, 22, 2706-2708.	1.8	22
177	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. Bioinformatics, 2006, 22, 2532-2538.	1.8	292
178	PRODISTIN Web Site: a tool for the functional classification of proteins from interaction networks. Bioinformatics, 2006, 22, 248-250.	1.8	20
179	Expression and functional profiling reveal distinct gene classes involved in fatty acid metabolism. Molecular Systems Biology, 2006, 2, 2006.0009.	3.2	44
180	Bioinformatics Approaches to Integrate Metabolomics and Other Systems Biology Data. , 2006, , 105-115.		14
181	Computational Tools for Modeling Protein Networks. Current Proteomics, 2006, 3, 181-197.	0.1	18
182	Dry work in a wet world: computation in systems biology. Molecular Systems Biology, 2006, 2, 40.	3.2	17
183	A Network-based Analysis of Polyanion-binding Proteins Utilizing Yeast Protein Arrays. Molecular and Cellular Proteomics, 2006, 5, 2263-2278.	2.5	15

#	ARTICLE	IF	CITATIONS
184	Unraveling transcription regulatory networks by protein-DNA and protein-protein interaction mapping. <i>Genome Research</i> , 2006, 16, 1445-1454.	2.4	136
185	Transcriptional Coordination of the Metabolic Network in Arabidopsis. <i>Plant Physiology</i> , 2006, 142, 762-774.	2.3	178
186	Development and Implementation of the PSI MI Standard for Molecular Interaction. , 2006, , .		1
187	MULTIPLEXED PROTEIN ARRAY PLATFORMS FOR ANALYSIS OF AUTOIMMUNE DISEASES. <i>Annual Review of Immunology</i> , 2006, 24, 391-418.	9.5	102
188	BiologicalNetworks: visualization and analysis tool for systems biology. <i>Nucleic Acids Research</i> , 2006, 34, W466-W471.	6.5	83
189	The tYNA platform for comparative interactomics: a web tool for managing, comparing and mining multiple networks. <i>Bioinformatics</i> , 2006, 22, 2968-2970.	1.8	63
190	Representing, storing and accessing molecular interaction data: a review of models and tools. <i>Briefings in Bioinformatics</i> , 2006, 7, 331-338.	3.2	35
191	GenePro: a cytoscape plug-in for advanced visualization and analysis of interaction networks. <i>Bioinformatics</i> , 2006, 22, 2178-2179.	1.8	47
192	BioNetBuilder: automatic integration of biological networks. <i>Bioinformatics</i> , 2007, 23, 392-393.	1.8	82
193	Integration of expression profiles and genetic mapping data to identify candidate genes in intracranial aneurysm. <i>Physiological Genomics</i> , 2007, 32, 45-57.	1.0	32
194	Bacteriome.org an integrated protein interaction database for E. coli. <i>Nucleic Acids Research</i> , 2007, 36, D632-D636.	6.5	47
195	IntAct--open source resource for molecular interaction data. <i>Nucleic Acids Research</i> , 2007, 35, D561-D565.	6.5	701
196	Making database systems usable. , 2007, , .		177
197	Network Genomics. , 2007, , 89-115.		14
198	Systems Analysis of Chaperone Networks in the Malarial Parasite Plasmodium falciparum. <i>PLoS Computational Biology</i> , 2007, 3, e168.	1.5	109
199	Identification of Putative Androgen Receptor Interaction Protein Modules. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 252-271.	2.5	51
200	Sungear: interactive visualization and functional analysis of genomic datasets. <i>Bioinformatics</i> , 2007, 23, 259-261.	1.8	35
201	Inferring genome-wide functional linkages in E. coli by combining improved genome context methods: Comparison with high-throughput experimental data. <i>Genome Research</i> , 2007, 17, 527-535.	2.4	57



#	ARTICLE	IF	CITATIONS
202	A Predicted Interactome for Arabidopsis. <i>Plant Physiology</i> , 2007, 145, 317-329.	2.3	285
203	Michigan Molecular Interactions (MiMI): putting the jigsaw puzzle together. <i>Nucleic Acids Research</i> , 2007, 35, D566-D571.	6.5	98
204	Systematic discovery of functional modules and context-specific functional annotation of human genome. <i>Bioinformatics</i> , 2007, 23, i222-i229.	1.8	73
205	Expression of a Tumor-Related Gene Network Increases in the Mammalian Hypothalamus at the Time of Female Puberty. <i>Endocrinology</i> , 2007, 148, 5147-5161.	1.4	79
206	The Rice Kinase Database. A Phylogenomic Database for the Rice Kinome. <i>Plant Physiology</i> , 2007, 143, 579-586.	2.3	127
207	T1DBase: integration and presentation of complex data for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2007, 35, D742-D746.	6.5	60
208	Regulation of yeast oscillatory dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2241-2246.	3.3	133
209	The Research on the Relationship Between Adrenergic Receptor Subtypes. , 2007, , .		0
210	A Network of Genes Regulated by Light in Cyanobacteria. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 166-185.	1.0	12
211	SEBINI-CABIN: An Analysis Pipeline for Biological Network Inference, with a Case Study in Protein-Protein Interaction Network Reconstruction. , 2007, , .		3
212	Kinetic Modeling Using BioPAX Ontology. , 2007, 2007, 339-348.		10
213	A Graph-Theoretic Analysis of the Human Protein-Interaction Network Using Multicore Parallel Algorithms. , 2007, , .		6
214	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4730-4735.	3.3	369
215	A Large-scale Protein-protein Interaction Analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , 2007, 14, 207-216.	1.5	170
216	Onto-Tools: new additions and improvements in 2006. <i>Nucleic Acids Research</i> , 2007, 35, W206-W211.	6.5	87
217	Current progress in network research: toward reference networks for key model organisms. <i>Briefings in Bioinformatics</i> , 2007, 8, 318-332.	3.2	46
218	Resources, standards and tools for systems biology. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2007, 6, 240-251.	3.8	63
219	In-depth Analysis of the Adipocyte Proteome by Mass Spectrometry and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1257-1273.	2.5	101

#	ARTICLE	IF	CITATIONS
220	Literature-based compound profiling: application to toxicogenomics. <i>Pharmacogenomics</i> , 2007, 8, 1521-1534.	0.6	22
221	The BioGRID Interaction Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D637-D640.	6.5	610
222	Transcriptional responses to fatty acid are coordinated by combinatorial control. <i>Molecular Systems Biology</i> , 2007, 3, 115.	3.2	58
223	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007, 35, W625-W632.	6.5	66
224	NetMatch: a Cytoscape plugin for searching biological networks. <i>Bioinformatics</i> , 2007, 23, 910-912.	1.8	75
225	COlOrize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. <i>Bioinformatics</i> , 2007, 23, 394-396.	1.8	105
226	Cerebral: a Cytoscape plugin for layout of and interaction with biological networks using subcellular localization annotation. <i>Bioinformatics</i> , 2007, 23, 1040-1042.	1.8	163
227	structureViz: linking Cytoscape and UCSF Chimera. <i>Bioinformatics</i> , 2007, 23, 2345-2347.	1.8	71
228	The MiSink Plugin: Cytoscape as a graphical interface to the Database of Interacting Proteins. <i>Bioinformatics</i> , 2007, 23, 2193-2195.	1.8	19
229	Quantitative Phosphoproteome Profiling of Wnt3a-mediated Signaling Network. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1952-1967.	2.5	57
230	Reliable prediction of regulator targets using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1919-1931.	2.4	141
231	Cyclone: java-based querying and computing with Pathway/Genome databases. <i>Bioinformatics</i> , 2007, 23, 1299-1300.	1.8	11
232	Pathway-based Approaches to Pharmacogenomics. <i>Current Pharmacogenomics and Personalized Medicine: the International Journal for Expert Reviews in Pharmacogenomics</i> , 2007, 5, 79-86.	0.3	9
233	A Tandem Affinity Purification-based Technology Platform to Study the Cell Cycle Interactome in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1226-1238.	2.5	196
234	Assessing Significance of Connectivity and Conservation in Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2007, 14, 747-764.	0.8	52
235	Identification of tightly regulated groups of genes during <i>Drosophila melanogaster</i> embryogenesis. <i>Molecular Systems Biology</i> , 2007, 3, 72.	3.2	67
236	Analyzing Protein Interaction Networks. , 0, , 1121-1177.		5
237	Inferring protein-protein interaction networks from protein complex data. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 480.	0.1	3

#	ARTICLE	IF	CITATIONS
238	Visualization of Biological Data. , 0, , 1573-1626.		1
239	The OXL format for the exchange of integrated datasets. Journal of Integrative Bioinformatics, 2007, 4, 27-40.	1.0	10
240	CellCircuits: a database of protein network models. Nucleic Acids Research, 2007, 35, D538-D545.	6.5	22
241	Analyzing Gene Relationships for Down Syndrome with Labeled Transition Graphs. , 2007, , .		1
242	Getting connected: analysis and principles of biological networks. Genes and Development, 2007, 21, 1010-1024.	2.7	477
243	Comparative genomics of elastin: Sequence analysis of a highly repetitive protein. Matrix Biology, 2007, 26, 524-540.	1.5	67
244	Broad network-based predictability of Saccharomyces cerevisiae gene loss-of-function phenotypes. Genome Biology, 2007, 8, R258.	13.9	87
245	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. Genome Biology, 2007, 8, R253.	13.9	52
246	PAZAR: a framework for collection and dissemination of cis-regulatory sequence annotation. Genome Biology, 2007, 8, R207.	13.9	89
247	Cross-species cluster co-conservation: a new method for generating protein interaction networks. Genome Biology, 2007, 8, R185.	13.9	12
248	Metabolic peculiarities of Aspergillus niger disclosed by comparative metabolic genomics. Genome Biology, 2007, 8, R182.	13.9	51
249	Network motif analysis of a multi-mode genetic-interaction network. Genome Biology, 2007, 8, R160.	13.9	14
250	A functional map of NF $\kappa$ B signaling identifies novel modulators and multiple system controls. Genome Biology, 2007, 8, R104.	13.9	20
251	Toxicogenomic analysis of Caenorhabditis elegans reveals novel genes and pathways involved in the resistance to cadmium toxicity. Genome Biology, 2007, 8, R122.	13.9	148
252	Reactome: a knowledge base of biologic pathways and processes. Genome Biology, 2007, 8, R39.	13.9	539
253	Genome mapping and expression analyses of human intronic noncoding RNAs reveal tissue-specific patterns and enrichment in genes related to regulation of transcription. Genome Biology, 2007, 8, R43.	13.9	209
254	Qualitative network models and genome-wide expression data define carbon/nitrogen-responsive molecular machines in Arabidopsis. Genome Biology, 2007, 8, R7.	13.9	289
255	Clustering of genes into regulons using integrated modeling-COGRIM. Genome Biology, 2007, 8, R4.	3.8	52

#	ARTICLE	IF	CITATIONS
256	Network visualization and network analysis. , 2007, 97, 245-275.		22
257	Analysis of Expression Data: An Overview. Current Protocols in Human Genetics, 2007, 54, Unit11.4.	3.5	5
258	How to infer gene networks from expression profiles. Molecular Systems Biology, 2007, 3, 78.	3.2	563
259	Selective Raf inhibition in cancer therapy. Expert Opinion on Therapeutic Targets, 2007, 11, 1587-1609.	1.5	63
260	Proteomics in 2005/2006:Â Developments, Applications and Challenges. Analytical Chemistry, 2007, 79, 4325-4344.	3.2	57
261	Pathway analysis software as a tool for drug target selection, prioritization and validation of drug mechanism. Expert Opinion on Therapeutic Targets, 2007, 11, 411-421.	1.5	27
262	GraphScope: integrated multivariate network visualization. , 2007, , .		7
263	Comparing Protein Interaction Networks via a Graph Match-and-Split Algorithm. Journal of Computational Biology, 2007, 14, 892-907.	0.8	61
264	Enabling high-throughput data management for systems biology: The Bioinformatics Resource Manager. Bioinformatics, 2007, 23, 906-909.	1.8	45
265	Understanding Challenges in Preserving and Reconstructing Computer-Assisted Medical Decision Processes. , 2007, , .		0
266	MotifNetwork: Genome-Wide Domain Analysis using Grid-enabled Workflows. , 2007, , .		4
267	Biomedical ontologies: a functional perspective. Briefings in Bioinformatics, 2007, 9, 75-90.	3.2	218
268	Regulation of gene expression by small nonâ€œcoding RNAs: a quantitative view. Molecular Systems Biology, 2007, 3, 138.	3.2	284
269	Protein interactions and disease: computational approaches to uncover the etiology of diseases. Briefings in Bioinformatics, 2007, 8, 333-346.	3.2	190
270	Tools for visually exploring biological networks. Bioinformatics, 2007, 23, 2651-2659.	1.8	220
271	A systems biology approach for pathway level analysis. Genome Research, 2007, 17, 1537-1545.	2.4	1,036
272	Comparative proteome analysis of human epithelial ovarian cancer. Proteome Science, 2007, 5, 16.	0.7	47
273	The intracellular region of Notch ligands: does the tail make the difference?. Biology Direct, 2007, 2, 19.	1.9	42

#	ARTICLE	IF	CITATIONS
274	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007, 3, 88.	3.2	918
275	<i>E. coli</i> metabolomics: capturing the complexity of a "simple" model. <i>Topics in Current Genetics</i> , 2007, , 189-234.	0.7	3
276	Analysis of Expression Data: An Overview. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 7.1.	25.8	9
277	Brain Expressed microRNAs Implicated in Schizophrenia Etiology. <i>PLoS ONE</i> , 2007, 2, e873.	1.1	235
278	Proteomic Shifts in Embryonic Stem Cells with Gene Dose Modifications Suggest the Presence of Balancer Proteins in Protein Regulatory Networks. <i>PLoS ONE</i> , 2007, 2, e1218.	1.1	24
279	Transcriptional Networks in <i>S. cerevisiae</i> Linked to an Accumulation of Base Excision Repair Intermediates. <i>PLoS ONE</i> , 2007, 2, e1252.	1.1	14
280	Public Databases and Software for the Pathway Analysis of Cancer Genomes. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	9
281	Genes2Networks: Connecting Lists of Proteins by Using Background Literature-based Mammalian Networks. <i>Nature Precedings</i> , 2007, , .	0.1	0
282	Integrative database management for mouse development: Systems and concepts. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2007, 81, 1-19.	3.6	5
283	Systems level analysis of osteoclastogenesis reveals intrinsic and extrinsic regulatory interactions. <i>Developmental Dynamics</i> , 2007, 236, 2181-2197.	0.8	26
284	CABIN: Collective Analysis of Biological Interaction Networks. <i>Computational Biology and Chemistry</i> , 2007, 31, 222-225.	1.1	20
285	An integrative in silico approach for discovering candidates for drug-targetable protein-protein interactions in interactome data. <i>BMC Pharmacology</i> , 2007, 7, 10.	0.4	20
286	The urologic epithelial stem cell database (UESC) "a web tool for cell type-specific gene expression and immunohistochemistry images of the prostate and bladder. <i>BMC Urology</i> , 2007, 7, 19.	0.6	28
287	Broadening the horizon " level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	1.7	237
288	A global analysis of genetic interactions in <i>Caenorhabditis elegans</i> . <i>Journal of Biology</i> , 2007, 6, 8.	2.7	144
289	A 1.55 Å... resolution X-ray crystal structure of HEF2/ERH and insights into its transcriptional and cell-cycle interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 427-437.	1.5	21
290	Systematic investigation of lycopene effects in LNCaP cells by use of novel large-scale proteomic analysis software. <i>Proteomics - Clinical Applications</i> , 2007, 1, 513-523.	0.8	34
291	Nine steps to proteomic wisdom: A practical guide to using protein-protein interaction networks and molecular pathways as a framework for interpreting disease proteomic profiles. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1156-1168.	0.8	6

#	ARTICLE	IF	CITATIONS
292	The extant core bacterial proteome is an archive of the origin of life. <i>Proteomics</i> , 2007, 7, 875-889.	1.3	49
293	WI-PHI: A weighted yeast interactome enriched for direct physical interactions. <i>Proteomics</i> , 2007, 7, 932-943.	1.3	83
294	Identifying functional modules in the physical interactome of <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2007, 7, 944-960.	1.3	135
295	Computational analysis of human protein interaction networks. <i>Proteomics</i> , 2007, 7, 2541-2552.	1.3	70
296	Discovering functions and revealing mechanisms at molecular level from biological networks. <i>Proteomics</i> , 2007, 7, 2856-2869.	1.3	110
297	Quantitative proteomics using uniform <sup>15</sup> N-labeling, MASCOT, and the transproteomic pipeline. <i>Proteomics</i> , 2007, 7, 3462-3469.	1.3	41
298	Relating protein pharmacology by ligand chemistry. <i>Nature Biotechnology</i> , 2007, 25, 197-206.	9.4	1,722
299	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. <i>Nature Biotechnology</i> , 2007, 25, 345-352.	9.4	156
300	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007, 25, 547-554.	9.4	84
301	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
302	Functional atlas of the integrin adhesome. <i>Nature Cell Biology</i> , 2007, 9, 858-867.	4.6	1,033
303	Prediction and assignment of function for a divergent N-succinyl amino acid racemase. <i>Nature Chemical Biology</i> , 2007, 3, 486-491.	3.9	98
304	Scaffold composition and biological relevance of screening libraries. <i>Nature Chemical Biology</i> , 2007, 3, 442-446.	3.9	164
305	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	5.5	2,275
306	MetaNetwork: a computational protocol for the genetic study of metabolic networks. <i>Nature Protocols</i> , 2007, 2, 685-694.	5.5	30
307	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. <i>Nature Protocols</i> , 2007, 2, 727-738.	5.5	757
308	Beyond standardization: dynamic software infrastructures for systems biology. <i>Nature Reviews Genetics</i> , 2007, 8, 235-243.	7.7	55
309	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 74-86.	4.1	386

#	ARTICLE	IF	CITATIONS
310	Model-based clustering for social networks. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2007, 170, 301-354.	0.6	482
311	Metabolic network visualization eliminating node redundance and preserving metabolic pathways. <i>BMC Systems Biology</i> , 2007, 1, 29.	3.0	35
312	A systems biology approach to modelling tea ( <i>Camellia sinensis</i> ). <i>BMC Systems Biology</i> , 2007, 1, .	3.0	3
313	BioPP: a tool for web-publication of biological networks. <i>BMC Bioinformatics</i> , 2007, 8, 168.	1.2	14
314	Discovering functional linkages and uncharacterized cellular pathways using phylogenetic profile comparisons: a comprehensive assessment. <i>BMC Bioinformatics</i> , 2007, 8, 173.	1.2	71
315	Genome Expression Pathway Analysis Tool – Analysis and visualization of microarray gene expression data under genomic, proteomic and metabolic context. <i>BMC Bioinformatics</i> , 2007, 8, 179.	1.2	19
316	GenMAPP 2: new features and resources for pathway analysis. <i>BMC Bioinformatics</i> , 2007, 8, 217.	1.2	224
317	Characterization of protein-interaction networks in tumors. <i>BMC Bioinformatics</i> , 2007, 8, 224.	1.2	100
318	A high-accuracy consensus map of yeast protein complexes reveals modular nature of gene essentiality. <i>BMC Bioinformatics</i> , 2007, 8, 236.	1.2	239
319	An exploration of alternative visualisations of the basic helix-loop-helix protein interaction network. <i>BMC Bioinformatics</i> , 2007, 8, 289.	1.2	7
320	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , 2007, 8, 35.	1.2	191
321	BNDB – The Biochemical Network Database. <i>BMC Bioinformatics</i> , 2007, 8, 367.	1.2	36
322	Genes2Networks: connecting lists of gene symbols using mammalian protein interactions databases. <i>BMC Bioinformatics</i> , 2007, 8, 372.	1.2	130
323	The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. <i>BMC Bioinformatics</i> , 2007, 8, 456.	1.2	30
324	An efficient grid layout algorithm for biological networks utilizing various biological attributes. <i>BMC Bioinformatics</i> , 2007, 8, 76.	1.2	27
325	Inferring biological networks with output kernel trees. <i>BMC Bioinformatics</i> , 2007, 8, S4.	1.2	20
326	Shared transcriptional correlations in seed formation and in plants response to drought. <i>BMC Bioinformatics</i> , 2007, 8, .	1.2	1
327	BioCAD: an information fusion platform for bio-network inference and analysis. <i>BMC Bioinformatics</i> , 2007, 8, S2.	1.2	18

#	ARTICLE	IF	CITATIONS
328	CAG-encoded polyglutamine length polymorphism in the human genome. <i>BMC Genomics</i> , 2007, 8, 126.	1.2	78
329	Evidence for systems-level molecular mechanisms of tumorigenesis. <i>BMC Genomics</i> , 2007, 8, 185.	1.2	31
330	EGFR associated expression profiles vary with breast tumor subtype. <i>BMC Genomics</i> , 2007, 8, 258.	1.2	234
331	Genes involved in TGF $\beta$ 1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. <i>BMC Genomics</i> , 2007, 8, 383.	1.2	20
332	Investigation of factors affecting prediction of protein-protein interaction networks by phylogenetic profiling. <i>BMC Genomics</i> , 2007, 8, 393.	1.2	16
333	A systems biology analysis of protein-protein interactions between yeast superoxide dismutases and DNA repair pathways. <i>Free Radical Biology and Medicine</i> , 2007, 43, 557-567.	1.3	22
334	Global mapping of gene/protein interactions in PubMed abstracts: A framework and an experiment with P53 interactions. <i>Journal of Biomedical Informatics</i> , 2007, 40, 453-464.	2.5	12
335	A new framework for identifying combinatorial regulation of transcription factors: A case study of the yeast cell cycle. <i>Journal of Biomedical Informatics</i> , 2007, 40, 707-725.	2.5	31
336	Expanding the metabolic engineering toolbox: more options to engineer cells. <i>Trends in Biotechnology</i> , 2007, 25, 132-137.	4.9	200
337	A Framework for Elucidating Regulatory Networks Based on Prior Information and Expression Data. <i>Annals of the New York Academy of Sciences</i> , 2007, 1115, 240-248.	1.8	20
338	Dialogue on Reverse-Engineering Assessment and Methods. <i>Annals of the New York Academy of Sciences</i> , 2007, 1115, 1-22.	1.8	318
339	PhosphoPep—a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. <i>Molecular Systems Biology</i> , 2007, 3, 139.	3.2	168
340	The virtual human: Towards a global systems biology of multiscale, distributed biochemical network models. <i>IUBMB Life</i> , 2007, 59, 689-695.	1.5	45
341	Inferring the skeleton cell cycle regulatory network of malaria parasite using comparative genomic and variational Bayesian approaches. <i>Genetica</i> , 2007, 132, 131-142.	0.5	10
342	Genomics and functional genomics with haloarchaea. <i>Archives of Microbiology</i> , 2008, 190, 197-215.	1.0	42
343	Uncovering the gene knockout landscape for improved lycopene production in <i>E. coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 801-810.	1.7	54
344	Differential Plasma Glycoproteome of p19ARF Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. <i>Clinical Proteomics</i> , 2008, 4, 105-116.	1.1	11
345	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	1.3	201



#	ARTICLE	IF	CITATIONS
346	Functional genomics in radiation biology: a gateway to cellular systems-level studies. <i>Radiation and Environmental Biophysics</i> , 2008, 47, 25-31.	0.6	47
347	Monitoring of multiple sclerosis immunotherapy. <i>Journal of Neurology</i> , 2008, 255, 48-57.	1.8	84
348	A global view of drug-therapy interactions. <i>BMC Pharmacology</i> , 2008, 8, 5.	0.4	81
349	Efficiency of the immunome protein interaction network increases during evolution. <i>Immunome Research</i> , 2008, 4, 4.	0.1	15
350	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. <i>BMC Medical Genomics</i> , 2008, 1, 62.	0.7	13
351	A survey of visualization tools for biological network analysis. <i>BioData Mining</i> , 2008, 1, 12.	2.2	173
352	Mining tissue specificity, gene connectivity and disease association to reveal a set of genes that modify the action of disease causing genes. <i>BioData Mining</i> , 2008, 1, 8.	2.2	32
353	PTP $\mu$ has a critical role in signaling transduction pathways and phosphoprotein network topology in red cells. <i>Proteomics</i> , 2008, 8, 4695-4708.	1.3	37
354	Proteomic approaches to the analysis of multiprotein signaling complexes. <i>Proteomics</i> , 2008, 8, 832-851.	1.3	45
355	Protein networking: insights into global functional organization of proteomes. <i>Proteomics</i> , 2008, 8, 799-816.	1.3	74
356	PATIKAmad: Putting microarray data into pathway context. <i>Proteomics</i> , 2008, 8, 2196-2198.	1.3	8
357	Phosphoproteomics: A possible route to novel biomarkers of breast cancer. <i>Proteomics - Clinical Applications</i> , 2008, 2, 181-194.	0.8	9
358	Transcriptional profiling of the megabladder mouse: A unique model of bladder dysmorphogenesis. <i>Developmental Dynamics</i> , 2008, 237, 170-186.	0.8	11
359	Proteomic analysis to characterize differential mouse strain sensitivity to cadmium-induced forelimb teratogenesis. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2008, 82, 187-199.	1.6	13
360	Applications of domain-domain interactions in pathway study. <i>Computational Biology and Chemistry</i> , 2008, 32, 81-87.	1.1	3
361	Gene module level analysis: identification to networks and dynamics. <i>Current Opinion in Biotechnology</i> , 2008, 19, 482-491.	3.3	90
362	A graph-theoretic analysis of the human protein-interaction network using multicore parallel algorithms. <i>Parallel Computing</i> , 2008, 34, 627-639.	1.3	19
363	Selected reaction monitoring for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2008, 4, 222.	3.2	1,215

#	ARTICLE	IF	CITATIONS
364	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
365	A systems biology approach to prediction of oncogenes and molecular perturbation targets in B-cell lymphomas. <i>Molecular Systems Biology</i> , 2008, 4, 169.	3.2	191
366	Comprehensive MicroRNA Profiling Reveals a Unique Human Embryonic Stem Cell Signature Dominated by a Single Seed Sequence. <i>Stem Cells</i> , 2008, 26, 1506-1516.	1.4	202
367	Phylogenetic Profiling. <i>Methods in Molecular Biology</i> , 2008, 453, 201-216.	0.4	4
368	Walking the Interactome for Prioritization of Candidate Disease Genes. <i>American Journal of Human Genetics</i> , 2008, 82, 949-958.	2.6	1,111
369	The Human Phenotype Ontology: A Tool for Annotating and Analyzing Human Hereditary Disease. <i>American Journal of Human Genetics</i> , 2008, 83, 610-615.	2.6	797
370	Understanding biological functions through molecular networks. <i>Cell Research</i> , 2008, 18, 224-237.	5.7	147
371	Yamanaka factors critically regulate the developmental signaling network in mouse embryonic stem cells. <i>Cell Research</i> , 2008, 18, 1177-1189.	5.7	117
372	Mapping the human protein interactome. <i>Cell Research</i> , 2008, 18, 716-724.	5.7	44
373	The fibromatosis signature defines a robust stromal response in breast carcinoma. <i>Laboratory Investigation</i> , 2008, 88, 591-601.	1.7	100
374	Regulatory potential for concerted modulation of Nrf2- and Nfkb1-mediated gene expression in inflammation and carcinogenesis. <i>British Journal of Cancer</i> , 2008, 99, 2070-2082.	2.9	143
375	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530
376	Network pharmacology: the next paradigm in drug discovery. <i>Nature Chemical Biology</i> , 2008, 4, 682-690.	3.9	3,165
377	Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. <i>Nature Reviews Genetics</i> , 2008, 9, 678-688.	7.7	145
378	Global monitoring of autumn gene expression within and among phenotypically divergent populations of Sitka spruce ( <i>Picea sitchensis</i> ). <i>New Phytologist</i> , 2008, 178, 103-122.	3.5	111
379	Comprehensive gene expression atlas for the <i>Arabidopsis</i> MAP kinase signalling pathways. <i>New Phytologist</i> , 2008, 179, 643-662.	3.5	105
380	Visualizing Genome Expression and Regulatory Network Dynamics in Genomic and Metabolic Context. <i>Computer Graphics Forum</i> , 2008, 27, 887-894.	1.8	19
381	Molecular and cellular approaches for the detection of protein-protein interactions: latest techniques and current limitations. <i>Plant Journal</i> , 2008, 53, 610-635.	2.8	177

#	ARTICLE	IF	CITATIONS
382	SPIKE – a database, visualization and analysis tool of cellular signaling pathways. BMC Bioinformatics, 2008, 9, 110.	1.2	65
383	Inferring the role of transcription factors in regulatory networks. BMC Bioinformatics, 2008, 9, 228.	1.2	11
384	A visual analytics approach for understanding biclustering results from microarray data. BMC Bioinformatics, 2008, 9, 247.	1.2	46
385	GenCLIP: a software program for clustering gene lists by literature profiling and constructing gene co-occurrence networks related to custom keywords. BMC Bioinformatics, 2008, 9, 308.	1.2	40
386	FERN – a Java framework for stochastic simulation and evaluation of reaction networks. BMC Bioinformatics, 2008, 9, 356.	1.2	26
387	Methodology capture: discriminating between the "best" and the rest of community practice. BMC Bioinformatics, 2008, 9, 359.	1.2	15
388	Predicting protein linkages in bacteria: Which method is best depends on task. BMC Bioinformatics, 2008, 9, 397.	1.2	16
389	Presenting and exploring biological pathways with PathVisio. BMC Bioinformatics, 2008, 9, 399.	1.2	305
390	iRefIndex: A consolidated protein interaction database with provenance. BMC Bioinformatics, 2008, 9, 405.	1.2	488
391	GeneTrailExpress: a web-based pipeline for the statistical evaluation of microarray experiments. BMC Bioinformatics, 2008, 9, 552.	1.2	69
392	RPPAML/RIMS: A metadata format and an information management system for reverse phase protein arrays. BMC Bioinformatics, 2008, 9, 555.	1.2	13
393	Building pathway clusters from Random Forests classification using class votes. BMC Bioinformatics, 2008, 9, 87.	1.2	28
394	SynechoNET: integrated protein-protein interaction database of a model cyanobacterium Synechocystis sp. PCC 6803. BMC Bioinformatics, 2008, 9, S20.	1.2	23
395	A protein interaction based model for schizophrenia study. BMC Bioinformatics, 2008, 9, S23.	1.2	13
396	RDFScape: Semantic Web meets Systems Biology. BMC Bioinformatics, 2008, 9, S6.	1.2	24
397	ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. BMC Bioinformatics, 2008, 9, S5.	1.2	30
398	Linking Cytoscape and the corynebacterial reference database CoryneRegNet. BMC Genomics, 2008, 9, 184.	1.2	32
399	Arabidopsis mRNA polyadenylation machinery: comprehensive analysis of protein-protein interactions and gene expression profiling. BMC Genomics, 2008, 9, 220.	1.2	94

#	ARTICLE	IF	CITATIONS
400	The topology of the bacterial co-conserved protein network and its implications for predicting protein function. BMC Genomics, 2008, 9, 313.	1.2	16
401	T2D-Db: An integrated platform to study the molecular basis of Type 2 diabetes. BMC Genomics, 2008, 9, 320.	1.2	36
402	Transcription factor control of growth rate dependent genes in <i>Saccharomyces cerevisiae</i> : A three factor design. BMC Genomics, 2008, 9, 341.	1.2	50
403	Sequence conservation and combinatorial complexity of <i>Drosophila</i> neural precursor cell enhancers. BMC Genomics, 2008, 9, 371.	1.2	8
404	Comparative analysis of function and interaction of transcription factors in nematodes: Extensive conservation of orthology coupled to rapid sequence evolution. BMC Genomics, 2008, 9, 399.	1.2	44
405	DroID: the <i>Drosophila</i> Interactions Database, a comprehensive resource for annotated gene and protein interactions. BMC Genomics, 2008, 9, 461.	1.2	107
406	The prediction of protein-protein interaction networks in rice blast fungus. BMC Genomics, 2008, 9, 519.	1.2	77
407	A cross-species transcriptomics approach to identify genes involved in leaf development. BMC Genomics, 2008, 9, 589.	1.2	37
408	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. BMC Genomics, 2008, 9, 630.	1.2	55
409	Inferring gene regulatory networks by thermodynamic modeling. BMC Genomics, 2008, 9, S19.	1.2	15
410	In silico comparison of transcript abundances during <i>Arabidopsis thaliana</i> and <i>Glycine max</i> resistance to <i>Fusarium virguliforme</i> . BMC Genomics, 2008, 9, S6.	1.2	20
411	<i>Mycobacterium tuberculosis</i> interactome analysis unravels potential pathways to drug resistance. BMC Microbiology, 2008, 8, 234.	1.3	86
412	Identification of a set of genes showing regionally enriched expression in the mouse brain. BMC Neuroscience, 2008, 9, 66.	0.8	25
413	Genetic and systems level analysis of <i>Drosophila</i> sticky/citron kinase and dFmr1 mutants reveals common regulation of genetic networks. BMC Systems Biology, 2008, 2, 101.	3.0	8
414	Arena3D: visualization of biological networks in 3D. BMC Systems Biology, 2008, 2, 104.	3.0	95
415	Interactive analysis of systems biology molecular expression data. BMC Systems Biology, 2008, 2, 23.	3.0	9
416	An integrated genetic, genomic and systems approach defines gene networks regulated by the interaction of light and carbon signaling pathways in <i>Arabidopsis</i> . BMC Systems Biology, 2008, 2, 31.	3.0	55
417	The Systems Biology Research Tool: evolvable open-source software. BMC Systems Biology, 2008, 2, 55.	3.0	45

#	ARTICLE	IF	CITATIONS
418	Seeded Bayesian Networks: Constructing genetic networks from microarray data. <i>BMC Systems Biology</i> , 2008, 2, 57.	3.0	86
419	The genome-scale metabolic model iIN800 of <i>Saccharomyces cerevisiae</i> and its validation: a scaffold to query lipid metabolism. <i>BMC Systems Biology</i> , 2008, 2, 71.	3.0	141
420	Rapidly exploring structural and dynamic properties of signaling networks using PathwayOracle. <i>BMC Systems Biology</i> , 2008, 2, 76.	3.0	12
421	Large-scale prediction of drug-target relationships. <i>FEBS Letters</i> , 2008, 582, 1283-1290.	1.3	84
422	ROS-deficient monocytes have aberrant gene expression that correlates with inflammatory disorders of chronic granulomatous disease. <i>Clinical Immunology</i> , 2008, 129, 90-102.	1.4	86
423	Advanced microarray analysis highlights modified neuro-immune signaling in nucleated blood cells from Parkinson's disease patients. <i>Journal of Neuroimmunology</i> , 2008, 201-202, 227-236.	1.1	49
424	Integrating metabolomics and phenomics with systems models of cardiac hypoxia. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 96, 209-225.	1.4	17
425	Scale relativity theory and integrative systems biology: 1. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 97, 79-114.	1.4	75
426	Low duplicability and network fragility of cancer genes. <i>Trends in Genetics</i> , 2008, 24, 427-430.	2.9	64
427	Relationships among carbohydrate intermediate metabolites and DNA damage and repair in yeast from a systems biology perspective. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 642, 43-56.	0.4	14
428	<i>Candida albicans</i> macrophage interactions: genomic and proteomic insights. <i>Future Microbiology</i> , 2008, 3, 661-681.	1.0	18
429	Protein Interaction Data Set Highlighted with Human Ras-MAPK/PI3K Signaling Pathways. <i>Journal of Proteome Research</i> , 2008, 7, 3879-3889.	1.8	38
432	Cardioinductive Network Guiding Stem Cell Differentiation Revealed by Proteomic Cartography of Tumor Necrosis Factor $\alpha$ -Primed Endodermal Secretome. <i>Stem Cells</i> , 2008, 26, 387-400.	1.4	68
433	WGCNA: an R package for weighted correlation network analysis. <i>BMC Bioinformatics</i> , 2008, 9, 559.	1.2	17,294
434	Characterization of the Mouse Pancreatic Islet Proteome and Comparative Analysis with Other Mouse Tissues. <i>Journal of Proteome Research</i> , 2008, 7, 3114-3126.	1.8	47
435	Proteomics of Cancer of Hormone-Dependent Tissues. <i>Advances in Experimental Medicine and Biology</i> , 2008, 630, 133-147.	0.8	8
436	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. <i>Physiological Genomics</i> , 2008, 33, 18-25.	1.0	137
437	In Vivo Identification of the Outer Membrane Protein OmcA-MtrC Interaction Network in <i>Shewanella oneidensis</i> MR-1 Cells Using Novel Hydrophobic Chemical Cross-Linkers. <i>Journal of Proteome Research</i> , 2008, 7, 1712-1720.	1.8	78

#	ARTICLE	IF	CITATIONS
438	Essential Concepts in Toxicogenomics. <i>Methods in Molecular Biology</i> , 2008, , .	0.4	1
439	KEGG spider: interpretation of genomics data in the context of the global gene metabolic network. <i>Genome Biology</i> , 2008, 9, R179.	13.9	58
440	ArrayPlex: distributed, interactive and programmatic access to genome sequence, annotation, ontology, and analytical toolsets. <i>Genome Biology</i> , 2008, 9, R159.	13.9	1
441	Functional architecture of <i>Escherichia coli</i> : new insights provided by a natural decomposition approach. <i>Genome Biology</i> , 2008, 9, R154.	13.9	56
442	NetGrep: fast network schema searches in interactomes. <i>Genome Biology</i> , 2008, 9, R138.	13.9	34
443	The hidden universal distribution of amino acids biosynthetic networks: a genomic perspective on its origins and evolution. <i>Genome Biology</i> , 2008, 9, R95.	13.9	37
444	Perceiving molecular evolution processes in <i>Escherichia coli</i> by comprehensive metabolite and gene expression profiling. <i>Genome Biology</i> , 2008, 9, R72.	13.9	17
445	Text-mining assisted regulatory annotation. <i>Genome Biology</i> , 2008, 9, R31.	13.9	34
446	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. <i>Genome Biology</i> , 2008, 9, R1.	13.9	18
447	Adipose tissue transcriptomic signature highlights the pathological relevance of extracellular matrix in human obesity. <i>Genome Biology</i> , 2008, 9, R14.	13.9	372
448	Handling Diverse Protein Interaction Data: Integration, Storage and Retrieval. <i>Computational Biology</i> , 2008, , 33-51.	0.1	0
449	Exploring Biological Networks with Cytoscape Software. <i>Current Protocols in Bioinformatics</i> , 2008, 23, Unit 8.13.	25.8	60
450	A Personal Journey of Discovery: Developing Technology and Changing Biology. <i>Annual Review of Analytical Chemistry</i> , 2008, 1, 1-43.	2.8	62
451	A systems biology analysis of proteinâ€“protein interactions in the APOBEC family. <i>Life Sciences</i> , 2008, 83, 521-530.	2.0	2
452	Protease proteomics: Revealing protease in vivo functions using systems biology approaches. <i>Molecular Aspects of Medicine</i> , 2008, 29, 339-358.	2.7	84
453	Functional organisation of <i>Escherichia coli</i> transcriptional regulatory network. <i>Journal of Molecular Biology</i> , 2008, 381, 238-247.	2.0	143
454	The Expression Level of the Chromatin-Associated HMGB1 Protein Influences Growth, Stress Tolerance, and Transcriptome in <i>Arabidopsis</i> . <i>Journal of Molecular Biology</i> , 2008, 384, 9-21.	2.0	56
455	Challenges in plant cellular pathway reconstruction based on gene expression profiling. <i>Trends in Plant Science</i> , 2008, 13, 44-50.	4.3	20

#	ARTICLE	IF	CITATIONS
456	Canonical WNT/ $\beta$ -catenin signaling is required for ureteric branching. <i>Developmental Biology</i> , 2008, 317, 83-94.	0.9	141
457	Identification of dilated cardiomyopathy signature genes through gene expression and network data integration. <i>Genomics</i> , 2008, 92, 404-413.	1.3	43
458	Global Bayesian Models for the Prioritization of Antitubercular Agents. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 2362-2370.	2.5	89
459	Transcriptional regulatory networks in haematopoiesis. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 530-535.	1.5	32
460	An Extended Transcriptional Network for Pluripotency of Embryonic Stem Cells. <i>Cell</i> , 2008, 132, 1049-1061.	13.5	1,226
461	Global Sequencing of Proteolytic Cleavage Sites in Apoptosis by Specific Labeling of Protein N Termini. <i>Cell</i> , 2008, 134, 866-876.	13.5	429
462	Taming Data. <i>Cell Host and Microbe</i> , 2008, 4, 312-313.	5.1	1
463	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , 2008, 15, 781-791.	3.1	196
464	Network Analysis Tools: from biological networks to clusters and pathways. <i>Nature Protocols</i> , 2008, 3, 1616-1629.	5.5	101
465	Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2008, 14, 1253-1260.	2.9	89
466	Dynamic Visualization of Coexpression in Systems Genetics Data. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2008, 14, 1081-1095.	2.9	4
467	Differential use of protease families for invasion by schistosome cercariae. <i>Biochimie</i> , 2008, 90, 345-358.	1.3	100
468	TiO <sub>2</sub> -Based Phosphoproteomic Analysis of the Plasma Membrane and the Effects of Phosphatase Inhibitor Treatment. <i>Journal of Proteome Research</i> , 2008, 7, 3304-3313.	1.8	94
469	Network integration and graph analysis in mammalian molecular systems biology. <i>IET Systems Biology</i> , 2008, 2, 206-221.	0.8	42
470	Complexity and modularity of intracellular networks: a systematic approach for modelling and simulation. <i>IET Systems Biology</i> , 2008, 2, 363-368.	0.8	24
471	Interactive Three-Dimensional Visualization and Contextual Analysis of Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2008, 7, 104-112.	1.8	37
472	SIRENE: supervised inference of regulatory networks. <i>Bioinformatics</i> , 2008, 24, i76-i82.	1.8	155
473	A Comparative Study of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus SCX-IMAC-Based Methods for Phosphopeptide Isolation/Enrichment. <i>Journal of Proteome Research</i> , 2008, 7, 4869-4877.	1.8	88



#	ARTICLE	IF	CITATIONS
474	Model-based prediction of cis-acting RNA elements regulating tissue-specific alternative splicing. , 2008, , .		1
475	An outlook into ultra-scale visualization of large-scale biological data. , 2008, , .		4
476	Up-Regulation of Genes Related to the Ubiquitin-Proteasome System in the Brown Adipose Tissue of 24-h-Fasted Rats. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 139-148.	0.6	34
477	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Proteome Quantitation of Mouse Embryonic Stem Cells to a Depth of 5,111 Proteins. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 672-683.	2.5	261
478	Natural selection on gene function drives the evolution of LTR retrotransposon families in the rice genome. <i>Genome Research</i> , 2009, 19, 243-254.	2.4	82
479	Arabidopsis Mitogen-Activated Protein Kinase Kinases MKK1 and MKK2 Have Overlapping Functions in Defense Signaling Mediated by MEKK1, MPK4, and MKS1. <i>Plant Physiology</i> , 2008, 148, 212-222.	2.3	266
480	60S ribosomal subunit assembly dynamics defined by semi-quantitative mass spectrometry of purified complexes. <i>Nucleic Acids Research</i> , 2008, 36, 4988-4999.	6.5	47
481	Phosphoproteome Analysis of E. coli Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	2.5	385
482	MetaNetter: inference and visualization of high-resolution metabolomic networks. <i>Bioinformatics</i> , 2008, 24, 143-145.	1.8	56
483	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. <i>Bioinformatics</i> , 2008, 24, i223-i231.	1.8	485
484	OmicsViz: Cytoscape plug-in for visualizing omics data across species. <i>Bioinformatics</i> , 2008, 24, 2557-2558.	1.8	8
485	Fast grid layout algorithm for biological networks with sweep calculation. <i>Bioinformatics</i> , 2008, 24, 1433-1441.	1.8	18
486	The fusidic acid stimulon of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 62, 1207-1214.	1.3	24
487	QGene 4.0, an extensible Java QTL-analysis platform. <i>Bioinformatics</i> , 2008, 24, 2788-2789.	1.8	340
488	The protein information and property explorer: an easy-to-use, rich-client web application for the management and functional analysis of proteomic data. <i>Bioinformatics</i> , 2008, 24, 2110-2111.	1.8	30
489	ProCope-protein complex prediction and evaluation. <i>Bioinformatics</i> , 2008, 24, 2115-2116.	1.8	32
490	Probabilistic assembly of human protein interaction networks from label-free quantitative proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1454-1459.	3.3	220
491	FunNet: an integrative tool for exploring transcriptional interactions. <i>Bioinformatics</i> , 2008, 24, 2636-2638.	1.8	78



#	ARTICLE	IF	CITATIONS
492	New Regulators of Wnt/ $\beta$ -Catenin Signaling Revealed by Integrative Molecular Screening. <i>Science Signaling</i> , 2008, 1, ra12.	1.6	135
493	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	6.5	445
494	Pathway knowledge base: An integrated pathway resource using BioPAX. <i>Applied Ontology</i> , 2008, 3, 235-245.	1.0	1
495	Genome-Scale Simulation Analysis: The Impact of Gene Deletion on the Metabolic Flux of E.coli and Its Flux-backbone. , 2008, , .		0
496	Genomic analysis of estrogen cascade reveals histone variant H2A.Z associated with breast cancer progression. <i>Molecular Systems Biology</i> , 2008, 4, 188.	3.2	158
497	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008, 4, 173.	3.2	113
498	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. <i>Nucleic Acids Research</i> , 2008, 36, 2777-2786.	6.5	19
499	Impact Analysis of Gene Deletion on the Metabolic Flux Distribution of E.coli and on Its Flux-Backbone: Genome-Scale Simulation Approach. , 2008, , .		0
500	A <i>C. elegans</i> genome-scale microRNA network contains composite feedback motifs with high flux capacity. <i>Genes and Development</i> , 2008, 22, 2535-2549.	2.7	207
501	GraphClust: A Method for Clustering Database of Graphs. <i>Journal of Information and Knowledge Management</i> , 2008, 07, 231-241.	0.8	7
502	Cytoprophet: a Cytoscape plug-in for protein and domain interaction networks inference. <i>Bioinformatics</i> , 2008, 24, 2265-2266.	1.8	11
503	The Glomerular Transcriptome and a Predicted Protein-Protein Interaction Network. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 260-268.	3.0	33
504	Computing topological parameters of biological networks. <i>Bioinformatics</i> , 2008, 24, 282-284.	1.8	1,601
505	Design and Application of Genome-Scale Reconstructed Metabolic Models. <i>Methods in Molecular Biology</i> , 2008, 416, 409-431.	0.4	47
506	Genome-wide analysis of signaling networks regulating fatty acid-induced gene expression and organelle biogenesis. <i>Journal of Cell Biology</i> , 2008, 181, 281-292.	2.3	55
507	Global transcriptomic analysis of <i>Cyanotheca</i> 51142 reveals robust diurnal oscillation of central metabolic processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6156-6161.	3.3	162
508	Perceptual dependencies in information visualization assessed by complex visual search. <i>ACM Transactions on Applied Perception</i> , 2008, 4, 1-21.	1.2	8
509	Unraveling transcriptional regulatory programs by integrative analysis of microarray and transcription factor binding data. <i>Bioinformatics</i> , 2008, 24, 1874-1880.	1.8	29

#	ARTICLE	IF	CITATIONS
510	Network Inference Algorithms Elucidate Nrf2 Regulation of Mouse Lung Oxidative Stress. PLoS Computational Biology, 2008, 4, e1000166.	1.5	78
511	Uncovering a Macrophage Transcriptional Program by Integrating Evidence from Motif Scanning and Expression Dynamics. PLoS Computational Biology, 2008, 4, e1000021.	1.5	173
512	Global Transcriptome and Deletome Profiles of Yeast Exposed to Transition Metals. PLoS Genetics, 2008, 4, e1000053.	1.5	140
513	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. Nucleic Acids Research, 2008, 36, W444-W451.	6.5	81
514	Functional Maps of Protein Complexes from Quantitative Genetic Interaction Data. PLoS Computational Biology, 2008, 4, e1000065.	1.5	128
515	A Specificity Map for the PDZ Domain Family. PLoS Biology, 2008, 6, e239.	2.6	410
516	Unraveling Protein Networks with Power Graph Analysis. PLoS Computational Biology, 2008, 4, e1000108.	1.5	105
517	Dynamic Changes in Protein Functional Linkage Networks Revealed by Integration with Gene Expression Data. PLoS Computational Biology, 2008, 4, e1000237.	1.5	32
518	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. Genome Research, 2008, 18, 1092-1099.	2.4	105
519	NetworkBLAST: comparative analysis of protein networks. Bioinformatics, 2008, 24, 594-596.	1.8	105
520	Identification and Functional Analysis of Light-Responsive Unique Genes and Gene Family Members in Rice. PLoS Genetics, 2008, 4, e1000164.	1.5	69
521	The Landscape of Human Proteins Interacting with Viruses and Other Pathogens. PLoS Pathogens, 2008, 4, e32.	2.1	297
522	Cytoscape ESP: simple search of complex biological networks. Bioinformatics, 2008, 24, 1465-1466.	1.8	11
523	The Protein Interaction Network of the Epithelial Junctional Complex: A System-Level Analysis. Molecular Biology of the Cell, 2008, 19, 5409-5421.	0.9	28
524	A global pathway crosstalk network. Bioinformatics, 2008, 24, 1442-1447.	1.8	145
525	VisANT: an integrative framework for networks in systems biology. Briefings in Bioinformatics, 2008, 9, 317-325.	3.2	121
526	Proteome-wide identification of poly(ADP-ribose) binding proteins and poly(ADP-ribose)-associated protein complexes. Nucleic Acids Research, 2008, 36, 6959-6976.	6.5	359
527	jSquid: a Java applet for graphical on-line network exploration. Bioinformatics, 2008, 24, 1467-1468.	1.8	16

#	ARTICLE	IF	CITATIONS
528	Genome-wide hepatitis C virus amino acid covariance networks can predict response to antiviral therapy in humans. <i>Journal of Clinical Investigation</i> , 2008, 119, 225-36.	3.9	76
529	Reconstruction of genetic association networks from microarray data: a partial least squares approach. <i>Bioinformatics</i> , 2008, 24, 561-568.	1.8	60
530	DrugViz: a Cytoscape plugin for visualizing and analyzing small molecule drugs in biological networks. <i>Bioinformatics</i> , 2008, 24, 2117-2118.	1.8	14
531	Integrating Global Gene Expression and Radiation Survival Parameters across the 60 Cell Lines of the National Cancer Institute Anticancer Drug Screen. <i>Cancer Research</i> , 2008, 68, 415-424.	0.4	226
532	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. <i>Plant Cell</i> , 2008, 20, 1426-1436.	3.1	52
533	A Dynamic Multiscale Magnifying Tool for Exploring Large Sparse Graphs. <i>Information Visualization</i> , 2008, 7, 105-117.	1.2	9
534	Fish and chips: functional genomics of social plasticity in an African cichlid fish. <i>Journal of Experimental Biology</i> , 2008, 211, 3041-3056.	0.8	166
535	VistaClara: an expression browser plug-in for Cytoscape. <i>Bioinformatics</i> , 2008, 24, 2112-2114.	1.8	23
536	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008, 24, 876-877.	1.8	97
537	Systems biology at the Institute for Systems Biology. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2008, 7, 239-248.	3.8	65
538	Global Analysis of Yeast Endosomal Transport Identifies the Vps55/68 Sorting Complex. <i>Molecular Biology of the Cell</i> , 2008, 19, 1282-1294.	0.9	33
539	Mass media influence spreading in social networks with community structure. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2008, 2008, P07007.	0.9	22
540	CompariMotif: quick and easy comparisons of sequence motifs. <i>Bioinformatics</i> , 2008, 24, 1307-1309.	1.8	47
541	Graph summarization with bounded error. , 2008, , .		234
542	CressExpress: A Tool For Large-Scale Mining of Expression Data from Arabidopsis. <i>Plant Physiology</i> , 2008, 147, 1004-1016.	2.3	103
543	Information Systems for Cancer Research. <i>Cancer Investigation</i> , 2008, 26, 1060-1067.	0.6	11
544	An Extensible, Scalable Architecture for Managing Bioinformatics Data and Analyses. , 2008, , .		7
545	Network-Constrained Support Vector Machine for Classification. , 2008, , .		0

#	ARTICLE	IF	CITATIONS
546	Novel Proteins, Putative Membrane Transporters, and an Integrated Metabolic Network Are Revealed by Quantitative Proteomic Analysis of Arabidopsis Cell Culture Peroxisomes. <i>Plant Physiology</i> , 2008, 148, 1809-1829.	2.3	169
547	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. <i>Molecular Systems Biology</i> , 2008, 4, 218.	3.2	330
548	QUERYING PARSE TREE DATABASE OF MEDLINE TEXT TO SYNTHESIZE USER-SPECIFIC BIOMOLECULAR NETWORKS. , 2008, , .		10
549	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
550	Deep cap analysis gene expression (CAGE): genome-wide identification of promoters, quantification of their expression, and network inference. <i>BioTechniques</i> , 2008, 44, 627-632.	0.8	87
551	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , 2008, 4, 209.	3.2	69
552	The MAPK Signaling Cascade is a Central Hub in the Regulation of Cell Cycle, Apoptosis and Cytoskeleton Remodeling by Tripeptidyl-Peptidase II. <i>Gene Regulation and Systems Biology</i> , 2008, 2, GRSB.S882.	2.3	9
553	Systems Pharmacology, Biomarkers, and Biomolecular Networks. , 0, , 75-113.		0
554	Assuring Consumer Safety without Animal Testing: A Feasibility Case Study for Skin Sensitisation. <i>ATLA Alternatives To Laboratory Animals</i> , 2008, 36, 557-568.	0.7	21
555	Organization of Physical Interactomes as Uncovered by Network Schemas. <i>PLoS Computational Biology</i> , 2008, 4, e1000203.	1.5	16
556	The Binary Protein Interactome of <i>Treponema pallidum</i> – The Syphilis Spirochete. <i>PLoS ONE</i> , 2008, 3, e2292.	1.1	92
557	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. <i>PLoS ONE</i> , 2008, 3, e3112.	1.1	35
558	Discovery and Expansion of Gene Modules by Seeking Isolated Groups in a Random Graph Process. <i>PLoS ONE</i> , 2008, 3, e3358.	1.1	3
559	Bioinformatics Tools for Plant Genomics. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-2.	2.2	4
560	M. tuberculosis interactome analysis unravels potential pathways to drug resistance. <i>Nature Precedings</i> , 2008, , .	0.1	1
561	EXPLORING BIOLOGICAL NETWORK DYNAMICS WITH ENSEMBLES OF GRAPH PARTITIONS. , 2009, , 166-177.		9
562	Non-Animal Approaches for Consumer Safety Risk Assessments: Unilever's Scientific Research Programme. <i>ATLA Alternatives To Laboratory Animals</i> , 2009, 37, 595-610.	0.7	16
563	Data Mining in the Molecular Biology Era – A Study Directed to Carbohydrates Biosynthesis and Accumulation in Plants. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
564	Network Properties for Ranking Predicted miRNA Targets in Breast Cancer. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-7.	5.7	3
565	Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. <i>PLoS Genetics</i> , 2009, 5, e1000479.	1.5	118
566	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	1.5	318
567	Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. <i>PLoS Genetics</i> , 2009, 5, e1000740.	1.5	145
568	Correlated Mutation Analysis on the Catalytic Domains of Serine/Threonine Protein Kinases. <i>PLoS ONE</i> , 2009, 4, e5913.	1.1	9
569	Maximum Entropy Reconstructions of Dynamic Signaling Networks from Quantitative Proteomics Data. <i>PLoS ONE</i> , 2009, 4, e6522.	1.1	31
570	Something Old, Something New, Something Borrowed; How the Thermoacidophilic Archaeon <i>Sulfolobus solfataricus</i> Responds to Oxidative Stress. <i>PLoS ONE</i> , 2009, 4, e6964.	1.1	70
571	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. <i>PLoS ONE</i> , 2009, 4, e7162.	1.1	18
572	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	1.1	35
573	Proteomic and Phospho-Proteomic Profile of Human Platelets in Basal, Resting State: Insights into Integrin Signaling. <i>PLoS ONE</i> , 2009, 4, e7627.	1.1	124
574	Stability of Metabolic Correlations under Changing Environmental Conditions in <i>Escherichia coli</i> – A Systems Approach. <i>PLoS ONE</i> , 2009, 4, e7441.	1.1	39
575	Meta-analysis of kindling-induced gene expression changes in the rat hippocampus. <i>Frontiers in Neuroscience</i> , 2009, 3, 53.	1.4	8
576	Reconstruction of an in silico metabolic model of <i>Arabidopsis thaliana</i> through database integration. <i>Nature Precedings</i> , 2009, , .	0.1	1
577	Practical network approaches and biologic interpretations of co-expression analyses in plants. <i>Plant Biotechnology</i> , 2009, 26, 3-7.	0.5	3
578	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009, 37, D412-D416.	6.5	2,195
579	Metabolic Flux Correlations, Genetic Interactions, and Disease. <i>Journal of Computational Biology</i> , 2009, 16, 291-302.	0.8	6
580	Revealing Social Networks of Spammers Through Spectral Clustering. , 2009, , .		11
581	Collection of Disease Networks by Hybrid Curation Method and the Application for Pathway Analysis. , 2009, , .		3

#	ARTICLE	IF	CITATIONS
582	Visualizing Temporal Dynamics at the Genomic and Metabolic Level. , 2009, , .		7
583	ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. <i>Bioinformatics</i> , 2009, 25, 1091-1093.	1.8	5,348
584	CTFMining: A Method to Predict Candidate Disease Genes Based on the Combined Network Topological Features Mining. , 2009, , .		1
585	PMAP: databases for analyzing proteolytic events and pathways. <i>Nucleic Acids Research</i> , 2009, 37, D611-D618.	6.5	57
586	Data integration for plant genomics—exemplars from the integration of <i>Arabidopsis thaliana</i> databases. <i>Briefings in Bioinformatics</i> , 2009, 10, 676-693.	3.2	21
587	Dysregulated gene expression networks in human acute myelogenous leukemia stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3396-3401.	3.3	253
588	Analyzing biological network parameters with CentiScaPe. <i>Bioinformatics</i> , 2009, 25, 2857-2859.	1.8	469
589	The Thioredoxin-like Protein Rod-derived Cone Viability Factor (RdCVFL) Interacts with TAU and Inhibits Its Phosphorylation in the Retina. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1206-1218.	2.5	52
590	Derivation of Transcriptional Regulatory Relationships by Partial Least Squares Regression. , 2009, , .		1
591	Assessing the Most Effective Depth for PPI Analysis. , 2009, , .		0
592	Simplevisgrid: Grid services for visualization of diverse biomedical knowledge and molecular systems data. , 2009, 2009, 4178-81.		2
593	Prediction of therapeutic mechanisms of tripterygium wilfordii in rheumatoid arthritis using text mining and network-based analysis. , 2009, , .		4
594	Gene Network Study Revealed Molecular Links Among Genes for Alcohol Metabolism and Breast Cancer Susceptibility. , 2009, , .		2
595	The Receptor Tyrosine Kinase EPHB4 Has Tumor Suppressor Activities in Intestinal Tumorigenesis. <i>Cancer Research</i> , 2009, 69, 7430-7438.	0.4	58
596	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. <i>Bioinformatics</i> , 2009, 25, 1470-1471.	1.8	285
597	An integrated network approach identifies the isobutanol response network of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2009, 5, 277.	3.2	175
598	Coexpression network based on natural variation in human gene expression reveals gene interactions and functions. <i>Genome Research</i> , 2009, 19, 1953-1962.	2.4	112
599	Clustering of Gene Expression Data Based on Shape Similarity. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 195712.	1.4	22

#	ARTICLE	IF	CITATIONS
600	Using a State-Space Model and Location Analysis to Infer Time-Delayed Regulatory Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 1-14.	1.4	10
601	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap011.	1.4	18
602	Blocking the Metabolism of Starch Breakdown Products in Arabidopsis Leaves Triggers Chloroplast Degradation. <i>Molecular Plant</i> , 2009, 2, 1233-1246.	3.9	127
603	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. <i>Molecular Systems Biology</i> , 2009, 5, 331.	3.2	308
604	Torque: topology-free querying of protein interaction networks. <i>Nucleic Acids Research</i> , 2009, 37, W106-W108.	6.5	30
605	DASMI: exchanging, annotating and assessing molecular interaction data. <i>Bioinformatics</i> , 2009, 25, 1321-1328.	1.8	15
606	The First Draft of the Endostatin Interaction Network. <i>Journal of Biological Chemistry</i> , 2009, 284, 22041-22047.	1.6	78
607	Reconstruction of the yeast Snf1 kinase regulatory network reveals its role as a global energy regulator. <i>Molecular Systems Biology</i> , 2009, 5, 319.	3.2	97
608	Application of an integrated physical and functional screening approach to identify inhibitors of the Wnt pathway. <i>Molecular Systems Biology</i> , 2009, 5, 315.	3.2	44
609	Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4 <sup>Δ2</sup> using proteome arrays. <i>Molecular Systems Biology</i> , 2009, 5, 333.	3.2	128
610	Integrating and annotating the interactome using the MiMI plugin for cytoscape. <i>Bioinformatics</i> , 2009, 25, 137-138.	1.8	144
611	Genoscope: a Cytoscape plug-in to automate the retrieval and integration of gene expression data and molecular networks. <i>Bioinformatics</i> , 2009, 25, 2617-2618.	1.8	12
612	Mechanisms of tumor resistance to EGFR-targeted therapies. <i>Expert Opinion on Therapeutic Targets</i> , 2009, 13, 339-362.	1.5	77
613	NAVIGATOR: Network Analysis, Visualization and Graphing Toronto. <i>Bioinformatics</i> , 2009, 25, 3327-3329.	1.8	234
614	A Pathway-Based View of Human Diseases and Disease Relationships. <i>PLoS ONE</i> , 2009, 4, e4346.	1.1	158
615	The Proteome of Seed Development in the Model Legume <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2009, 149, 1325-1340.	2.3	76
616	Global Gene Expression Analysis of Reactive Stroma in Prostate Cancer. <i>Clinical Cancer Research</i> , 2009, 15, 3979-3989.	3.2	140
617	Regulators of yeast endocytosis identified by systematic quantitative analysis. <i>Journal of Cell Biology</i> , 2009, 185, 1097-1110.	2.3	109



#	ARTICLE	IF	CITATIONS
618	EclID. A database for the inference of functional interactions in E. coli. <i>Nucleic Acids Research</i> , 2009, 37, D629-D635.	6.5	28
619	SNOW, a web-based tool for the statistical analysis of protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2009, 37, W109-W114.	6.5	45
620	Cell biologists expand their networks. <i>Journal of Cell Biology</i> , 2009, 186, 305-311.	2.3	7
621	Sys-BodyFluid: a systematical database for human body fluid proteome research. <i>Nucleic Acids Research</i> , 2009, 37, D907-D912.	6.5	79
622	Identification of an inter-transcription factor regulatory network in human hepatoma cells by Matrix RNAi. <i>Nucleic Acids Research</i> , 2009, 37, 1049-1060.	6.5	32
623	Microarray and Bioinformatics Analysis of Gene Expression in Experimental Membranous Nephropathy. <i>Nephron Experimental Nephrology</i> , 2009, 112, e43-e58.	2.4	33
624	An Integrated Systems Analysis Implicates EGR1 Downregulation in Simian Immunodeficiency Virus Encephalitis-Induced Neural Dysfunction. <i>Journal of Neuroscience</i> , 2009, 29, 12467-12476.	1.7	37
625	An analysis pipeline for the inference of protein-protein interaction networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 409.	0.1	3
626	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1908-1920.	2.5	94
627	Defining Elastic Fiber Interactions by Molecular Fishing. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2715-2732.	2.5	27
628	MatrixDB, a database focused on extracellular protein-protein and protein-carbohydrate interactions. <i>Bioinformatics</i> , 2009, 25, 690-691.	1.8	88
629	Rapid Evolution of Functional Complexity in a Domain Family. <i>Science Signaling</i> , 2009, 2, ra50.	1.6	57
630	Integrative Analysis of Genome-Wide RNA Interference Screens. <i>Science Signaling</i> , 2009, 2, pt4.	1.6	8
631	Graph Partitioning Method for Functional Module Detections of Protein Interaction Network. , 2009, , ,		9
632	Change in gene expression of mouse embryonic stem cells derived from parthenogenetic activation. <i>Human Reproduction</i> , 2009, 24, 805-814.	0.4	22
633	L'écriture augmentée. , 2009, , ,		1
634	Longitudinal system-based analysis of transcriptional responses to type I interferons. <i>Physiological Genomics</i> , 2009, 38, 362-371.	1.0	32
635	Physiological and toxicological transcriptome changes in HepG2 cells exposed to copper. <i>Physiological Genomics</i> , 2009, 38, 386-401.	1.0	60



#	ARTICLE	IF	CITATIONS
636	Global Analysis of Protein Damage by the Lipid Electrophile 4-Hydroxy-2-nonenal. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 670-680.	2.5	130
637	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009, 19, 1107-1116.	2.4	137
638	Novel Regulators of Fgf23 Expression and Mineralization in Hyp Bone. <i>Molecular Endocrinology</i> , 2009, 23, 1505-1518.	3.7	110
639	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. <i>Nucleic Acids Research</i> , 2009, 37, W115-W121.	6.5	170
640	Bruton's Tyrosine Kinase Revealed as a Negative Regulator of Wnt $\beta$ -Catenin Signaling. <i>Science Signaling</i> , 2009, 2, ra25.	1.6	56
641	Cohesive versus Flexible Evolution of Functional Modules in Eukaryotes. <i>PLoS Computational Biology</i> , 2009, 5, e1000276.	1.5	19
642	Evolutionarily Conserved Herpesviral Protein Interaction Networks. <i>PLoS Pathogens</i> , 2009, 5, e1000570.	2.1	162
643	Biomedical Discovery Acceleration, with Applications to Craniofacial Development. <i>PLoS Computational Biology</i> , 2009, 5, e1000215.	1.5	57
644	Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2009, 5, e1000605.	1.5	587
645	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	2.6	172
646	Webb Miller and Trey Ideker To Receive Top International Bioinformatics Awards for 2009 from the International Society for Computational Biology. <i>PLoS Computational Biology</i> , 2009, 5, e1000375.	1.5	0
647	Biomedical Text Mining and Its Applications. <i>PLoS Computational Biology</i> , 2009, 5, e1000597.	1.5	85
648	Integrating Computational Biology and Forward Genetics in Drosophila. <i>PLoS Genetics</i> , 2009, 5, e1000351.	1.5	27
649	Genome-Wide Association Data Reveal a Global Map of Genetic Interactions among Protein Complexes. <i>PLoS Genetics</i> , 2009, 5, e1000782.	1.5	52
650	A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for serious adverse drug reaction. <i>Bioinformatics</i> , 2009, 25, 2244-2250.	1.8	25
651	A Differential Wiring Analysis of Expression Data Correctly Identifies the Gene Containing the Causal Mutation. <i>PLoS Computational Biology</i> , 2009, 5, e1000382.	1.5	211
652	Interactome Analyses Identify Ties of PrPC and Its Mammalian Paralogs to Oligomannosidic N-Glycans and Endoplasmic Reticulum-Derived Chaperones. <i>PLoS Pathogens</i> , 2009, 5, e1000608.	2.1	108
653	Coordinated Regulation of Virulence during Systemic Infection of Salmonella enterica Serovar Typhimurium. <i>PLoS Pathogens</i> , 2009, 5, e1000306.	2.1	143

#	ARTICLE	IF	CITATIONS
654	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. <i>Science Signaling</i> , 2009, 2, ra39.	1.6	171
655	Sexually dimorphic gene expression in the chick brain before gonadal differentiation. <i>Poultry Science</i> , 2009, 88, 1003-1015.	1.5	36
656	Challenges and Rewards of Interaction Proteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 3-18.	2.5	78
657	SciMiner: web-based literature mining tool for target identification and functional enrichment analysis. <i>Bioinformatics</i> , 2009, 25, 838-840.	1.8	78
658	Michigan molecular interactions r2: from interacting proteins to pathways. <i>Nucleic Acids Research</i> , 2009, 37, D642-D646.	6.5	85
659	Human Cancer Protein-Protein Interaction Network: A Structural Perspective. <i>PLoS Computational Biology</i> , 2009, 5, e1000601.	1.5	202
660	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. <i>PLoS Computational Biology</i> , 2009, 5, e1000311.	1.5	28
661	Capturing the Spectrum of Interaction Effects in Genetic Association Studies by Simulated Evaporative Cooling Network Analysis. <i>PLoS Genetics</i> , 2009, 5, e1000432.	1.5	72
662	Plasmold: A <i>P. falciparum</i> Information Discovery Tool. <i>In Silico Biology</i> , 2009, 9, 195-202.	0.4	5
663	A Mapping of Drug Space from the Viewpoint of Small Molecule Metabolism. <i>PLoS Computational Biology</i> , 2009, 5, e1000474.	1.5	34
664	Identifying Drug Effects via Pathway Alterations using an Integer Linear Programming Optimization Formulation on Phosphoproteomic Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000591.	1.5	112
665	Functional States of the Genome-Scale <i>Escherichia Coli</i> Transcriptional Regulatory System. <i>PLoS Computational Biology</i> , 2009, 5, e1000403.	1.5	34
666	Shwachman-Bodian Diamond syndrome is a multi-functional protein implicated in cellular stress responses. <i>Human Molecular Genetics</i> , 2009, 18, 3684-3695.	1.4	65
667	Construction and application of a protein and genetic interaction network (yeast interactome). <i>Nucleic Acids Research</i> , 2009, 37, e54-e54.	6.5	9
668	A Comparative Genomics, Network-Based Approach to Understanding Virulence in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2009, 191, 6262-6272.	1.0	10
669	Computational Identification of Potential Molecular Interactions in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2009, 151, 34-46.	2.3	25
670	PathBuilder™ open source software for annotating and developing pathway resources. <i>Bioinformatics</i> , 2009, 25, 2860-2862.	1.8	40
671	Systems-Level Comparison of Host-Responses Elicited by Avian H5N1 and Seasonal H1N1 Influenza Viruses in Primary Human Macrophages. <i>PLoS ONE</i> , 2009, 4, e8072.	1.1	109

#	ARTICLE	IF	CITATIONS
672	The Macrophage Colony-Stimulating Factor 1 Response Signature in Breast Carcinoma. <i>Clinical Cancer Research</i> , 2009, 15, 778-787.	3.2	177
673	RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. <i>Nucleic Acids Research</i> , 2009, 37, D996-D1000.	6.5	10
674	Dynamic and complex transcription factor binding during an inducible response in yeast. <i>Genes and Development</i> , 2009, 23, 1351-1363.	2.7	89
675	Comparative analysis and unification of domain-domain interaction networks. <i>Bioinformatics</i> , 2009, 25, 3020-3025.	1.8	26
676	Polar Mapper: a computational tool for integrated visualization of protein interaction networks and mRNA expression data. <i>Journal of the Royal Society Interface</i> , 2009, 6, 881-896.	1.5	12
677	Large-scale Proteomics Analysis of the Human Kinome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1751-1764.	2.5	257
678	The human protein coevolution network. <i>Genome Research</i> , 2009, 19, 1861-1871.	2.4	48
679	Model-based redesign of global transcription regulation. <i>Nucleic Acids Research</i> , 2009, 37, e38-e38.	6.5	28
680	Dynamic reprogramming of transcription factors to and from the subtelomere. <i>Genome Research</i> , 2009, 19, 1014-1025.	2.4	15
681	Combinatorial network of primary and secondary microRNA-driven regulatory mechanisms. <i>Nucleic Acids Research</i> , 2009, 37, 5969-5980.	6.5	68
682	Human microRNAs co-silence in well-separated groups and have different predicted essentialities. <i>Bioinformatics</i> , 2009, 25, 1063-1069.	1.8	35
683	Detection of Treatment-Induced Changes in Signaling Pathways in Gastrointestinal Stromal Tumors Using Transcriptomic Data. <i>Cancer Research</i> , 2009, 69, 9125-9132.	0.4	54
684	Mapping and characterization of two relevance networks from SNP and gene levels. <i>Progress in Natural Science: Materials International</i> , 2009, 19, 653-657.	1.8	1
685	The global cysteine peptidase landscape in parasites. <i>Trends in Parasitology</i> , 2009, 25, 573-581.	1.5	88
686	Early gene expression changes during embryonic stem cell differentiation into cardiomyocytes and their modulation by monobutyl phthalate. <i>Reproductive Toxicology</i> , 2009, 27, 93-102.	1.3	69
687	Aging defined by a chronologic replicative protein network in <i>Saccharomyces cerevisiae</i> : An interactome analysis. <i>Mechanisms of Ageing and Development</i> , 2009, 130, 444-460.	2.2	15
688	POINeT: protein interactome with sub-network analysis and hub prioritization. <i>BMC Bioinformatics</i> , 2009, 10, 114.	1.2	47
689	Seeking unique and common biological themes in multiple gene lists or datasets: pathway pattern extraction pipeline for pathway-level comparative analysis. <i>BMC Bioinformatics</i> , 2009, 10, 200.	1.2	16

#	ARTICLE	IF	CITATIONS
690	mSpecs: a software tool for the administration and editing of mass spectral libraries in the field of metabolomics. BMC Bioinformatics, 2009, 10, 229.	1.2	5
691	The B6 database: a tool for the description and classification of vitamin B6-dependent enzymatic activities and of the corresponding protein families. BMC Bioinformatics, 2009, 10, 273.	1.2	240
692	VANLO - Interactive visual exploration of aligned biological networks. BMC Bioinformatics, 2009, 10, 327.	1.2	10
693	Arabidopsis gene co-expression network and its functional modules. BMC Bioinformatics, 2009, 10, 346.	1.2	163
694	Phylogeny-guided interaction mapping in seven eukaryotes. BMC Bioinformatics, 2009, 10, 393.	1.2	15
695	Bioclipse 2: A scriptable integration platform for the life sciences. BMC Bioinformatics, 2009, 10, 397.	1.2	52
696	Exploring complex miRNA-mRNA interactions with Bayesian networks by splitting-averaging strategy. BMC Bioinformatics, 2009, 10, 408.	1.2	72
697	In Silico Evaluation of Predicted Regulatory Interactions in Arabidopsis thaliana. BMC Bioinformatics, 2009, 10, 435.	1.2	3
698	Gene set-based module discovery in the breast cancer transcriptome. BMC Bioinformatics, 2009, 10, 71.	1.2	28
699	Disease candidate gene identification and prioritization using protein interaction networks. BMC Bioinformatics, 2009, 10, 73.	1.2	293
700	JNets: Exploring networks by integrating annotation. BMC Bioinformatics, 2009, 10, 95.	1.2	10
701	Markov clustering versus affinity propagation for the partitioning of protein interaction graphs. BMC Bioinformatics, 2009, 10, 99.	1.2	187
702	A new graph-based method for pairwise global network alignment. BMC Bioinformatics, 2009, 10, S59.	1.2	162
703	NATbox: a network analysis toolbox in R. BMC Bioinformatics, 2009, 10, S14.	1.2	9
704	Structural and functional-annotation of an equine whole genome oligoarray. BMC Bioinformatics, 2009, 10, S8.	1.2	21
705	Protopia: a protein-protein interaction tool. BMC Bioinformatics, 2009, 10, S17.	1.2	9
706	Identification of functionally related genes using data mining and data integration: a breast cancer case study. BMC Bioinformatics, 2009, 10, S8.	1.2	20
707	Leveraging existing biological knowledge in the identification of candidate genes for facial dysmorphism. BMC Bioinformatics, 2009, 10, S12.	1.2	14

#	ARTICLE	IF	CITATIONS
708	GIBA: a clustering tool for detecting protein complexes. BMC Bioinformatics, 2009, 10, S11.	1.2	20
709	From SNPs to pathways: integration of functional effect of sequence variations on models of cell signalling pathways. BMC Bioinformatics, 2009, 10, S6.	1.2	24
710	A systems biology approach to the identification and analysis of transcriptional regulatory networks in osteocytes. BMC Bioinformatics, 2009, 10, S5.	1.2	15
711	Uncovering new signaling proteins and potential drug targets through the interactome analysis of Mycobacterium tuberculosis. BMC Genomics, 2009, 10, 118.	1.2	79
712	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. BMC Genomics, 2009, 10, 126.	1.2	47
713	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. BMC Genomics, 2009, 10, 13.	1.2	80
714	A network-based integrative approach to prioritize reliable hits from multiple genome-wide RNAi screens in Drosophila. BMC Genomics, 2009, 10, 220.	1.2	37
715	BioQuali Cytoscape plugin: analysing the global consistency of regulatory networks. BMC Genomics, 2009, 10, 244.	1.2	21
716	A genome-wide deletion mutant screen identifies pathways affected by nickel sulfate in Saccharomyces cerevisiae. BMC Genomics, 2009, 10, 524.	1.2	44
717	Colorectal cancer cell-derived microvesicles are enriched in cell cycle-related mRNAs that promote proliferation of endothelial cells. BMC Genomics, 2009, 10, 556.	1.2	361
718	Transcriptomic response of the mycoparasitic fungus Trichoderma atroviride to the presence of a fungal prey. BMC Genomics, 2009, 10, 567.	1.2	141
719	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. BMC Genomics, 2009, 10, 595.	1.2	65
720	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. BMC Genomics, 2009, 10, 596.	1.2	11
721	Genome-wide prediction of cis-acting RNA elements regulating tissue-specific pre-mRNA alternative splicing. BMC Genomics, 2009, 10, S4.	1.2	26
722	BioNetBuilder2.0: bringing systems biology to chicken and other model organisms. BMC Genomics, 2009, 10, S6.	1.2	21
723	Alternative paths in HIV-1 targeted human signal transduction pathways. BMC Genomics, 2009, 10, S30.	1.2	20
724	Five QTL hotspots for yield in short rotation coppice bioenergy poplar: The Poplar Biomass Loci. BMC Plant Biology, 2009, 9, 23.	1.6	68
725	Identification of tyrosine-phosphorylated proteins associated with metastasis and functional analysis of FER in human hepatocellular carcinoma cells. BMC Cancer, 2009, 9, 366.	1.1	63

#	ARTICLE	IF	CITATIONS
726	SNAVI: Desktop application for analysis and visualization of large-scale signaling networks. <i>BMC Systems Biology</i> , 2009, 3, 10.	3.0	28
727	Human synthetic lethal inference as potential anti-cancer target gene detection. <i>BMC Systems Biology</i> , 2009, 3, 116.	3.0	45
728	FORG3D: Force-directed 3D graph editor for visualization of integrated genome scale data. <i>BMC Systems Biology</i> , 2009, 3, 26.	3.0	11
729	Identifying disease-specific genes based on their topological significance in protein networks. <i>BMC Systems Biology</i> , 2009, 3, 36.	3.0	108
730	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. <i>BMC Systems Biology</i> , 2009, 3, 37.	3.0	391
731	Genetic and environmental pathways to complex diseases. <i>BMC Systems Biology</i> , 2009, 3, 46.	3.0	65
732	A system biology approach highlights a hormonal enhancer effect on regulation of genes in a nitrate responsive "biomodule". <i>BMC Systems Biology</i> , 2009, 3, 59.	3.0	48
733	The Symbiosis Interactome: a computational approach reveals novel components, functional interactions and modules in <i>Sinorhizobium meliloti</i> . <i>BMC Systems Biology</i> , 2009, 3, 63.	3.0	24
734	BowTieBuilder: modeling signal transduction pathways. <i>BMC Systems Biology</i> , 2009, 3, 67.	3.0	42
735	Adapted Boolean network models for extracellular matrix formation. <i>BMC Systems Biology</i> , 2009, 3, 77.	3.0	15
736	Visualizing post genomics data-sets on customized pathway maps by ProMeTra – aeration-dependent gene expression and metabolism of <i>Corynebacterium glutamicum</i> as an example. <i>BMC Systems Biology</i> , 2009, 3, 82.	3.0	61
737	The crosstalk between EGF, IGF, and Insulin cell signaling pathways - computational and experimental analysis. <i>BMC Systems Biology</i> , 2009, 3, 88.	3.0	56
738	Network module detection: Affinity search technique with the multi-node topological overlap measure. <i>BMC Research Notes</i> , 2009, 2, 142.	0.6	67
739	Computing Consistency Between Microarray Data and Known Gene Regulation Relationships. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2009, 13, 1075-1082.	3.6	2
740	Differential HIV-1 integration targets more actively transcribed host genes in neonatal than adult blood mononuclear cells. <i>Virology</i> , 2009, 385, 28-38.	1.1	13
741	Transcriptional signature of human adipose tissue-derived stem cells (hASCs) preconditioned for chondrogenesis in hypoxic conditions. <i>Experimental Cell Research</i> , 2009, 315, 1937-1952.	1.2	46
742	Screening a genome-wide <i>S. pombe</i> deletion library identifies novel genes and pathways involved in genome stability maintenance. <i>DNA Repair</i> , 2009, 8, 672-679.	1.3	68
743	Bioinformatics analysis of mass spectrometry-based proteomics data sets. <i>FEBS Letters</i> , 2009, 583, 1703-1712.	1.3	147

#	ARTICLE	IF	CITATIONS
744	Filling and mining the reactive metabolite target protein database. <i>Chemico-Biological Interactions</i> , 2009, 179, 38-44.	1.7	31
746	Identification of novel hub genes associated with liver metastasis of gastric cancer. <i>International Journal of Cancer</i> , 2009, 125, 2844-2853.	2.3	74
747	Developmental shifts in gene expression in the auditory forebrain during the sensitive period for song learning. <i>Developmental Neurobiology</i> , 2009, 69, 437-450.	1.5	48
748	Dynamical approaches to modeling developmental gene regulatory networks. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 131-142.	3.6	16
749	Information theoretical methods to deconvolute genetic regulatory networks applied to thyroid neoplasms. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 5057-5069.	1.2	24
750	Computational challenges in systems biology. <i>Computer Science Review</i> , 2009, 3, 1-17.	10.2	38
751	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 107-125.	1.2	25
752	A survey of integral $\alpha$ -helical membrane proteins. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 269-280.	1.2	12
753	InÂSilico Construction of a Protein Interaction Landscape for Nucleotide Excision Repair. <i>Cell Biochemistry and Biophysics</i> , 2009, 53, 101-114.	0.9	2
754	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. <i>Biophysical Reviews</i> , 2009, 1, 43-49.	1.5	49
755	PIAS proteins: pleiotropic interactors associated with SUMO. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3029-3041.	2.4	230
756	Desmosomal interactome in keratinocytes: a systems biology approach leading to an understanding of the pathogenesis of skin disease. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3517-3533.	2.4	29
758	Dissecting the human plasma proteome and inflammatory response biomarkers. <i>Proteomics</i> , 2009, 9, 470-484.	1.3	20
759	Recent developments in public proteomic MS repositories and pipelines. <i>Proteomics</i> , 2009, 9, 861-881.	1.3	42
760	PPI spider: A tool for the interpretation of proteomics data in the context of proteinâ€“protein interaction networks. <i>Proteomics</i> , 2009, 9, 2740-2749.	1.3	63
761	The properties of hub proteins in a yeastâ€“aggregated cell cycle network and its phase subâ€“networks. <i>Proteomics</i> , 2009, 9, 4812-4824.	1.3	10
762	Highâ€“accuracy identification and bioinformatic analysis of <i>in vivo</i> protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009, 9, 4642-4652.	1.3	132
763	Systematic prediction of human membrane receptor interactions. <i>Proteomics</i> , 2009, 9, 5243-5255.	1.3	22



#	ARTICLE	IF	CITATIONS
764	The Interactorium: Visualising proteins, complexes and interaction networks in a virtual 3D cell. <i>Proteomics</i> , 2009, 9, 5309-5315.	1.3	8
765	Identification of group specific motifs in Beta-lactamase family of proteins. <i>Journal of Biomedical Science</i> , 2009, 16, 109.	2.6	20
766	myGRN: A database and visualisation system for the storage and analysis of developmental genetic regulatory networks. <i>BMC Developmental Biology</i> , 2009, 9, 33.	2.1	3
767	Bioinformatic analysis of xenobiotic reactive metabolite target proteins and their interacting partners. <i>BMC Chemical Biology</i> , 2009, 9, 5.	1.6	20
768	Construction of a polycystic ovarian syndrome (PCOS) pathway based on the interactions of PCOS-related proteins retrieved from bibliomic data. <i>Theoretical Biology and Medical Modelling</i> , 2009, 6, 18.	2.1	28
769	The apoptotic machinery as a biological complex system: analysis of its omics and evolution, identification of candidate genes for fourteen major types of cancer, and experimental validation in CML and neuroblastoma. <i>BMC Medical Genomics</i> , 2009, 2, 20.	0.7	20
770	Network analysis of human glaucomatous optic nerve head astrocytes. <i>BMC Medical Genomics</i> , 2009, 2, 24.	0.7	51
771	Identification of the <i>Arabidopsis thaliana</i> <i>dry2</i> mutant reveals a central role for sterols in drought tolerance and regulation of reactive oxygen species. <i>Plant Journal</i> , 2009, 59, 63-76.	2.8	114
772	Theoretical framework for the histone modification network: modifications in the unstructured histone tails form a robust scale-free network. <i>Genes To Cells</i> , 2009, 14, 789-806.	0.5	15
773	More synergetic cooperation of Yamanaka factors in induced pluripotent stem cells than in embryonic stem cells. <i>Cell Research</i> , 2009, 19, 1127-1138.	5.7	49
774	Temporal and spatial profiling of nuclei-associated proteins upon TNF- $\alpha$ /NF- $\kappa$ B signaling. <i>Cell Research</i> , 2009, 19, 651-664.	5.7	20
775	Genome-wide analysis of Notch signalling in <i>Drosophila</i> by transgenic RNAi. <i>Nature</i> , 2009, 458, 987-992.	13.7	283
776	Predicting new molecular targets for known drugs. <i>Nature</i> , 2009, 462, 175-181.	13.7	1,474
777	Dynamic modularity in protein interaction networks predicts breast cancer outcome. <i>Nature Biotechnology</i> , 2009, 27, 199-204.	9.4	654
778	Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. <i>Nature Biotechnology</i> , 2009, 27, 378-386.	9.4	519
779	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009, 6, 741-744.	9.0	141
780	Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms. <i>Nature Methods</i> , 2009, 6, 767-772.	9.0	802
781	My5C: web tools for chromosome conformation capture studies. <i>Nature Methods</i> , 2009, 6, 690-691.	9.0	86



#	ARTICLE	IF	CITATIONS
782	A general pipeline for quality and statistical assessment of protein interaction data using R and Bioconductor. <i>Nature Protocols</i> , 2009, 4, 535-546.	5.5	15
783	Dynamic proteomics in modeling of the living cell. Protein-protein interactions. <i>Biochemistry (Moscow)</i> , 2009, 74, 1586-1607.	0.7	35
784	Sequence, structure, function, immunity: structural genomics of costimulation. <i>Immunological Reviews</i> , 2009, 229, 356-386.	2.8	83
785	IDENTIFYING COEVOLUTIONARY PATTERNS IN HUMAN LEUKOCYTE ANTIGEN (HLA) MOLECULES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 64, 1429-45.	1.1	3
786	A Network Inference Workflow Applied to Virulence-Related Processes in <i>Salmonella typhimurium</i> . <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 143-158.	1.8	5
787	TRANSCRIPTIONAL ANALYSIS OF THE UNICELLULAR, DIAZOTROPHIC CYANOBACTERIUM <i>CYANOTHECE</i> SP. ATCC 51142 GROWN UNDER SHORT DAY/NIGHT CYCLES. <i>Journal of Phycology</i> , 2009, 45, 610-620.	1.0	28
788	Proteome analysis of a human liver carcinoma cell line stably expressing hepatitis delta virus ribonucleoproteins. <i>Journal of Proteomics</i> , 2009, 72, 616-627.	1.2	24
789	Nuclear factor- $\kappa$ B bioluminescence imaging-guided transcriptomic analysis for the assessment of host-biomaterial interaction in vivo. <i>Biomaterials</i> , 2009, 30, 3042-3049.	5.7	35
790	The Phagosomal Proteome in Interferon- $\beta$ -Activated Macrophages. <i>Immunity</i> , 2009, 30, 143-154.	6.6	206
791	Gene regulatory network inference: Data integration in dynamic models—A review. <i>BioSystems</i> , 2009, 96, 86-103.	0.9	663
792	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. <i>Blood</i> , 2009, 114, e20-e26.	0.6	224
793	Functional Analysis of OMICs Data and Small Molecule Compounds in an Integrated Knowledge-Based Platform. <i>Methods in Molecular Biology</i> , 2009, 563, 177-196.	0.4	75
794	Systems Approach for Understanding Metastasis. , 2009, , 383-394.		0
795	Integrating Proteomic, Transcriptional, and Interactome Data Reveals Hidden Components of Signaling and Regulatory Networks. <i>Science Signaling</i> , 2009, 2, ra40.	1.6	161
796	Systems biology approaches and pathway tools for investigating cardiovascular disease. <i>Molecular BioSystems</i> , 2009, 5, 588.	2.9	96
797	MAPK target networks in <i>Arabidopsis thaliana</i> revealed using functional protein microarrays. <i>Genes and Development</i> , 2009, 23, 80-92.	2.7	438
798	SYNTHESIS OF PHARMACOKINETIC PATHWAYS THROUGH KNOWLEDGE ACQUISITION AND AUTOMATED REASONING. , 2009, , 465-476.		19
799	Top-Down Identification of Protein Biomarkers in Bacteria with Unsequenced Genomes. <i>Analytical Chemistry</i> , 2009, 81, 9633-9642.	3.2	69

#	ARTICLE	IF	CITATIONS
800	Proteomic Analysis of Chemona~ve Pediatric Osteosarcomas and Corresponding Normal Bone Reveals Multiple Altered Molecular Targets. <i>Journal of Proteome Research</i> , 2009, 8, 3882-3888.	1.8	36
801	Annotating Enzymes of Uncertain Function: The Deacylation of <sup>d</sup>-Amino Acids by Members of the Amidohydrolase Superfamily<sup></sup>. <i>Biochemistry</i> , 2009, 48, 6469-6481.	1.2	15
802	FPPI: <i>Fusarium graminearum</i> Protein~Protein Interaction Database. <i>Journal of Proteome Research</i> , 2009, 8, 4714-4721.	1.8	85
803	ATP-Sensitive K<sup>+</sup> Channel Knockout Induces Cardiac Proteome Remodeling Predictive of Heart Disease Susceptibility. <i>Journal of Proteome Research</i> , 2009, 8, 4823-4834.	1.8	33
804	Knowledge-Based Characterization of Similarity Relationships in the Human Protein~Tyrosine Phosphatase Family for Rational Inhibitor Design. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 6649-6659.	2.9	14
805	Fishing the Target of Antitubercular Compounds: <i>In Silico</i> Target Deconvolution Model Development and Validation. <i>Journal of Proteome Research</i> , 2009, 8, 2788-2798.	1.8	27
806	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6477-6482.	3.3	154
807	PubChem as a Source of Polypharmacology. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2044-2055.	2.5	130
808	Assessing the impact of network depth on the analysis of PPI networks: A case study. , 2009, , .		2
809	Generating Abstract Networks Using Multi-relational Biological Data. , 2009, , .		1
810	<i>Caenorhabditis elegans</i> Has a Phosphoproteome Atypical for Metazoans That Is Enriched in Developmental and Sex Determination Proteins. <i>Journal of Proteome Research</i> , 2009, 8, 4039-4049.	1.8	66
811	Visualization, documentation, analysis, and communication of large-scale gene regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 363-374.	0.9	98
812	Shotgun Proteomics in Neuroscience. <i>Neuron</i> , 2009, 63, 12-26.	3.8	48
813	Systems based mapping demonstrates that recovery from alkylation damage requires DNA repair, RNA processing, and translation associated networks. <i>Genomics</i> , 2009, 93, 42-51.	1.3	17
814	Construction of a functional network for common DNA damage responses in <i>Escherichia coli</i> . <i>Genomics</i> , 2009, 93, 514-524.	1.3	10
815	14-3-3 proteins: Insights from genome-wide studies in yeast. <i>Genomics</i> , 2009, 94, 287-293.	1.3	57
816	Investigating transcriptional regulation: From analysis of complex networks to discovery of cis-regulatory elements. <i>Methods</i> , 2009, 48, 277-286.	1.9	4
817	Enabling a systems biology approach to immunology: focus on innate immunity. <i>Trends in Immunology</i> , 2009, 30, 249-262.	2.9	122

#	ARTICLE	IF	CITATIONS
818	Transcript Elongation Factor TFIIIS Is Involved in Arabidopsis Seed Dormancy. <i>Journal of Molecular Biology</i> , 2009, 386, 598-611.	2.0	73
819	Transcriptional response to mitochondrial NADH kinase deficiency in <i>Saccharomyces cerevisiae</i> . <i>Mitochondrion</i> , 2009, 9, 211-221.	1.6	6
820	Cytoscape: A Community-Based Framework for Network Modeling. <i>Methods in Molecular Biology</i> , 2009, 563, 219-239.	0.4	191
821	Biological Network Inference and Analysis Using SEBINI and CABIN. <i>Methods in Molecular Biology</i> , 2009, 541, 551-576.	0.4	10
822	Solution and Crystal Molecular Dynamics Simulation Study of m4-Cyanovirin-N Mutants Complexed with Di-Mannose. <i>Biophysical Journal</i> , 2009, 97, 2532-2540.	0.2	36
824	Predicting drug side-effects by chemical systems biology. <i>Genome Biology</i> , 2009, 10, 238.	13.9	59
825	Glutathione Transferases Are Structural and Functional Outliers in the Thioredoxin Fold. <i>Biochemistry</i> , 2009, 48, 11108-11116.	1.2	125
826	An Atlas of the Thioredoxin Fold Class Reveals the Complexity of Function-Enabling Adaptations. <i>PLoS Computational Biology</i> , 2009, 5, e1000541.	1.5	114
827	Mapping Adverse Drug Reactions in Chemical Space. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 3103-3107.	2.9	156
828	Systems biology evaluation of immune responses induced by human host defence peptide LL-37 in mononuclear cells. <i>Molecular BioSystems</i> , 2009, 5, 483.	2.9	92
829	Deciphering peculiar protein-protein interacting modules in <i>Deinococcus radiodurans</i> . <i>Biology Direct</i> , 2009, 4, 12.	1.9	3
830	Evolution of Enzymatic Activities in the Enolase Superfamily: Stereochemically Distinct Mechanisms in Two Families of <i>cis</i> - <i>cis</i> -Muconate Lactonizing Enzymes. <i>Biochemistry</i> , 2009, 48, 1445-1453.	1.2	36
831	The EVER Proteins as a Natural Barrier against Papillomaviruses: a New Insight into the Pathogenesis of Human Papillomavirus Infections. <i>Microbiology and Molecular Biology Reviews</i> , 2009, 73, 348-370.	2.9	119
832	A global view of protein expression in human cells, tissues, and organs. <i>Molecular Systems Biology</i> , 2009, 5, 337.	3.2	175
833	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. <i>Molecular BioSystems</i> , 2009, 5, 1456.	2.9	8
834	Network-assisted protein identification and data interpretation in shotgun proteomics. <i>Molecular Systems Biology</i> , 2009, 5, 303.	3.2	59
835	Identification of cis-Regulatory Elements in Gene Co-expression Networks Using A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 541, 3-22.	0.4	14
836	Breaking the hierarchy - a new cluster selection mechanism for hierarchical clustering methods. <i>Algorithms for Molecular Biology</i> , 2009, 4, 12.	0.3	14

#	ARTICLE	IF	CITATIONS
837	Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi analysis. <i>Genome Biology</i> , 2009, 10, R121.	13.9	16
838	Reverse-engineering the <i>Arabidopsis thaliana</i> transcriptional network under changing environmental conditions. <i>Genome Biology</i> , 2009, 10, R96.	13.9	81
839	Gene networks in <i>Drosophila melanogaster</i> : integrating experimental data to predict gene function. <i>Genome Biology</i> , 2009, 10, R97.	13.9	44
840	The conservation and evolutionary modularity of metabolism. <i>Genome Biology</i> , 2009, 10, R63.	13.9	134
841	Insights into female sperm storage from the spermathecal fluid proteome of the honeybee <i>Apis mellifera</i> . <i>Genome Biology</i> , 2009, 10, R67.	13.9	116
842	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	13.9	138
843	The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. <i>Genome Biology</i> , 2009, 10, R58.	13.9	38
844	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	13.9	67
845	Reconstructing the ubiquitin network - cross-talk with other systems and identification of novel functions. <i>Genome Biology</i> , 2009, 10, R33.	13.9	33
846	Using prior knowledge and genome-wide association to identify pathways involved in multiple sclerosis. <i>Genome Medicine</i> , 2009, 1, 65.	3.6	21
847	Systems medicine: the future of medical genomics and healthcare. <i>Genome Medicine</i> , 2009, 1, 2.	3.6	333
848	Strategies for efficient disruption of metabolism in <i>Mycobacterium tuberculosis</i> from network analysis. <i>Molecular BioSystems</i> , 2009, 5, 1740.	2.9	35
849	Pattern Discovery in Expression Profiling Data. <i>Current Protocols in Molecular Biology</i> , 2009, 85, Unit 22.5.	2.9	8
850	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. <i>Methods in Enzymology</i> , 2009, 467, 583-599.	0.4	23
851	Enzyme Relational Network Reveals Target Enzymes within Metabolic Submodules. , 2009, , .		0
852	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. <i>Molecular BioSystems</i> , 2009, 6, 175-181.	2.9	16
853	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009, 25, 2955-2961.	1.8	34
854	A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
855	Possible Occurrence of Scale-Free Topology in Highly Statistically Associated Polymorphic Positions in Two Potyviral Proteins. , 2009, , .		2
856	Predicting Yeast Synthetic Lethal Genetic Interactions Using Protein Domains. , 2009, , .		0
857	Applying Graph Theory on Protein - Protein Interaction Data. , 2009, , .		0
858	MetNetGE: Visualizing biological networks in hierarchical views and 3D tiered layouts. , 2009, , .		4
859	The Storage, Retrieval, and Visualization of Biological Pathway Data. , 2009, , .		0
860	Interaction Based Functional Clustering of Genomic Data. , 2009, , .		1
861	Visualizing a Correlative Multi-level Graph of Biology Entity Interactions. , 2009, , .		0
862	Revealing Biological Modules via Graph Summarization. Journal of Computational Biology, 2009, 16, 253-264.	0.8	47
863	Comprehensive evaluation of a novel nuclear factor- $\kappa$ B inhibitor, quinoclamine, by transcriptomic analysis. British Journal of Pharmacology, 2009, 157, 746-756.	2.7	12
864	GeneShelf: A Web-based Visual Interface for Large Gene Expression Time-Series Data Repositories. IEEE Transactions on Visualization and Computer Graphics, 2009, 15, 905-912.	2.9	12
865	Prioritizing Genes for Pathway Impact Using Network Analysis. Methods in Molecular Biology, 2009, 563, 141-156.	0.4	5
866	Pathway Enrichment Based on Text Mining and Its Validation on Carotenoid and Vitamin A Metabolism. OMICS A Journal of Integrative Biology, 2009, 13, 367-379.	1.0	14
867	Mapping Human Metabolic Pathways in the Small Molecule Chemical Space. Journal of Chemical Information and Modeling, 2009, 49, 2272-2289.	2.5	14
868	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. Molecular Systems Biology, 2009, 5, 290.	3.2	173
869	Biological Resource Centers and Systems Biology. BioScience, 2009, 59, 113-125.	2.2	3
870	Histogenomics: Association of Gene Expression Patterns With Histological Parameters in Kidney Biopsies. Transplantation, 2009, 87, 290-295.	0.5	38
871	Network Graph Analysis of Category Fluency Testing. Cognitive and Behavioral Neurology, 2009, 22, 45-52.	0.5	43
872	Computational Methods to Identify Transcription Factor Binding Sites Using CAGE Information. , 2009, , 137-151.		0

#	ARTICLE	IF	CITATIONS
873	Tomato Transcriptional Responses to a Foliar and a Vascular Fungal Pathogen Are Distinct. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 245-258.	1.4	61
874	Grafta: A 3D environment for biomolecular networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 564.	0.1	0
876	An Efficient Method to Identify Conditionally Activated Transcription Factors and their Corresponding Signal Transduction Pathway Segments. <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S3485.	1.0	0
877	Muscle genome-wide expression profiling during disease evolution in mdx mice. <i>Physiological Genomics</i> , 2009, 37, 119-132.	1.0	50
878	Genomics software: The view from 10,000 feet. <i>Human Genomics</i> , 2009, 4, 56-8.	1.4	0
879	Isolation stress for 30 days alters hepatic gene expression profiles, especially with reference to lipid metabolism in mice. <i>Physiological Genomics</i> , 2009, 37, 79-87.	1.0	21
880	AtPIN: Arabidopsis thaliana Protein Interaction Network. <i>BMC Bioinformatics</i> , 2009, 10, 454.	1.2	107
881	Graph methods for the investigation of metabolic networks in parasitology. <i>Parasitology</i> , 2010, 137, 1393-1407.	0.7	21
882	Functional modularity of nuclear hormone receptors in a <i>Caenorhabditis elegans</i> metabolic gene regulatory network. <i>Molecular Systems Biology</i> , 2010, 6, 367.	3.2	93
883	Strategies for online inference of model-based clustering in large and growing networks. <i>Annals of Applied Statistics</i> , 2010, 4, .	0.5	19
885	Novel systems biology insights using antifibrotic approaches for diabetic kidney disease. <i>Expert Review of Endocrinology and Metabolism</i> , 2010, 5, 127-135.	1.2	1
886	An integrated model for visualizing biclusters from gene expression data and PPI networks. , 2010, , .		0
887	Systems Biology and TOR. <i>The Enzymes</i> , 2010, 28, 317-348.	0.7	1
888	Structure, evolution and dynamics of transcriptional regulatory networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1155-1178.	1.6	21
889	Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 101.	0.1	3
890	Predicting protein complexes by data integration of different types of interactions. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 19.	0.3	7
891	Multi-level integrative analysis of Protein Protein Interaction networks: connecting completeness, depth and robustness. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 31.	0.3	1
892	Meta analysis algorithms for microarray gene expression data using Gene Regulatory Networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 487.	0.1	3

#	ARTICLE	IF	CITATIONS
893	Exploring Target-Selectivity Patterns of Molecular Scaffolds. ACS Medicinal Chemistry Letters, 2010, 1, 54-58.	1.3	14
894	Protein-Protein Interaction Network and Gene Ontology. , 2010, , 159-169.		1
895	The use of network analyses for elucidating mechanisms in cardiovascular disease. Molecular BioSystems, 2010, 6, 289-304.	2.9	81
896	From experimental setup to bioinformatics: An RNAi screening platform to identify host factors involved in HIV-1 replication. Biotechnology Journal, 2010, 5, 39-49.	1.8	39
897	Protein-to-protein interactions. ACM Computing Surveys, 2010, 43, 1-36.	16.1	122
898	Current Progress in Static and Dynamic Modeling of Biological Networks. Systems Biology, 2010, , 13-73.	0.1	4
900	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR $\beta$ . Cellular and Molecular Life Sciences, 2010, 67, 4049-4064.	2.4	38
901	Proteomics for quality-control processes in transfusion medicine. Analytical and Bioanalytical Chemistry, 2010, 398, 111-124.	1.9	14
902	Temporal Patterns in Glycolate-Utilizing Bacterial Community Composition Correlate with Phytoplankton Population Dynamics in Humic Lakes. Microbial Ecology, 2010, 60, 406-418.	1.4	37
903	Analysis of gene expression pattern reveals potential targets of dietary oleoylethanolamide in reducing body fat gain in C3H mice. Journal of Nutritional Biochemistry, 2010, 21, 922-928.	1.9	30
904	Integrated protein network and microarray analysis to identify potential biomarkers after myocardial infarction. Functional and Integrative Genomics, 2010, 10, 329-337.	1.4	36
905	The NetAge database: a compendium of networks for longevity, age-related diseases and associated processes. Biogerontology, 2010, 11, 513-522.	2.0	71
906	Interaction networks as a tool to investigate the mechanisms of aging. Biogerontology, 2010, 11, 463-473.	2.0	14
907	A mouse protein interactome through combined literature mining with multiple sources of interaction evidence. Amino Acids, 2010, 38, 1237-1252.	1.2	28
908	Enriching the viral-host interactomes with interactions mediated by SH3 domains. Amino Acids, 2010, 38, 1541-1547.	1.2	9
909	Cytochrome P450 networks in chemical space. Archives of Pharmacal Research, 2010, 33, 1361-1374.	2.7	3
910	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. Protein and Cell, 2010, 1, 675-687.	4.8	22
911	Revealing system-level correlations between aging and calorie restriction using a mouse transcriptome. Age, 2010, 32, 15-30.	3.0	18



#	ARTICLE	IF	CITATIONS
912	Metagenomics: Facts and Artifacts, and Computational Challenges. Journal of Computer Science and Technology, 2010, 25, 71-81.	0.9	132
913	A linear programming model based on network flow for pathway inference. Journal of Systems Science and Complexity, 2010, 23, 971-977.	1.6	0
914	Protein-protein interaction networks suggest different targets have different propensities for triggering drug resistance. Systems and Synthetic Biology, 2010, 4, 311-322.	1.0	21
915	A preliminary approach to creating an overview of lactoferrin multi-functionality utilizing a text mining method. BioMetals, 2010, 23, 453-463.	1.8	2
916	Use of reconstituted metabolic networks to assist in metabolomic data visualization and mining. Metabolomics, 2010, 6, 312-321.	1.4	29
917	A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. Plant Molecular Biology, 2010, 72, 369-380.	2.0	70
918	Belief Propagation Estimation of Protein and Domain Interactions Using the Sum-Product Algorithm. IEEE Transactions on Information Theory, 2010, 56, 742-755.	1.5	6
919	Information technology solutions for integration of biomolecular and clinical data in the identification of new cancer biomarkers and targets for therapy. , 2010, 128, 488-498.		13
920	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. BMC Bioinformatics, 2010, 11, 117.	1.2	92
921	SCPS: a fast implementation of a spectral method for detecting protein families on a genome-wide scale. BMC Bioinformatics, 2010, 11, 120.	1.2	54
922	Response network analysis of differential gene expression in human epithelial lung cells during avian influenza infections. BMC Bioinformatics, 2010, 11, 170.	1.2	18
923	Consolidating metabolite identifiers to enable contextual and multi-platform metabolomics data analysis. BMC Bioinformatics, 2010, 11, 214.	1.2	38
924	GOAL: A software tool for assessing biological significance of genes groups. BMC Bioinformatics, 2010, 11, 229.	1.2	27
925	Towards the systematic discovery of signal transduction networks using phosphorylation dynamics data. BMC Bioinformatics, 2010, 11, 232.	1.2	15
926	Detecting disease associated modules and prioritizing active genes based on high throughput data. BMC Bioinformatics, 2010, 11, 26.	1.2	70
927	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. BMC Bioinformatics, 2010, 11, 265.	1.2	16
928	LucidDraw: Efficiently visualizing complex biochemical networks within MATLAB. BMC Bioinformatics, 2010, 11, 31.	1.2	9
929	Introducing W.A.T.E.R.S.: a Workflow for the Alignment, Taxonomy, and Ecology of Ribosomal Sequences. BMC Bioinformatics, 2010, 11, 317.	1.2	29



#	ARTICLE	IF	CITATIONS
930	An efficient biological pathway layout algorithm combining grid-layout and spring embedder for complicated cellular location information. BMC Bioinformatics, 2010, 11, 335.	1.2	6
931	Identifying differentially regulated subnetworks from phosphoproteomic data. BMC Bioinformatics, 2010, 11, 351.	1.2	35
932	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360.	1.2	0
933	Integration and visualization of systems biology data in context of the genome. BMC Bioinformatics, 2010, 11, 382.	1.2	31
934	Consistency, comprehensiveness, and compatibility of pathway databases. BMC Bioinformatics, 2010, 11, 449.	1.2	60
935	MetNetGE: interactive views of biological networks and ontologies. BMC Bioinformatics, 2010, 11, 469.	1.2	6
936	Protein network prediction and topological analysis in Leishmania major as a tool for drug target selection. BMC Bioinformatics, 2010, 11, 484.	1.2	81
937	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. BMC Bioinformatics, 2010, 11, 5.	1.2	180
938	MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. BMC Bioinformatics, 2010, 11, 504.	1.2	63
939	Inferring gene regression networks with model trees. BMC Bioinformatics, 2010, 11, 517.	1.2	25
940	Biana: a software framework for compiling biological interactions and analyzing networks. BMC Bioinformatics, 2010, 11, 56.	1.2	85
941	BiologicalNetworks 2.0 - an integrative view of genome biology data. BMC Bioinformatics, 2010, 11, 610.	1.2	21
942	A temporal precedence based clustering method for gene expression microarray data. BMC Bioinformatics, 2010, 11, 68.	1.2	9
943	Lists2Networks: Integrated analysis of gene/protein lists. BMC Bioinformatics, 2010, 11, 87.	1.2	38
944	BisoGenet: a new tool for gene network building, visualization and analysis. BMC Bioinformatics, 2010, 11, 91.	1.2	294
945	A statistical framework for differential network analysis from microarray data. BMC Bioinformatics, 2010, 11, 95.	1.2	134
946	An ontology-based search engine for protein-protein interactions. BMC Bioinformatics, 2010, 11, S23.	1.2	5
947	NeMo: Network Module identification in Cytoscape. BMC Bioinformatics, 2010, 11, S61.	1.2	104

#	ARTICLE	IF	CITATIONS
948	Modularity of Escherichia coli sRNA regulation revealed by sRNA-target and protein network analysis. BMC Bioinformatics, 2010, 11, S11.	1.2	8
949	Positive selection of HIV host factors and the evolution of lentivirus genes. BMC Evolutionary Biology, 2010, 10, 186.	3.2	15
950	Assembling networks of microbial genomes using linear programming. BMC Evolutionary Biology, 2010, 10, 360.	3.2	4
951	Transcriptomic changes arising during light-induced sporulation in Physarum polycephalum. BMC Genomics, 2010, 11, 115.	1.2	23
952	Transcriptional profiling of an Fd-GOGAT1/GLU1 mutant in Arabidopsis thaliana reveals a multiple stress response and extensive reprogramming of the transcriptome. BMC Genomics, 2010, 11, 190.	1.2	36
953	The ancient mammalian KRAB zinc finger gene cluster on human chromosome 8q24.3 illustrates principles of C2H2 zinc finger evolution associated with unique expression profiles in human tissues. BMC Genomics, 2010, 11, 206.	1.2	26
954	Computational prediction of the osmoregulation network in Synechococcus sp. WH8102. BMC Genomics, 2010, 11, 291.	1.2	14
955	Prednisolone-induced differential gene expression in mouse liver carrying wild type or a dimerization-defective glucocorticoid receptor. BMC Genomics, 2010, 11, 359.	1.2	107
956	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in Arabidopsis thaliana. BMC Genomics, 2010, 11, 411.	1.2	21
957	A potential role for intragenic miRNAs on their hosts' interactome. BMC Genomics, 2010, 11, 533.	1.2	142
958	Genome-wide inference of regulatory networks in Streptomyces coelicolor. BMC Genomics, 2010, 11, 578.	1.2	38
959	Gene duplications in prokaryotes can be associated with environmental adaptation. BMC Genomics, 2010, 11, 588.	1.2	102
960	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. BMC Genomics, 2010, 11, 654.	1.2	15
961	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. BMC Genomics, 2010, 11, 685.	1.2	77
962	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. BMC Genomics, 2010, 11, 71.	1.2	24
963	Data integration and exploration for the identification of molecular mechanisms in tumor-immune cells interaction. BMC Genomics, 2010, 11, S7.	1.2	16
964	Expression profile and specific network features of the apoptotic machinery explain relapse of acute myeloid leukemia after chemotherapy. BMC Cancer, 2010, 10, 377.	1.1	26
965	Investigation of PARP-1, PARP-2, and PARC interactomes by affinity-purification mass spectrometry. Proteome Science, 2010, 8, 22.	0.7	133

#	ARTICLE	IF	CITATIONS
966	ReCGiP, a database of reproduction candidate genes in pigs based on bibliomics. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 96.	1.4	7
967	Snazer: the simulations and networks analyzer. <i>BMC Systems Biology</i> , 2010, 4, 1.	3.0	175
968	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. <i>BMC Systems Biology</i> , 2010, 4, 15.	3.0	18
969	Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. <i>BMC Systems Biology</i> , 2010, 4, 170.	3.0	40
970	Integrated cellular network of transcription regulations and protein-protein interactions. <i>BMC Systems Biology</i> , 2010, 4, 20.	3.0	57
971	Building and analyzing protein interactome networks by cross-species comparisons. <i>BMC Systems Biology</i> , 2010, 4, 36.	3.0	55
972	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010, 4, 45.	3.0	321
973	Construction of a large scale integrated map of macrophage pathogen recognition and effector systems. <i>BMC Systems Biology</i> , 2010, 4, 63.	3.0	35
974	Identifying potential survival strategies of HIV-1 through virus-host protein interaction networks. <i>BMC Systems Biology</i> , 2010, 4, 96.	3.0	31
975	MetNetAPI: A flexible method to access and manipulate biological network data from MetNet. <i>BMC Research Notes</i> , 2010, 3, 312.	0.6	4
976	Construction and analysis of protein-protein interaction networks. <i>Automated Experimentation</i> , 2010, 2, 2.	2.0	139
977	Loss of <i>Caenorhabditis elegans</i> UNG-1 uracil-DNA glycosylase affects apoptosis in response to DNA damaging agents. <i>DNA Repair</i> , 2010, 9, 861-870.	1.3	17
978	Pharmacoproteomics: a chess game on a protein field. <i>Drug Discovery Today</i> , 2010, 15, 1015-1023.	3.2	26
979	Protein interaction network underpins concordant prognosis among heterogeneous breast cancer signatures. <i>Journal of Biomedical Informatics</i> , 2010, 43, 385-396.	2.5	49
980	Gene pathways and subnetworks distinguish between major glioma subtypes and elucidate potential underlying biology. <i>Journal of Biomedical Informatics</i> , 2010, 43, 945-952.	2.5	12
981	Low malignant potential tumors with micropapillary features are molecularly similar to low-grade serous carcinoma of the ovary. <i>Gynecologic Oncology</i> , 2010, 117, 9-17.	0.6	61
982	Analysis of chemotherapy response programs in ovarian cancers by the next-generation sequencing technologies. <i>Gynecologic Oncology</i> , 2010, 117, 159-169.	0.6	64
983	A systems biology approach to understanding atherosclerosis. <i>EMBO Molecular Medicine</i> , 2010, 2, 79-89.	3.3	69

#	ARTICLE	IF	CITATIONS
984	Sensing the mechanical state of the axoneme and integration of Ca <sup>2+</sup> signaling by outer arm dynein. <i>Cytoskeleton</i> , 2010, 67, 207-213.	1.0	22
985	Scaffold Distributions in Bioactive Molecules, Clinical Trials Compounds, and Drugs. <i>ChemMedChem</i> , 2010, 5, 187-190.	1.6	22
986	Modulators of cancer cell invasiveness. <i>Journal of Cellular Biochemistry</i> , 2010, 111, 791-796.	1.2	9
987	Architectural Repertoire of Ligand-Binding Pockets on Protein Surfaces. <i>ChemBioChem</i> , 2010, 11, 556-563.	1.3	22
988	Network-Based Modeling of the Human Gut Microbiome. <i>Chemistry and Biodiversity</i> , 2010, 7, 1040-1050.	1.0	48
989	Subcellular phosphoproteomics. <i>Mass Spectrometry Reviews</i> , 2010, 29, 962-990.	2.8	36
990	Drug-Target Networks. <i>Molecular Informatics</i> , 2010, 29, 10-14.	1.4	73
991	Iterative Shannon Entropy – a Methodology to Quantify the Information Content of Value Range Dependent Data Distributions. Application to Descriptor and Compound Selectivity Profiling. <i>Molecular Informatics</i> , 2010, 29, 432-440.	1.4	1
992	Missing Value Estimation for Compound-Target Activity Data. <i>Molecular Informatics</i> , 2010, 29, 678-684.	1.4	9
993	Tocotrienols activity in MCF7 breast cancer cells: Involvement of ER <sup>1/2</sup> signal transduction. <i>Molecular Nutrition and Food Research</i> , 2010, 54, 669-678.	1.5	29
994	Rescue of F508del-CFTR by RXR motif inactivation triggers proteome modulation associated with the unfolded protein response. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 856-865.	1.1	31
995	Proteomics data repositories: Providing a safe haven for your data and acting as a springboard for further research. <i>Journal of Proteomics</i> , 2010, 73, 2136-2146.	1.2	61
996	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , 2010, 73, 2171-2185.	1.2	138
997	Regulatory dynamics of standard two-component systems in bacteria. <i>Journal of Theoretical Biology</i> , 2010, 264, 560-569.	0.8	8
998	eNelator: A simulation system for large-scale vulnerability analysis of species-, disease- and process-specific protein networks. <i>Journal of Computational Science</i> , 2010, 1, 197-205.	1.5	6
999	A new analysis of debris mitigation and removal using networks. <i>Acta Astronautica</i> , 2010, 66, 257-268.	1.7	4
1000	Ground testing of Arabidopsis preservation protocol for the microarray analysis to be used in the ISS EMCS Multigen-2 experiment. <i>Advances in Space Research</i> , 2010, 46, 1249-1256.	1.2	7
1001	Natural immunity to cancer in humans. <i>Current Opinion in Immunology</i> , 2010, 22, 215-222.	2.4	153

#	ARTICLE	IF	CITATIONS
1002	Incorporating multiple genomic features with the utilization of interacting domain patterns to improve the prediction of protein-protein interactions. <i>Information Sciences</i> , 2010, 180, 3955-3973.	4.0	6
1003	Modifiers of notch transcriptional activity identified by genome-wide RNAi. <i>BMC Developmental Biology</i> , 2010, 10, 107.	2.1	20
1004	Hydrocarbon phenotyping of algal species using pyrolysis-gas chromatography mass spectrometry. <i>BMC Biotechnology</i> , 2010, 10, 40.	1.7	26
1005	Concept and application of a computational vaccinology workflow. <i>Immunome Research</i> , 2010, 6, S7.	0.1	32
1006	GTC: A web server for integrating systems biology data with web tools and desktop applications. <i>Source Code for Biology and Medicine</i> , 2010, 5, 7.	1.7	2
1007	Open source tool for prediction of genome wide protein-protein interaction network based on ortholog information. <i>Source Code for Biology and Medicine</i> , 2010, 5, 8.	1.7	34
1008	A Novel microRNA and transcription factor mediated regulatory network in schizophrenia. <i>BMC Systems Biology</i> , 2010, 4, 10.	3.0	145
1009	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. <i>BMC Systems Biology</i> , 2010, 4, 114.	3.0	79
1010	Curating the innate immunity interactome. <i>BMC Systems Biology</i> , 2010, 4, 117.	3.0	68
1011	The mEPN scheme: an intuitive and flexible graphical system for rendering biological pathways. <i>BMC Systems Biology</i> , 2010, 4, 65.	3.0	18
1012	Co-expression module analysis reveals biological processes, genomic gain, and regulatory mechanisms associated with breast cancer progression. <i>BMC Systems Biology</i> , 2010, 4, 74.	3.0	117
1013	The biological context of HIV-1 host interactions reveals subtle insights into a system hijack. <i>BMC Systems Biology</i> , 2010, 4, 80.	3.0	28
1014	Identification of transcription factor's targets using tissue-specific transcriptomic data in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2010, 4, S2.	3.0	35
1015	Shrunken methodology to genome-wide SNPs selection and construction of SNPs networks. <i>BMC Systems Biology</i> , 2010, 4, S5.	3.0	8
1016	Gene regulatory network reveals oxidative stress as the underlying molecular mechanism of type 2 diabetes and hypertension. <i>BMC Medical Genomics</i> , 2010, 3, 45.	0.7	46
1017	mspecLINE: bridging knowledge of human disease with the proteome. <i>BMC Medical Genomics</i> , 2010, 3, 7.	0.7	9
1018	Predicting cytotoxicity from heterogeneous data sources with Bayesian learning. <i>Journal of Cheminformatics</i> , 2010, 2, 11.	2.8	32
1019	Comparison of human solute carriers. <i>Protein Science</i> , 2010, 19, 412-428.	3.1	99

#	ARTICLE	IF	CITATIONS
1020	Domain distribution and intrinsic disorder in hubs in the human protein-protein interaction network. <i>Protein Science</i> , 2010, 19, 1461-1468.	3.1	62
1021	From proteome lists to biological impact: tools and strategies for the analysis of large MS data sets. <i>Proteomics</i> , 2010, 10, 1270-1283.	1.3	54
1022	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. <i>Proteomics</i> , 2010, 10, 1316-1327.	1.3	55
1023	The impact of miR-34a on protein output in hepatocellular carcinoma HepG2 cells. <i>Proteomics</i> , 2010, 10, 1557-1572.	1.3	65
1024	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 2010, 10, 2719-2722.	1.3	20
1025	N-terminal strands of filamin Ig domains act as a conformational switch under biological forces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 12-24.	1.5	29
1026	Regional covariation and its application for predicting protein contact patches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 548-558.	1.5	6
1027	The evolutionary landscape of the chromatin modification machinery reveals lineage specific gains, expansions, and losses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2075-2089.	1.5	17
1028	Undifferentiated Embryonic Cell Transcription Factor 1 Regulates ESC Chromatin Organization and Gene Expression. <i>Stem Cells</i> , 2010, 28, 1703-1714.	1.4	30
1029	<i>In silico</i> models of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 438-459.	6.6	103
1030	Genome-wide analysis of caesium and strontium accumulation in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2010, 27, 817-835.	0.8	15
1031	Genome wide expression analysis of the effect of <i>Pinelliae Rhizoma</i> extract on psychological stress. <i>Phytotherapy Research</i> , 2010, 24, 384-392.	2.8	5
1032	Reciprocal regulation of gene expression by <i>Ephedra herba</i> in mouse brain. <i>Phytotherapy Research</i> , 2010, 24, 531-537.	2.8	1
1033	A comprehensive and non-prefractionation on the protein level approach for the human urinary proteome: touching phosphorylation in urine. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 823-832.	0.7	79
1034	Hubs and bottlenecks in plant molecular signalling networks. <i>New Phytologist</i> , 2010, 188, 919-938.	3.5	75
1035	An update on clinical proteomics in Alzheimer's research. <i>Journal of Neurochemistry</i> , 2010, 112, 1386-1414.	2.1	82
1036	Global gene profiling and comprehensive bioinformatics analysis of a 46,XY female with pericentric inversion of the Y chromosome. <i>Congenital Anomalies (discontinued)</i> , 2010, 50, 40-51.	0.3	3
1037	Immunoinformatics: an integrated scenario. <i>Immunology</i> , 2010, 131, 153-168.	2.0	116

#	ARTICLE	IF	CITATIONS
1038	The proximal signaling network of the BCR-ABL1 oncogene shows a modular organization. <i>Oncogene</i> , 2010, 29, 5895-5910.	2.6	35
1039	Phylogenetic diversity and community structure of anaerobic gut fungi (phylum Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50,702 Td	4.4	239
1040	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
1041	Transcriptional profiling of growth perturbations of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Biotechnology</i> , 2010, 28, 91-98.	9.4	196
1042	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
1043	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 990-1003.	2.8	47
1044	New perspectives on the biology of acute GVHD. <i>Bone Marrow Transplantation</i> , 2010, 45, 1-11.	1.3	158
1045	ProHits: integrated software for mass spectrometry-based interaction proteomics. <i>Nature Biotechnology</i> , 2010, 28, 1015-1017.	9.4	202
1046	A basic helix-loop-helix transcription factor controls cell growth and size in root hairs. <i>Nature Genetics</i> , 2010, 42, 264-267.	9.4	295
1047	A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. <i>Nature Immunology</i> , 2010, 11, 635-643.	7.0	475
1048	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010, 7, S56-S68.	9.0	548
1049	Visualizing biological data—now and in the future. <i>Nature Methods</i> , 2010, 7, S2-S4.	9.0	115
1050	Detecting interactions with membrane proteins using a membrane two-hybrid assay in yeast. <i>Nature Protocols</i> , 2010, 5, 1281-1293.	5.5	115
1051	Statistical analysis strategies for association studies involving rare variants. <i>Nature Reviews Genetics</i> , 2010, 11, 773-785.	7.7	426
1052	Analysing biological pathways in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 843-854.	7.7	722
1053	Differential bacterial dynamics promote emergent community robustness to lake mixing: an epilimnion to hypolimnion transplant experiment. <i>Environmental Microbiology</i> , 2010, 12, 455-466.	1.8	44
1054	SmallWorlds: Visualizing Social Recommendations. <i>Computer Graphics Forum</i> , 2010, 29, 833-842.	1.8	79
1055	Pathline: A Tool For Comparative Functional Genomics. <i>Computer Graphics Forum</i> , 2010, 29, 1043-1052.	1.8	57

#	ARTICLE	IF	CITATIONS
1056	A network analysis of the single nucleotide polymorphisms in acute allergic diseases. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2010, 65, 40-47.	2.7	11
1057	Charting the NF- $\kappa$ B pathway interactome map. <i>Nature Precedings</i> , 2010, , .	0.1	1
1058	Protein Interaction Data Resources. , 2010, , 1375-1385.		1
1060	A membrane protein / signaling protein interaction network for Arabidopsis version AMPv2. <i>Frontiers in Physiology</i> , 2010, 1, 24.	1.3	131
1061	Current Trends and New Challenges of Databases and Web Applications for Systems Driven Biological Research. <i>Frontiers in Physiology</i> , 2010, 1, 147.	1.3	12
1062	Systems Biology: The Next Frontier for Bioinformatics. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-10.	5.7	51
1063	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput $\omicron$ omics Data. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-19.	5.7	19
1064	Automated Network Analysis Identifies Core Pathways in Glioblastoma. <i>PLoS ONE</i> , 2010, 5, e8918.	1.1	318
1065	A Boolean Model of the <i>Pseudomonas syringae</i> hrp Regulon Predicts a Tightly Regulated System. <i>PLoS ONE</i> , 2010, 5, e9101.	1.1	19
1066	<i>Xenopus</i> Meiotic Microtubule-Associated Interactome. <i>PLoS ONE</i> , 2010, 5, e9248.	1.1	40
1067	A Comprehensive Resource of Interacting Protein Regions for Refining Human Transcription Factor Networks. <i>PLoS ONE</i> , 2010, 5, e9289.	1.1	56
1068	Cancer-Drug Associations: A Complex System. <i>PLoS ONE</i> , 2010, 5, e10031.	1.1	18
1069	A Comprehensive Molecular Interaction Map for Rheumatoid Arthritis. <i>PLoS ONE</i> , 2010, 5, e10137.	1.1	51
1070	Identifying Molecular Effects of Diet through Systems Biology: Influence of Herring Diet on Sterol Metabolism and Protein Turnover in Mice. <i>PLoS ONE</i> , 2010, 5, e12361.	1.1	17
1071	Network Analysis Identifies ELF3 as a QTL for the Shade Avoidance Response in Arabidopsis. <i>PLoS Genetics</i> , 2010, 6, e1001100.	1.5	120
1072	Structural and Functional Roles of Coevolved Sites in Proteins. <i>PLoS ONE</i> , 2010, 5, e8591.	1.1	52
1073	Inference of Cancer-specific Gene Regulatory Networks Using Soft Computing Rules. <i>Gene Regulation and Systems Biology</i> , 2010, 4, GRSB.S4509.	2.3	12
1074	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. <i>Aging</i> , 2010, 2, 133-159.	1.4	23



#	ARTICLE	IF	CITATIONS
1075	Investigating the correlations among the chemical structures, bioactivity profiles and molecular targets of small molecules. <i>Bioinformatics</i> , 2010, 26, 2881-2888.	1.8	26
1076	Interactome Mapping of the Phosphatidylinositol 3-Kinase-Mammalian Target of Rapamycin Pathway Identifies Deformed Epidermal Autoregulatory Factor-1 as a New Glycogen Synthase Kinase-3 Interactor. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1578-1593.	2.5	51
1077	Functional Modules in the <i>Arabidopsis</i> Core Cell Cycle Binary Protein-Protein Interaction Network. <i>Plant Cell</i> , 2010, 22, 1264-1280.	3.1	168
1078	Molecular and Physiological Analysis of Drought Stress in <i>Arabidopsis</i> Reveals Early Responses Leading to Acclimation in Plant Growth. <i>Plant Physiology</i> , 2010, 154, 1254-1271.	2.3	580
1079	Recent progress in automatically extracting information from the pharmacogenomic literature. <i>Pharmacogenomics</i> , 2010, 11, 1467-1489.	0.6	63
1080	Coexpression Analysis Identifies Rice Starch Regulator1, a Rice AP2/EREBP Family Transcription Factor, as a Novel Rice Starch Biosynthesis Regulator. <i>Plant Physiology</i> , 2010, 154, 927-938.	2.3	325
1081	DRYGIN: a database of quantitative genetic interaction networks in yeast. <i>Nucleic Acids Research</i> , 2010, 38, D502-D507.	6.5	75
1082	Comorbidity: A network perspective. <i>Behavioral and Brain Sciences</i> , 2010, 33, 137-150.	0.4	1,043
1083	EGAN: exploratory gene association networks. <i>Bioinformatics</i> , 2010, 26, 285-286.	1.8	51
1084	geWorkbench: an open source platform for integrative genomics. <i>Bioinformatics</i> , 2010, 26, 1779-1780.	1.8	82
1085	Genomic cis-regulatory networks in the early <i>Ciona intestinalis</i> embryo. <i>Development (Cambridge)</i> , 2010, 137, 1613-1623.	1.2	61
1086	A Novel Grid-Based Visualization Approach for Metabolic Networks with Advanced Focus&Context View. <i>Lecture Notes in Computer Science</i> , 2010, , 268-279.	1.0	14
1087	ToppCluster: a multiple gene list feature analyzer for comparative enrichment clustering and network-based dissection of biological systems. <i>Nucleic Acids Research</i> , 2010, 38, W96-W102.	6.5	325
1088	PROFESS: a PROtein Function, Evolution, Structure and Sequence database. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq011-baq011.	1.4	6
1089	GeneMANIA Cytoscape plugin: fast gene function predictions on the desktop. <i>Bioinformatics</i> , 2010, 26, 2927-2928.	1.8	552
1090	Trivalent Arsenic Inhibits the Functions of Chaperonin Complex. <i>Genetics</i> , 2010, 186, 725-734.	1.2	51
1091	SpotXplore: a Cytoscape plugin for visual exploration of hotspot expression in gene regulatory networks. <i>Bioinformatics</i> , 2010, 26, 2922-2923.	1.8	6
1092	Measuring the physical cohesiveness of proteins using physical interaction enrichment. <i>Bioinformatics</i> , 2010, 26, 2737-2743.	1.8	18

#	ARTICLE	IF	CITATIONS
1093	SimBoolNet—a Cytoscape plugin for dynamic simulation of signaling networks. <i>Bioinformatics</i> , 2010, 26, 141-142.	1.8	54
1094	CORNET: A User-Friendly Tool for Data Mining and Integration. <i>Plant Physiology</i> , 2010, 152, 1167-1179.	2.3	62
1095	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010, 38, 8141-8148.	6.5	17
1096	Upstream transcription factor 1 influences plasma lipid and metabolic traits in mice. <i>Human Molecular Genetics</i> , 2010, 19, 597-608.	1.4	30
1097	Regulators of cyclin-dependent kinases are crucial for maintaining genome integrity in S phase. <i>Journal of Cell Biology</i> , 2010, 188, 629-638.	2.3	146
1098	MicroRNA miR-183 Functions as an Oncogene by Targeting the Transcription Factor <i>EGR1</i> and Promoting Tumor Cell Migration. <i>Cancer Research</i> , 2010, 70, 9570-9580.	0.4	277
1099	Defining the budding yeast chromatin-associated interactome. <i>Molecular Systems Biology</i> , 2010, 6, 448.	3.2	58
1100	Mapping Plant Interactomes Using Literature Curated and Predicted Protein-Protein Interaction Data Sets. <i>Plant Cell</i> , 2010, 22, 997-1005.	3.1	33
1101	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14793-14798.	3.3	234
1102	Quantitative Site-specific Phosphorylation Dynamics of Human Protein Kinases during Mitotic Progression. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1167-1181.	2.5	46
1103	Computational Tools for the Interactive Exploration of Proteomic and Structural Data. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1703-1715.	2.5	9
1104	R spider: a network-based analysis of gene lists by combining signaling and metabolic pathways from Reactome and KEGG databases. <i>Nucleic Acids Research</i> , 2010, 38, W78-W83.	6.5	62
1105	RNA G-Quadruplexes in the model plant species <i>Arabidopsis thaliana</i> : prevalence and possible functional roles. <i>Nucleic Acids Research</i> , 2010, 38, 8149-8163.	6.5	93
1106	GSearcher: Agile Attribute Querying for Biological Networks. <i>Bioinformatics</i> , 2010, 26, 3138-3139.	1.8	1
1107	Parallel Genetic and Proteomic Screens Identify Msps as a CLASP Abl Pathway Interactor in <i>Drosophila</i> . <i>Genetics</i> , 2010, 185, 1311-1325.	1.2	49
1108	Network-based Identification of Novel Cancer Genes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 648-655.	2.5	54
1109	Preferential use of protein domain pairs as interaction mediators: order and transitivity. <i>Bioinformatics</i> , 2010, 26, 2564-2570.	1.8	11
1110	Engineered Human Skin Substitutes Undergo Large-Scale Genomic Reprogramming and Normal Skin-Like Maturation after Transplantation to Athymic Mice. <i>Journal of Investigative Dermatology</i> , 2010, 130, 587-601.	0.3	38

#	ARTICLE	IF	CITATIONS
1111	Chemotherapy and signaling. <i>Cancer Biology and Therapy</i> , 2010, 10, 839-853.	1.5	88
1112	Extended Constraint-Based Boolean Analysis: A Computational Method in Genetic Network Inference. <i>Communications in Computer and Information Science</i> , 2010, , 71-82.	0.4	0
1113	<i>Biomedical Informatics for Cancer Research.</i> , 2010, , .		13
1114	Massively Parallel Signature Sequencing and Bioinformatics Analysis Identifies Up-Regulation of TGFBI and SOX4 in Human Glioblastoma. <i>PLoS ONE</i> , 2010, 5, e10210.	1.1	77
1115	MetExplore: a web server to link metabolomic experiments and genome-scale metabolic networks. <i>Nucleic Acids Research</i> , 2010, 38, W132-W137.	6.5	148
1116	DisGeNET: a Cytoscape plugin to visualize, integrate, search and analyze gene-disease networks. <i>Bioinformatics</i> , 2010, 26, 2924-2926.	1.8	180
1117	Metscape: a Cytoscape plug-in for visualizing and interpreting metabolomic data in the context of human metabolic networks. <i>Bioinformatics</i> , 2010, 26, 971-973.	1.8	196
1118	Evidence mining and novelty assessment of protein-protein interactions with the ConsensusPathDB plugin for Cytoscape. <i>Bioinformatics</i> , 2010, 26, 2796-2797.	1.8	30
1119	OmicsAnalyzer: a Cytoscape plug-in suite for modeling omics data. <i>Bioinformatics</i> , 2010, 26, 2995-2996.	1.8	24
1120	Unfolding of Metastable Linker Region Is at the Core of Hsp33 Activation as a Redox-regulated Chaperone. <i>Journal of Biological Chemistry</i> , 2010, 285, 11243-11251.	1.6	56
1121	MODEVO: exploring modularity and evolution of protein interaction networks. <i>Bioinformatics</i> , 2010, 26, 1790-1791.	1.8	15
1122	Synthetic Lethal Screen of an EGFR-Centered Network to Improve Targeted Therapies. <i>Science Signaling</i> , 2010, 3, ra67.	1.6	131
1123	GATE: software for the analysis and visualization of high-dimensional time series expression data. <i>Bioinformatics</i> , 2010, 26, 143-144.	1.8	29
1124	Genetic Associations of Variants in Genes Encoding HIV-Dependency Factors Required for HIV-1 Infection. <i>Journal of Infectious Diseases</i> , 2010, 202, 1836-1845.	1.9	29
1125	Molecular Association between Diabetes-Specific Local Gene Network and Nutrient Metabolism Modules. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010, , .	0.0	2
1126	seGOsa: Software environment for gene ontology-driven similarity assessment. , 2010, , .		4
1127	Classification of genome-wide copy number variations and their associated SNP and gene networks analysis. , 2010, , .		0
1128	Toward automatically drawn metabolic pathway atlas with peripheral node abstraction algorithm. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
1129	An Integrative Scoring Approach to Identify Transcriptional Regulations Controlling Lung Surfactant Homeostasis. , 2010, , .		0
1130	AtMetExpress Development: A Phytochemical Atlas of Arabidopsis Development. Plant Physiology, 2010, 152, 566-578.	2.3	161
1131	Functional genomics and networks: new approaches in the extraction of complex gene modules. Expert Review of Proteomics, 2010, 7, 55-63.	1.3	10
1132	Simulation and Analysis of the Network Model of the Quorum Sensing Process during Biofilm Creation. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
1133	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Journal of Computational Biology, 2010, 17, 443-457.	0.8	12
1134	Comparative Transcriptomic and Proteomic Profiling of Industrial Wine Yeast Strains. Applied and Environmental Microbiology, 2010, 76, 3911-3923.	1.4	43
1135	Flipping DNA to Generate and Regulate Microbial Consortia. Genetics, 2010, 184, 285-293.	1.2	6
1136	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. Molecular and Cellular Proteomics, 2010, 9, 1314-1323.	2.5	225
1137	Systematic Interpretation of Comutated Genes in Large-Scale Cancer Mutation Profiles. Molecular Cancer Therapeutics, 2010, 9, 2186-2195.	1.9	12
1138	Mass spectrometry-based proteomics in biomedical research: emerging technologies and future strategies. Expert Reviews in Molecular Medicine, 2010, 12, e30.	1.6	27
1139	Global approaches to study proteinâ€“protein interactions among viruses and hosts. Future Microbiology, 2010, 5, 289-301.	1.0	32
1140	Glioblastoma-Specific Protein Interaction Network Identifies PP1A and CSK21 as Connecting Molecules between Cell Cycleâ€“Associated Genes. Cancer Research, 2010, 70, 6437-6447.	0.4	27
1141	The Early Whole-Blood Transcriptional Signature of Dengue Virus and Features Associated with Progression to Dengue Shock Syndrome in Vietnamese Children and Young Adults. Journal of Virology, 2010, 84, 12982-12994.	1.5	108
1142	Software Tools for Systems Biology. , 2010, , 289-314.		7
1143	Synthetic Biology: Tools to Design, Build, and Optimize Cellular Processes. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-12.	3.0	54
1144	IQGAP1 and vimentin are key regulator genes in naturally occurring hepatotumorigenesis induced by oxidative stress. Carcinogenesis, 2010, 31, 504-511.	1.3	25
1145	PhenoHM: humanâ€“mouse comparative phenomeâ€“genome server. Nucleic Acids Research, 2010, 38, W165-W174.	6.5	19
1146	Network-based comparison of temporal gene expression patterns. Bioinformatics, 2010, 26, 2944-2951.	1.8	8

#	ARTICLE	IF	CITATIONS
1147	PhosphoGRID: a database of experimentally verified in vivo protein phosphorylation sites from the budding yeast <i>Saccharomyces cerevisiae</i> . Database: the Journal of Biological Databases and Curation, 2010, 2010, bap026-bap026.	1.4	90
1148	How to Understand the Cell by Breaking It: Network Analysis of Gene Perturbation Screens. PLoS Computational Biology, 2010, 6, e1000655.	1.5	51
1149	Network-Based Elucidation of Human Disease Similarities Reveals Common Functional Modules Enriched for Pluripotent Drug Targets. PLoS Computational Biology, 2010, 6, e1000662.	1.5	297
1150	Learning "cegraph-mer" Motifs that Predict Gene Expression Trajectories in Development. PLoS Computational Biology, 2010, 6, e1000761.	1.5	6
1151	Graph-Based Analysis of the Metabolic Exchanges between Two Co-Resident Intracellular Symbionts, <i>Baumannia cicadellinicola</i> and <i>Sulcia muelleri</i> , with Their Insect Host, <i>Homalodisca coagulata</i> . PLoS Computational Biology, 2010, 6, e1000904.	1.5	34
1152	Modeling Conformational Ensembles of Slow Functional Motions in Pin1-WW. PLoS Computational Biology, 2010, 6, e1001015.	1.5	76
1153	FuncBase : a resource for quantitative gene function annotation. Bioinformatics, 2010, 26, 1806-1807.	1.8	14
1154	Pivotal Advance: Avian colony-stimulating factor 1 ( <i>CSF-1</i> ), interleukin-34 ( <i>IL-34</i> ), and <i>CSF-1</i> receptor genes and gene products. Journal of Leukocyte Biology, 2010, 87, 753-764.	1.5	173
1155	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. PLoS Computational Biology, 2010, 6, e1001001.	1.5	23
1156	Prediction of human functional genetic networks from heterogeneous data using RVM-based ensemble learning. Bioinformatics, 2010, 26, 807-813.	1.8	28
1157	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. PLoS Biology, 2010, 8, e1000480.	2.6	142
1158	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. PLoS Computational Biology, 2010, 6, e1000730.	1.5	140
1159	Practical Application of Toxicogenomics for Profiling Toxicant-Induced Biological Perturbations. International Journal of Molecular Sciences, 2010, 11, 3397-3412.	1.8	21
1160	Functional Toxicogenomics: Mechanism-Centered Toxicology. International Journal of Molecular Sciences, 2010, 11, 4796-4813.	1.8	49
1161	Ontology- and graph-based similarity assessment in biological networks. Bioinformatics, 2010, 26, 2643-2644.	1.8	17
1162	A Scalable Approach for Discovering Conserved Active Subnetworks across Species. PLoS Computational Biology, 2010, 6, e1001028.	1.5	17
1163	Large-Scale Analysis of Network Bistability for Human Cancers. PLoS Computational Biology, 2010, 6, e1000851.	1.5	69
1164	Feedback between p21 and reactive oxygen production is necessary for cell senescence. Molecular Systems Biology, 2010, 6, 347.	3.2	754

#	ARTICLE	IF	CITATIONS
1165	A cytoscape based framework for efficient sub-graph isomorphic protein-protein interaction motif lookup. , 2010, , .		1
1166	A Global Census of Fission Yeast Deubiquitinating Enzyme Localization and Interaction Networks Reveals Distinct Compartmentalization Profiles and Overlapping Functions in Endocytosis and Polarity. PLoS Biology, 2010, 8, e1000471.	2.6	77
1167	Patterns of HIV-1 Protein Interaction Identify Perturbed Host-Cellular Subsystems. PLoS Computational Biology, 2010, 6, e1000863.	1.5	57
1168	Comparative Pathogenesis and Systems Biology for Biodefense Virus Vaccine Development. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-11.	3.0	10
1169	Proteinâ€“Protein Interactions Essentials: Key Concepts to Building and Analyzing Interactome Networks. PLoS Computational Biology, 2010, 6, e1000807.	1.5	496
1170	SBRML: a markup language for associating systems biology data with models. Bioinformatics, 2010, 26, 932-938.	1.8	54
1171	Constructing metabolic networks based on bipartite model within MATLAB. , 2010, , .		0
1172	Screening Chromosomal Aberrations by Array Comparative Genomic Hybridization in 80 Patients with Congenital Hypothyroidism and Thyroid Dysgenesis. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3446-3452.	1.8	28
1173	Construction of a Large Extracellular Protein Interaction Network and Its Resolution by Spatiotemporal Expression Profiling. Molecular and Cellular Proteomics, 2010, 9, 2654-2665.	2.5	37
1174	The IntAct molecular interaction database in 2010. Nucleic Acids Research, 2010, 38, D525-D531.	6.5	574
1175	Inference of RhoGAP/GTPase regulation using single-cell morphological data from a combinatorial RNAi screen. Genome Research, 2010, 20, 372-380.	2.4	25
1176	VirtualPlant: A Software Platform to Support Systems Biology Research Â Â. Plant Physiology, 2010, 152, 500-515.	2.3	254
1177	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis Â Â. Plant Physiology, 2010, 153, 642-651.	2.3	96
1178	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks Â Â. Plant Physiology, 2010, 154, 13-24.	2.3	93
1179	Emergence and Evolution of Modern Molecular Functions Inferred from Phylogenomic Analysis of Ontological Data. Molecular Biology and Evolution, 2010, 27, 1710-1733.	3.5	43
1180	PerturbationAnalyzer: a tool for investigating the effects of concentration perturbation on protein interaction networks. Bioinformatics, 2010, 26, 275-277.	1.8	15
1181	A novel cancer classifier based on differentially expressed gene network. , 2010, , .		0
1182	Networks Inferred from Biochemical Data Reveal Profound Differences in Toll-like Receptor and Inflammatory Signaling between Normal and Transformed Hepatocytes. Molecular and Cellular Proteomics, 2010, 9, 1849-1865.	2.5	95

#	ARTICLE	IF	CITATIONS
1183	Genes and Pathways Contributing to Obesity. <i>Progress in Molecular Biology and Translational Science</i> , 2010, 94, 9-38.	0.9	3
1184	Computational modeling of the effects of oxidative stress on the IGF-1 signaling pathway in human articular chondrocytes. , 2010, , .		0
1185	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010, 20, 1689-1699.	2.4	309
1186	Advanced querying interface for biochemical network databases. , 2010, , .		0
1187	Simple sequence-based kernels do not predict protein-protein interactions. <i>Bioinformatics</i> , 2010, 26, 2610-2614.	1.8	98
1188	Conservation and canalization of gene expression during angiosperm diversification accompany the origin and evolution of the flower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22570-22575.	3.3	68
1189	Microarray analysis reveals the inhibition of nuclear factor-kappa B signaling by aristolochic acid in normal human kidney (HK-2) cells. <i>Acta Pharmacologica Sinica</i> , 2010, 31, 227-236.	2.8	28
1190	BioMet Toolbox: genome-wide analysis of metabolism. <i>Nucleic Acids Research</i> , 2010, 38, W144-W149.	6.5	91
1191	PINT: Pathways INtegration Tool. <i>Nucleic Acids Research</i> , 2010, 38, W124-W131.	6.5	8
1192	Direct Transfer of $\alpha$ -Synuclein from Neuron to Astroglia Causes Inflammatory Responses in Synucleinopathies. <i>Journal of Biological Chemistry</i> , 2010, 285, 9262-9272.	1.6	704
1193	Joint Genome-Wide Profiling of miRNA and mRNA Expression in Alzheimer's Disease Cortex Reveals Altered miRNA Regulation. <i>PLoS ONE</i> , 2010, 5, e8898.	1.1	320
1194	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. <i>Journal of Proteome Research</i> , 2010, 9, 3280-3289.	1.8	253
1195	Systems biology of embryogenesis. <i>Reproduction, Fertility and Development</i> , 2010, 22, 98.	0.1	10
1196	Computational Challenges in Systems Biology. , 2010, , 175-223.		3
1198	An in silico analysis of microRNAs: Mining the miRNAome. <i>Molecular BioSystems</i> , 2010, 6, 1853.	2.9	42
1199	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
1200	Long-term genome-wide blood RNA expression profiles yield novel molecular response candidates for IFN- $\beta$ treatment in relapsing remitting MS. <i>Pharmacogenomics</i> , 2010, 11, 147-161.	0.6	42
1201	Synthetic Genetic Array (SGA) Analysis in <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>Methods in Enzymology</i> , 2010, 470, 145-179.	0.4	175



#	ARTICLE	IF	CITATIONS
1202	Microvesicles Derived from Adult Human Bone Marrow and Tissue Specific Mesenchymal Stem Cells Shuttle Selected Pattern of miRNAs. PLoS ONE, 2010, 5, e11803.	1.1	554
1203	Evolution of the 12-Spanner Drug:H+ Antiporter DHA1 Family in Hemiascomycetous Yeasts. OMICS A Journal of Integrative Biology, 2010, 14, 701-710.	1.0	20
1207	Analysis of the Bacterial Luciferase Mobile Loop by Replica-Exchange Molecular Dynamics. Biophysical Journal, 2010, 99, 4012-4019.	0.2	20
1208	Systems biology visualization tools for drug target discovery. Expert Opinion on Drug Discovery, 2010, 5, 425-439.	2.5	8
1209	Comparative Functional Genomics of Stress Responses in Yeasts. OMICS A Journal of Integrative Biology, 2010, 14, 501-515.	1.0	12
1210	MicroRNA-Regulated Protein-Protein Interaction Networks: How Could They Help in Searching for Pro-Longevity Targets?. Rejuvenation Research, 2010, 13, 373-377.	0.9	30
1211	Robust TLR4-induced gene expression patterns are not an accurate indicator of human immunity. Journal of Translational Medicine, 2010, 8, 6.	1.8	4
1212	Structural similarity-based predictions of protein interactions between HIV-1 and Homo sapiens. Virology Journal, 2010, 7, 82.	1.4	70
1213	Chaperone expression profiles correlate with distinct physiological states of Plasmodium falciparum in malaria patients. Malaria Journal, 2010, 9, 236.	0.8	43
1214	High-Throughput Biological Data Analysis. IEEE Control Systems, 2010, 30, 81-100.	1.0	2
1215	Hub Gene Selection Methods for the Reconstruction of Transcription Networks. Lecture Notes in Computer Science, 2010, , 506-521.	1.0	2
1216	Quantitative Analysis of HGF and EGF-Dependent Phosphotyrosine Signaling Networks. Journal of Proteome Research, 2010, 9, 2734-2742.	1.8	48
1217	Quantitative Proteomics Reveals a "Poised Quiescence" Cellular State after Triggering the DNA Replication Origin Activation Checkpoint. Journal of Proteome Research, 2010, 9, 5445-5460.	1.8	6
1218	Immunomodulatory effect of 5-azacytidine (5-azaC): potential role in the transplantation setting. Blood, 2010, 115, 107-121.	0.6	201
1219	Gene Network Visualization and Quantitative Synteny Analysis of more than 300 Marine T4-Like Phage Scaffolds from the GOS Metagenome. Molecular Biology and Evolution, 2010, 27, 1935-1944.	3.5	25
1220	Molecular Scaffolds with High Propensity to Form Multi-Target Activity Cliffs. Journal of Chemical Information and Modeling, 2010, 50, 500-510.	2.5	45
1221	Network-based modeling for analyzing the human skin microbiome. , 2010, , .		1
1222	Gene Association Networks from Microarray Data Using a Regularized Estimation of Partial Correlation Based on PLS Regression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 251-262.	1.9	31



#	ARTICLE	IF	CITATIONS
1223	Topology-Free Querying of Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2010, 17, 237-252.	0.8	99
1224	Polypharmacology Directed Compound Data Mining: Identification of Promiscuous Chemotypes with Different Activity Profiles and Comparison to Approved Drugs. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 2112-2118.	2.5	56
1225	Changes in Protein Expression Profiles between a Low Phytic Acid Rice ( <i>Oryza sativa</i> L. Ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T Agricultural and Food Chemistry, 2010, 58, 6912-6922.	2.4	16
1226	Association weight matrix for the genetic dissection of puberty in beef cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13642-13647.	3.3	127
1227	Proteomics and Transcriptomics Investigation on <i>longissimus</i> Muscles in Large White and Casertana Pig Breeds. <i>Journal of Proteome Research</i> , 2010, 9, 6450-6466.	1.8	58
1228	Molecular networks for the study of TCM Pharmacology. <i>Briefings in Bioinformatics</i> , 2010, 11, 417-430.	3.2	186
1229	Phospholipid Transfer Protein in Human Plasma Associates with Proteins Linked to Immunity and Inflammation. <i>Biochemistry</i> , 2010, 49, 7314-7322.	1.2	47
1230	<i>Disrupted-in-schizophrenia 1</i> (DISC1) plays essential roles in mitochondria in collaboration with Mitofilin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17785-17790.	3.3	133
1231	BioRuby: bioinformatics software for the Ruby programming language. <i>Bioinformatics</i> , 2010, 26, 2617-2619.	1.8	151
1232	Cytoscape Web: an interactive web-based network browser. <i>Bioinformatics</i> , 2010, 26, 2347-2348.	1.8	648
1233	PathwayAccess: CellDesigner plugins for pathway databases. <i>Bioinformatics</i> , 2010, 26, 2345-2346.	1.8	14
1234	Databases of Protein-Protein Interactions and Complexes. <i>Methods in Molecular Biology</i> , 2010, 609, 145-159.	0.4	20
1235	Geometric Similarities of Protein-Protein Interfaces at Atomic Resolution Are Only Observed within Homologous Families: An Exhaustive Structural Classification Study. <i>Journal of Molecular Biology</i> , 2010, 399, 526-540.	2.0	17
1236	Global Network Analysis of Lipid-Raft-Related Proteins Reveals Their Centrality in the Network and Their Roles in Multiple Biological Processes. <i>Journal of Molecular Biology</i> , 2010, 402, 761-773.	2.0	6
1237	Disease progression and solid tumor survival: A transcriptome decoherence model. <i>Molecular and Cellular Probes</i> , 2010, 24, 53-60.	0.9	5
1238	Prediction of regulatory networks in mouse abdominal wall. <i>Gene</i> , 2010, 469, 1-8.	1.0	5
1239	Expression of cytokine genes in the aorta is altered by the deficiency in MCP-1: Effect of a high-fat, high-cholesterol diet. <i>Cytokine</i> , 2010, 50, 121-128.	1.4	20
1240	Transcriptional Control of a Plant Stem Cell Niche. <i>Developmental Cell</i> , 2010, 18, 841-853.	3.1	221

#	ARTICLE	IF	CITATIONS
1241	A Combined Ex Vivo and In Vivo RNAi Screen for Notch Regulators in Drosophila Reveals an Extensive Notch Interaction Network. <i>Developmental Cell</i> , 2010, 18, 862-876.	3.1	139
1242	Identification of modules in <i>Aspergillus niger</i> by gene co-expression network analysis. <i>Fungal Genetics and Biology</i> , 2010, 47, 539-550.	0.9	15
1243	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	13.5	789
1244	An Alternative Splicing Network Links Cell-Cycle Control to Apoptosis. <i>Cell</i> , 2010, 142, 625-636.	13.5	273
1245	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650.	13.5	200
1246	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.	13.5	123
1247	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	1,564
1248	Carbon dioxide sequestration by carbon nanotubes: Application of graph theoretical approach. <i>Computational Materials Science</i> , 2010, 48, 402-408.	1.4	3
1249	Lab-Specific Gene Expression Signatures in Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 258-262.	5.2	195
1250	Investigation of low-dose ritonavir on human peripheral blood mononuclear cells using gene expression whole genome microarrays. <i>Genomics</i> , 2010, 96, 57-65.	1.3	8
1251	Gene set-level network analysis using a toxicogenomics database. <i>Genomics</i> , 2010, 96, 39-49.	1.3	14
1252	Systematic Analysis of Public Domain Compound Potency Data Identifies Selective Molecular Scaffolds across Druggable Target Families. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 752-758.	2.9	43
1253	Analysis of protein complexes through model-based biclustering of label-free quantitative AP-MS data. <i>Molecular Systems Biology</i> , 2010, 6, 385.	3.2	33
1254	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. <i>Science Signaling</i> , 2010, 3, rs3.	1.6	245
1255	Dynamic cross-talk analysis among TNF-R, TLR-4 and IL-1R signalings in TNF $\alpha$ -induced inflammatory responses. <i>BMC Medical Genomics</i> , 2010, 3, 19.	0.7	32
1256	A Decade of Systems Biology. <i>Annual Review of Cell and Developmental Biology</i> , 2010, 26, 721-744.	4.0	277
1257	Functional Modules in Protein-Protein Interaction Networks. <i>Systems Biology</i> , 2010, , 353-369.	0.1	0
1258	Interaction with Diurnal and Circadian Regulation Results in Dynamic Metabolic and Transcriptional Changes during Cold Acclimation in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2010, 5, e14101.	1.1	146

#	ARTICLE	IF	CITATIONS
1259	The Profile of Mitochondrial Proteins and Their Phosphorylation Signaling Network in INS-1 $\beta$ Cells. <i>Journal of Proteome Research</i> , 2010, 9, 2898-2908.	1.8	23
1260	Visual Integration of Quantitative Proteomic Data, Pathways, and Protein Interactions. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2010, 16, 609-620.	2.9	15
1261	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2010, 11, 40-79.	3.2	551
1262	Global Protein-Protein Interaction Network in the Human Pathogen <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Proteome Research</i> , 2010, 9, 6665-6677.	1.8	104
1263	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> . <i>Molecular Systems Biology</i> , 2010, 6, 397.	3.2	315
1264	Multilocus haplotypes reveal variable levels of diversity and population structure of <i>Plasmodium falciparum</i> in Papua New Guinea, a region of intense perennial transmission. <i>Malaria Journal</i> , 2010, 9, 336.	0.8	79
1265	Novel genes exhibit distinct patterns of function acquisition and network integration. <i>Genome Biology</i> , 2010, 11, R127.	13.9	71
1266	Constructing a fish metabolic network model. <i>Genome Biology</i> , 2010, 11, R115.	13.9	47
1267	A human functional protein interaction network and its application to cancer data analysis. <i>Genome Biology</i> , 2010, 11, R53.	13.9	591
1268	Characterizing regulatory path motifs in integrated networks using perturbational data. <i>Genome Biology</i> , 2010, 11, R32.	13.9	10
1269	CDCOCA: a statistical method to define complexity dependent co-occurring chromosomal aberrations. <i>Genome Biology</i> , 2010, 11, P23.	13.9	2
1270	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	13.9	456
1271	Proteomic Profile Regulated by the Anticancer Peptide CIGB-300 in Non-Small Cell Lung Cancer (NSCLC) Cells. <i>Journal of Proteome Research</i> , 2010, 9, 5473-5483.	1.8	26
1272	SARANEA: A Freely Available Program To Mine Structure-Activity and Structure-Selectivity Relationship Information in Compound Data Sets. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 68-78.	2.5	77
1273	Visualizing large-scale RDF data using Subsets, Summaries, and Sampling in Oracle. , 2010, , .		7
1274	BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 1129-1130.	1.8	215
1275	Global assessment of scaffold hopping potential for current pharmaceutical targets. <i>MedChemComm</i> , 2010, 1, 339-344.	3.5	25
1276	Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. <i>Molecular BioSystems</i> , 2010, 6, 1475.	2.9	12

#	ARTICLE	IF	CITATIONS
1277	Gene-centered regulatory networks. Briefings in Functional Genomics, 2010, 9, 4-12.	1.3	40
1278	Proteomic Profiling of Early Life Stages of European Grayling (<i>Thymallus thymallus</i>). Journal of Proteome Research, 2010, 9, 4790-4800.	1.8	9
1279	PBSK browser: Navigate biological pathways of PSI-MI, BioPAX, SBML and KGML formats. , 2010, , .		0
1280	Self-Organizing Fuzzy Graphs for Structure-Based Comparison of Protein Pockets. Journal of Proteome Research, 2010, 9, 6498-6510.	1.8	29
1281	Investigating microRNA-transcription factor mediated regulatory network in glioblastoma. , 2010, , .		1
1282	HepatoNet1: a comprehensive metabolic reconstruction of the human hepatocyte for the analysis of liver physiology. Molecular Systems Biology, 2010, 6, 411.	3.2	248
1283	Comparison of Co-temporal Modeling Algorithms on Sparse Experimental Time Series Data Sets. , 2010, 2010, 79-85.		2
1284	Interferonâ€inducible factor 16 is a novel modulator of glucocorticoid action. FASEB Journal, 2010, 24, 1700-1713.	0.2	13
1285	Isobaric labeling and tandem mass spectrometry: A novel approach for profiling and quantifying proteins differentially expressed in amniotic fluid in preterm labor with and without intra-amniotic infection/inflammation. Journal of Maternal-Fetal and Neonatal Medicine, 2010, 23, 261-280.	0.7	74
1286	Prediction of Protein-Protein Interaction Using Distance Frequency of Amino Acids Grouped with their Physicochemical Properties. , 2011, , .		2
1287	Secretory pathway genes assessed by high-throughput microscopy and synthetic genetic array analysis. Molecular BioSystems, 2011, 7, 2589.	2.9	39
1288	Obvious: A meta-toolkit to encapsulate information visualization toolkits &#x2014; One toolkit to bind them all. , 2011, , .		10
1289	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Research, 2011, 39, D561-D568.	6.5	3,014
1290	NAViGaTOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. Internet Mathematics, 2011, 7, 314-347.	0.7	13
1291	Dupuytren's: a systems biology disease. Arthritis Research and Therapy, 2011, 13, 238.	1.6	36
1292	A novel integrative network approach to understand the interplay between cardiovascular disease and other complex disorders. Molecular BioSystems, 2011, 7, 2205.	2.9	12
1293	G-PARE: A visual analytic tool for comparative analysis of uncertain graphs. , 2011, , .		13
1294	A predicted proteinâ€protein interaction network of the filamentous fungus Neurospora crassa. Molecular BioSystems, 2011, 7, 2278.	2.9	29

#	ARTICLE	IF	CITATIONS
1295	Rule-based modelling of iron homeostasis in tuberculosis. <i>Molecular BioSystems</i> , 2011, 7, 2750.	2.9	13
1296	Automated model-driven generation of software components for the simulation of epithelial tissues. , 2011, , .		0
1297	Identification and Modeling of Genes with Diurnal Oscillations from Microarray Time Series Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 108-121.	1.9	7
1298	RuleBender: Integrated visualization for biochemical rule-based modeling. , 2011, , .		4
1299	Visual exploration of microbial populations. , 2011, , .		6
1300	Large scale identification of protein-protein interaction of <i>Aspergillus terreus</i> NIH2624 using computational approaches. , 2011, , .		0
1301	The protein folding network indicates that the ultrafast folding mutant of villin headpiece subdomain has a deeper folding funnel. <i>Journal of Chemical Physics</i> , 2011, 134, 205104.	1.2	13
1302	EVEVis: A multi-scale visualization system for dense evolutionary data. , 2011, , .		4
1303	Characterizing the Diversity and Biological Relevance of the MLPCN Assay Manifold and Screening Set. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 1205-1215.	2.5	12
1304	Mapping the Subcellular Protein Distribution in Three Human Cell Lines. <i>Journal of Proteome Research</i> , 2011, 10, 3766-3777.	1.8	37
1305	FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6680-6685.	3.3	325
1306	Using the Human Plasma PeptideAtlas to Study Human Plasma Proteins. <i>Methods in Molecular Biology</i> , 2011, 728, 349-374.	0.4	22
1307	Community Structures of Fecal Bacteria in Cattle from Different Animal Feeding Operations. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2992-3001.	1.4	342
1308	NMR Analysis of a Stress Response Metabolic Signaling Network. <i>Journal of Proteome Research</i> , 2011, 10, 3743-3754.	1.8	46
1309	Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. <i>Molecular Systems Biology</i> , 2011, 7, 486.	3.2	80
1310	Combining Horizontal and Vertical Substructure Relationships in Scaffold Hierarchies for Activity Prediction. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 248-257.	2.5	13
1311	A Data Set of Human Endogenous Protein Ubiquitination Sites. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002089.	2.5	76
1312	Proteomic Analysis of Membrane Proteins from <i>Streptococcus pneumoniae</i> with Multiple Separation Methods Plus High Accuracy Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 683-694.	1.0	16

#	ARTICLE	IF	CITATIONS
1313	Enzymatic Deamination of the Epigenetic Base <i>N</i> -6-Methyladenine. <i>Journal of the American Chemical Society</i> , 2011, 133, 2080-2083.	6.6	24
1314	A Face in the Crowd: Recognizing Peptides Through Database Search. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R111.009522.	2.5	147
1315	G-DOC: A Systems Medicine Platform for Personalized Oncology. <i>Neoplasia</i> , 2011, 13, 771-783.	2.3	58
1316	Genome-Wide Analysis of MuDR-Related Transposable Elements Insertion Population in Maize. <i>Acta Agronomica Sinica</i> , 2011, 37, 772-777.	0.3	2
1317	Molecular Simulation Uncovers the Conformational Space of the $\hat{\nu}$ Cro Dimer in Solution. <i>Biophysical Journal</i> , 2011, 101, 2516-2524.	0.2	12
1318	PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274
1319	The Footprints of Gut Microbiota in Mammalian Co-Metabolism. <i>Journal of Proteome Research</i> , 2011, 10, 5512-5522.	1.8	268
1320	Enhanced Y1H assays for Arabidopsis. <i>Nature Methods</i> , 2011, 8, 1053-1055.	9.0	115
1321	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. <i>Molecular Systems Biology</i> , 2011, 7, 551.	3.2	33
1322	Topographical Continuity of Bacterial Populations in the Healthy Human Respiratory Tract. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 957-963.	2.5	912
1324	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	13.9	665
1325	Phosphoproteome profile of human lung cancer cell line A549. <i>Molecular BioSystems</i> , 2011, 7, 472-479.	2.9	13
1326	Computational tools for polypharmacology and repurposing. <i>Future Medicinal Chemistry</i> , 2011, 3, 961-968.	1.1	66
1327	Network Models of TEM $\beta$ -Lactamase Mutations Coevolving under Antibiotic Selection Show Modular Structure and Anticipate Evolutionary Trajectories. <i>PLoS Computational Biology</i> , 2011, 7, e1002184.	1.5	36
1328	MatrixDB, the extracellular matrix interaction database. <i>Nucleic Acids Research</i> , 2011, 39, D235-D240.	6.5	117
1329	A refinement and coarsening indicator algorithm for finding sparse solutions of inverse problems. <i>Inverse Problems and Imaging</i> , 2011, 5, 391-406.	0.6	3
1330	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. <i>Molecular BioSystems</i> , 2011, 7, 667-676.	2.9	39
1331	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712

#	ARTICLE	IF	CITATIONS
1332	Integrating Omics Data for Signaling Pathways, Interactome Reconstruction, and Functional Analysis. <i>Methods in Molecular Biology</i> , 2011, 719, 415-433.	0.4	24
1334	Constructing gene regulatory networks for long term photosynthetic light acclimation in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2011, 12, 335.	1.2	18
1335	gViz, a novel tool for the visualization of co-expression networks. <i>BMC Research Notes</i> , 2011, 4, 452.	0.6	9
1336	Displaying Chemical Information on a Biological Network Using Cytoscape. <i>Methods in Molecular Biology</i> , 2011, 781, 363-376.	0.4	7
1337	Yeast Protein-Protein Interaction Assays and Screens. <i>Methods in Molecular Biology</i> , 2011, 754, 145-165.	0.4	56
1338	MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011, 39, 825-836.	6.5	245
1339	Discovery of a Cytokinin Deaminase. <i>ACS Chemical Biology</i> , 2011, 6, 1036-1040.	1.6	15
1340	Mass Spectrometry-Driven Proteomics: An Introduction. <i>Methods in Molecular Biology</i> , 2011, 753, 1-27.	0.4	6
1341	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy. <i>Genome Biology</i> , 2011, 12, R61.	13.9	49
1342	A quantitative literature-curated gold standard for kinase-substrate pairs. <i>Genome Biology</i> , 2011, 12, R39.	13.9	56
1343	Bringing order to protein disorder through comparative genomics and genetic interactions. <i>Genome Biology</i> , 2011, 12, R14.	13.9	129
1344	Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .	13.9	89
1345	Are clinical genomes already becoming semi-routine for patient care?. <i>Genome Biology</i> , 2011, 12, .	13.9	0
1346	ScaffViz: visualizing metagenome assemblies. <i>Genome Biology</i> , 2011, 12, .	13.9	0
1347	An unusual suspect: an uncommon human-specific synonymous coding variant within the UGT1A6 gene explains a GWAS signal and protects against bladder cancer. <i>Genome Biology</i> , 2011, 12, .	3.8	0
1348	Network analysis of skin tumor progression identifies a rewired genetic architecture affecting inflammation and tumor susceptibility. <i>Genome Biology</i> , 2011, 12, R5.	13.9	41
1349	Gene-Centered Regulatory Network Mapping. <i>Methods in Cell Biology</i> , 2011, 106, 271-288.	0.5	19
1351	Relating protein adduction to gene expression changes: a systems approach. <i>Molecular BioSystems</i> , 2011, 7, 2118.	2.9	28



#	ARTICLE	IF	CITATIONS
1352	Gene expression profiling of the androgen receptor antagonists flutamide and vinclozolin in zebrafish ( <i>Danio rerio</i> ) gonads. <i>Aquatic Toxicology</i> , 2011, 101, 447-458.	1.9	50
1353	Shift in chicken intestinal gene association networks after infection with <i>Salmonella</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 339-347.	0.4	9
1354	Responses of threespine stickleback ( <i>Gasterosteus aculeatus</i> , L) transcriptome to hypoxia. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 370-381.	0.4	31
1355	Phenotypic Landscape of a Bacterial Cell. <i>Cell</i> , 2011, 144, 143-156.	13.5	623
1356	Mapping the NPHP-JBTS-MKS Protein Network Reveals Ciliopathy Disease Genes and Pathways. <i>Cell</i> , 2011, 145, 513-528.	13.5	531
1357	Genome-Wide RNAi Screens Identify Genes Required for Ricin and PE Intoxications. <i>Developmental Cell</i> , 2011, 21, 231-244.	3.1	61
1358	Networks in <i>Caenorhabditis elegans</i> . <i>Current Opinion in Genetics and Development</i> , 2011, 21, 787-798.	1.5	13
1359	Synthetic biosensing systems. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 310-319.	1.2	21
1360	Expression of HOXB genes is significantly different in acute myeloid leukemia with a partial tandem duplication of MLL vs. a MLL translocation: a cross-laboratory study. <i>Cancer Genetics</i> , 2011, 204, 252-259.	0.2	12
1361	Sex-Biased Protein Expression in Threespine Stickleback, <i>Gasterosteus aculeatus</i> . <i>Journal of Proteome Research</i> , 2011, 10, 4033-4040.	1.8	13
1362	Target Family-Directed Exploration of Scaffolds with Different SAR Profiles. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 3138-3148.	2.5	9
1363	Atrial Fibrillation. <i>Circulation</i> , 2011, 124, 1982-1993.	1.6	225
1364	Molecular Evolution and Network-Level Analysis of the N-Glycosylation Metabolic Pathway Across Primates. <i>Molecular Biology and Evolution</i> , 2011, 28, 813-823.	3.5	30
1365	Assembling global maps of cellular function through integrative analysis of physical and genetic networks. <i>Nature Protocols</i> , 2011, 6, 1308-1323.	5.5	23
1366	Spliceosomal RNA infrastructure: The Network of Splicing Components and Their Regulation by miRNAs. <i>Advances in Experimental Medicine and Biology</i> , 2011, 722, 86-102.	0.8	3
1367	A Comprehensive Genomic Binding Map of Gene and Chromatin Regulatory Proteins in <i>Saccharomyces</i> . <i>Molecular Cell</i> , 2011, 41, 480-492.	4.5	269
1368	The Specificity and Topology of Chromatin Interaction Pathways in Yeast. <i>Molecular Cell</i> , 2011, 42, 536-549.	4.5	225
1369	Functional analysis of beef tenderness. <i>Journal of Proteomics</i> , 2011, 75, 352-365.	1.2	106



#	ARTICLE	IF	CITATIONS
1370	TCM grammar systems: An approach to aid the interpretation of the molecular interactions in Chinese herbal medicine. <i>Journal of Ethnopharmacology</i> , 2011, 137, 77-84.	2.0	18
1371	Traditional phytotherapy remedies used in Southern Rwanda for the treatment of liver diseases. <i>Journal of Ethnopharmacology</i> , 2011, 138, 415-431.	2.0	56
1372	iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2011, 405, 1295-1310.	2.0	56
1373	Comprehensive Gene Expression Analysis of Human Embryonic Stem Cells during Differentiation into Neural Cells. <i>PLoS ONE</i> , 2011, 6, e22856.	1.1	72
1374	Cross-species Functionome analysis identifies proteins associated with DNA repair, translation and aerobic respiration as conserved modulators of UV-toxicity. <i>Genomics</i> , 2011, 97, 133-147.	1.3	6
1375	Identification of candidate genes in Arabidopsis and Populus cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. <i>Plant Science</i> , 2011, 181, 675-687.	1.7	44
1376	Computational Analysis of Drought Stress-Associated miRNAs and miRNA Co-Regulation Network in <i>Physcomitrella patens</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 37-44.	3.0	26
1377	Cytoscape: Software for Visualization and Analysis of Biological Networks. <i>Methods in Molecular Biology</i> , 2011, 696, 291-303.	0.4	1,068
1378	Application of systems biology approach identifies and validates GRB2 as a risk gene for schizophrenia in the Irish Case Control Study of Schizophrenia (ICCS) sample. <i>Schizophrenia Research</i> , 2011, 125, 201-208.	1.1	26
1379	Identification of 14q23 in human gastric cancer cells and its potency as a diagnostic and prognostic biomarker. <i>Proteomics</i> , 2011, 11, 2423-2439.	1.3	38
1380	Toxins and stress in fish: Proteomic analyses and response network. <i>Toxicon</i> , 2011, 57, 959-969.	0.8	33
1381	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. <i>Journal of Cell Biology</i> , 2011, 192, 615-629.	2.3	439
1382	Large scale microarray profiling and coexpression network analysis of CHO cells identifies transcriptional modules associated with growth and productivity. <i>Journal of Biotechnology</i> , 2011, 155, 350-359.	1.9	62
1383	Proteomics and Host-Pathogen Interactions. , 2011, , 263-303.		4
1384	Study of the Gene Expressions in Rheumatoid Arthritis Synovial Macrophages Using Network Analysis. <i>Journal of Rheumatic Diseases</i> , 2011, 18, 101.	0.4	0
1385	Identify potential chronic heart failure related transcription factors by network analysis. <i>African Journal of Microbiology Research</i> , 2011, 5, 3862-3869.	0.4	4
1386	3DScape: three dimensional visualization plug-in for Cytoscape. <i>Nature Precedings</i> , 2011, , .	0.1	2
1387	Topological Characterization of Protein-Protein Interaction Networks in Human and Mouse. <i>Nature Precedings</i> , 0, , .	0.1	1

#	ARTICLE	IF	CITATIONS
1388	The DNA-Damage Response to Ionizing Radiation in Human Lymphocytes. , 0, , .		0
1389	Data Retrieval and Visualization for Setting Research Priorities in Biomedical Research. , 2011, , .		0
1390	Cellular Automata Modeling of Biomolecular Networks. , 2011, , .		0
1391	Crosstalk between viruses and PML nuclear bodies: a network-based approach. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 2910.	3.0	12
1392	Seeking colorectal carcinoma related genes based on regulation network. <i>African Journal of Pharmacy and Pharmacology</i> , 2011, 5, 1467-1474.	0.2	0
1393	Grand Challenge: Accelerating Discovery through Technology Development. <i>Frontiers in Plant Science</i> , 2011, 2, 41.	1.7	3
1394	Functional Genomic and Proteomic Analysis Reveals Disruption of Myelin-Related Genes and Translation in a Mouse Model of Early Life Neglect. <i>Frontiers in Psychiatry</i> , 2011, 2, 18.	1.3	52
1395	Systems-Biology Approaches to Discover Anti-Viral Effectors of the Human Innate Immune Response. <i>Viruses</i> , 2011, 3, 1112-1130.	1.5	9
1396	Defining the Role of Essential Genes in Human Disease. <i>PLoS ONE</i> , 2011, 6, e27368.	1.1	89
1397	Diurnal Rhythms Result in Significant Changes in the Cellular Protein Complement in the Cyanobacterium <i>Cyanothece</i> 51142. <i>PLoS ONE</i> , 2011, 6, e16680.	1.1	51
1398	The Light Responsive Transcriptome of the Zebrafish: Function and Regulation. <i>PLoS ONE</i> , 2011, 6, e17080.	1.1	90
1399	MicroRNA Genes Derived from Repetitive Elements and Expanded by Segmental Duplication Events in Mammalian Genomes. <i>PLoS ONE</i> , 2011, 6, e17666.	1.1	77
1400	A Protein Domain Co-Occurrence Network Approach for Predicting Protein Function and Inferring Species Phylogeny. <i>PLoS ONE</i> , 2011, 6, e17906.	1.1	30
1401	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. <i>PLoS ONE</i> , 2011, 6, e17911.	1.1	361
1402	Computational Integration of Homolog and Pathway Gene Module Expression Reveals General Stemness Signatures. <i>PLoS ONE</i> , 2011, 6, e18968.	1.1	9
1403	A Bioinformatics Classifier and Database for Heme-Copper Oxygen Reductases. <i>PLoS ONE</i> , 2011, 6, e19117.	1.1	60
1404	Mapping the Conformational Dynamics and Pathways of Spontaneous Steric Zipper Peptide Oligomerization. <i>PLoS ONE</i> , 2011, 6, e19129.	1.1	45
1405	Quantitative Proteomic and Interaction Network Analysis of Cisplatin Resistance in HeLa Cells. <i>PLoS ONE</i> , 2011, 6, e19892.	1.1	37

#	ARTICLE	IF	CITATIONS
1406	Unraveling Molecular Signatures of Immunostimulatory Adjuvants in the Female Genital Tract through Systems Biology. PLoS ONE, 2011, 6, e20448.	1.1	17
1407	Design, Synthesis and Characterization of a Highly Effective Inhibitor for Analog-Sensitive (as) Kinases. PLoS ONE, 2011, 6, e20789.	1.1	7
1408	Intuitive Visualization and Analysis of Multi-Omics Data and Application to Escherichia coli Carbon Metabolism. PLoS ONE, 2011, 6, e21318.	1.1	15
1409	Induction of Immune Mediators in Glioma and Prostate Cancer Cells by Non-Lethal Photodynamic Therapy. PLoS ONE, 2011, 6, e21834.	1.1	45
1410	Proteomic Analysis Shows Synthetic Oleanane Triterpenoid Binds to mTOR. PLoS ONE, 2011, 6, e22862.	1.1	88
1411	Global Analysis of Proline-Rich Tandem Repeat Proteins Reveals Broad Phylogenetic Diversity in Plant Secretomes. PLoS ONE, 2011, 6, e23167.	1.1	16
1412	Genome-Wide Functional Profiling Reveals Genes Required for Tolerance to Benzene Metabolites in Yeast. PLoS ONE, 2011, 6, e24205.	1.1	49
1413	MicroRNA Regulation and Tissue-Specific Protein Interaction Network. PLoS ONE, 2011, 6, e25394.	1.1	19
1414	An Integrated Transcriptomic and Meta-Analysis of Hepatoma Cells Reveals Factors That Influence Susceptibility to HCV Infection. PLoS ONE, 2011, 6, e25584.	1.1	18
1415	Gene Expression Analysis Reveals the Cell Cycle and Kinetochore Genes Participating in Ischemia Reperfusion Injury and Early Development in Kidney. PLoS ONE, 2011, 6, e25679.	1.1	11
1416	A New Methodology to Associate SNPs with Human Diseases According to Their Pathway Related Context. PLoS ONE, 2011, 6, e26277.	1.1	52
1417	Modeling the Mechanism of Action of a DGAT1 Inhibitor Using a Causal Reasoning Platform. PLoS ONE, 2011, 6, e27009.	1.1	24
1418	Gene Expression Profile Change and Associated Physiological and Pathological Effects in Mouse Liver Induced by Fasting and Refeeding. PLoS ONE, 2011, 6, e27553.	1.1	49
1419	BinTree Seeking: A Novel Approach to Mine Both Bi-Sparse and Cohesive Modules in Protein Interaction Networks. PLoS ONE, 2011, 6, e27646.	1.1	6
1420	Transcriptional Regulation of Ribosome Components Are Determined by Stress According to Cellular Compartments in Arabidopsis thaliana. PLoS ONE, 2011, 6, e28070.	1.1	75
1421	Heterozygous Yeast Deletion Collection Screens Reveal Essential Targets of Hsp90. PLoS ONE, 2011, 6, e28211.	1.1	26
1422	A Brain Region-Specific Predictive Gene Map for Autism Derived by Profiling a Reference Gene Set. PLoS ONE, 2011, 6, e28431.	1.1	20
1423	Hypergraph visualization and enrichment statistics: how the EGAN paradigm facilitates organic discovery from big data. Proceedings of SPIE, 2011, , .	0.8	5

#	ARTICLE	IF	CITATIONS
1424	Prediction of the Mechanisms of <i>Salvia Miltiorrhiza</i> against Atherosclerosis Using Text Mining and Network-Based Analysis. <i>Journal of Algorithms and Computational Technology</i> , 2011, 5, 139-144.	0.4	3
1425	Applying information visualization principles to biological network displays. <i>Proceedings of SPIE</i> , 2011, , .	0.8	4
1426	Lipid Mediator Profiling in Pulmonary Disease. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 1026-1052.	0.9	59
1427	Analyzing Protein-Protein Interaction Networks with Web Tools. <i>Current Bioinformatics</i> , 2011, 6, 389-397.	0.7	3
1428	HMGA1-dependent and independent 7SK RNA gene regulatory activity. <i>RNA Biology</i> , 2011, 8, 143-157.	1.5	19
1429	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. <i>Blood</i> , 2011, 118, 5604-5612.	0.6	58
1430	Computational identification of potential microRNA network biomarkers for the progression stages of gastric cancer. <i>International Journal of Data Mining and Bioinformatics</i> , 2011, 5, 519.	0.1	8
1431	Using cellular network diagrams to interpret large-scale datasets: past progress and future challenges. <i>Proceedings of SPIE</i> , 2011, , .	0.8	1
1434	Dissecting the retinoid-induced differentiation of F9 embryonal stem cells by integrative genomics. <i>Molecular Systems Biology</i> , 2011, 7, 538.	3.2	76
1435	Flexibility and utility of the cell cycle ontology. <i>Applied Ontology</i> , 2011, 6, 247-261.	1.0	2
1436	Proteome-wide systems analysis of a cellulosic biofuel-producing microbe. <i>Molecular Systems Biology</i> , 2011, 7, 461.	3.2	81
1437	Exploring and challenging the network of angiogenesis. <i>Scientific Reports</i> , 2011, 1, 61.	1.6	10
1438	Pathway Preserving Representation of Metabolic Networks. <i>Computer Graphics Forum</i> , 2011, 30, 1021-1030.	1.8	15
1439	Genomic expression profiles of blood and placenta reveal significant immune-related pathways and categories in Chinese women with gestational diabetes mellitus. <i>Diabetic Medicine</i> , 2011, 28, 237-246.	1.2	45
1440	Strong male/male competition allows for nonchoosy females: high levels of polygynandry in a territorial frog with paternal care. <i>Molecular Ecology</i> , 2011, 20, 1759-1771.	2.0	81
1441	Using a genetic network to parameterize a landscape resistance surface for fishers, <i>Martes pennanti</i> . <i>Molecular Ecology</i> , 2011, 20, 3978-3988.	2.0	56
1442	The effects of mitochondrial genotype on hypoxic survival and gene expression in a hybrid population of the killifish, <i>Fundulus heteroclitus</i> . <i>Molecular Ecology</i> , 2011, 20, 4503-4520.	2.0	27
1443	Interactions between flowering and senescence regulation and the influence of low temperature in <i>Arabidopsis</i> and crop plants. <i>Annals of Applied Biology</i> , 2011, 159, 320-338.	1.3	26

#	ARTICLE	IF	CITATIONS
1444	A review of ecological models for brown trout: towards a new demogenetic model. <i>Ecology of Freshwater Fish</i> , 2011, 20, 167-198.	0.7	33
1445	Isoform-specific Localization of the Deubiquitinase USP33 to the Golgi Apparatus. <i>Traffic</i> , 2011, 12, 1563-1574.	1.3	24
1446	Antagonistic interaction networks among bacteria from a cold soil environment. <i>FEMS Microbiology Ecology</i> , 2011, 78, 376-385.	1.3	20
1447	Activation of nuclear factor-kappa B signalling promotes cellular senescence. <i>Oncogene</i> , 2011, 30, 2356-2366.	2.6	158
1448	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. <i>European Journal of Human Genetics</i> , 2011, 19, 1082-1089.	1.4	39
1449	Peripheral blood gene expression profiles in metabolic syndrome, coronary artery disease and type 2 diabetes. <i>Genes and Immunity</i> , 2011, 12, 341-351.	2.2	55
1450	Analysis of human and animal fecal microbiota for microbial source tracking. <i>ISME Journal</i> , 2011, 5, 362-365.	4.4	87
1451	Coral-mucus-associated <i>Vibrio</i> integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. <i>ISME Journal</i> , 2011, 5, 962-972.	4.4	37
1452	Marine bacterial, archaeal and protistan association networks reveal ecological linkages. <i>ISME Journal</i> , 2011, 5, 1414-1425.	4.4	560
1453	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. <i>Nature Biotechnology</i> , 2011, 29, 505-511.	9.4	90
1454	Reconstruction of the regulatory network of <i>Lactobacillus plantarum</i> WCFS1 on basis of correlated gene expression and conserved regulatory motifs. <i>Microbial Biotechnology</i> , 2011, 4, 333-344.	2.0	26
1455	Drawing networks of rejection - a systems biological approach to the identification of candidate genes in heart transplantation. <i>Journal of Cellular and Molecular Medicine</i> , 2011, 15, 949-956.	1.6	10
1456	The effects of deoxynivalenol on gene expression in the murine thymus. <i>Toxicology and Applied Pharmacology</i> , 2011, 250, 299-311.	1.3	25
1457	Exposure of Jurkat cells to bis (tri-n-butyltin) oxide (TBTO) induces transcriptomics changes indicative for ER- and oxidative stress, T cell activation and apoptosis. <i>Toxicology and Applied Pharmacology</i> , 2011, 254, 311-322.	1.3	46
1458	Analyzing and visualizing residue networks of protein structures. <i>Trends in Biochemical Sciences</i> , 2011, 36, 179-182.	3.7	244
1459	<i>Plasmodium falciparum</i> enolase complements yeast enolase functions and associates with the parasite food vacuole. <i>Molecular and Biochemical Parasitology</i> , 2011, 179, 8-17.	0.5	12
1460	Predicting interactions between T cell receptors and MHC-peptide complexes. <i>Molecular Immunology</i> , 2011, 48, 553-562.	1.0	14
1461	Proteomic profiling of the human T-cell nucleolus. <i>Molecular Immunology</i> , 2011, 49, 441-452.	1.0	47

#	ARTICLE	IF	CITATIONS
1462	Chemical class-specific gene expression changes in the zebrafish embryo after exposure to glycol ether alkoxy acids and 1,2,4-triazole antifungals. <i>Reproductive Toxicology</i> , 2011, 32, 245-252.	1.3	46
1463	Preconceptional paternal glycidamide exposure affects embryonic gene expression: Single embryo gene expression study following in vitro fertilization. <i>Reproductive Toxicology</i> , 2011, 32, 463-471.	1.3	10
1464	A Network Representation of Households by Health Exclusion, Poverty, and Unemployment. <i>Procedia, Social and Behavioral Sciences</i> , 2011, 22, 69-79.	0.5	0
1465	Metabolomics – A robust bioanalytical approach for the discovery of the modes-of-action of pesticides: A review. <i>Pesticide Biochemistry and Physiology</i> , 2011, 100, 105-117.	1.6	91
1466	Interactive, Graph-based Visual Analysis of High-dimensional, Multi-parameter Fluorescence Microscopy Data in Toponomics. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2011, 17, 1882-1891.	2.9	9
1467	CIGB-300, a proapoptotic peptide, inhibits angiogenesis in vitro and in vivo. <i>Experimental Cell Research</i> , 2011, 317, 1677-1688.	1.2	20
1468	Medusa: A tool for exploring and clustering biological networks. <i>BMC Research Notes</i> , 2011, 4, 384.	0.6	49
1469	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. <i>BMC Research Notes</i> , 2011, 4, 462.	0.6	17
1470	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011, 2, 4.	0.9	19
1471	Stringent response of <i>Escherichia coli</i> : revisiting the bibliome using literature mining. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 14.	7.6	9
1472	Dynamic gene network reconstruction from gene expression data in mice after influenza A (H1N1) infection. <i>Journal of Clinical Bioinformatics</i> , 2011, 1, 27.	1.2	14
1473	Population genetic structure and history of a generalist parasite infecting multiple sympatric host species. <i>International Journal for Parasitology</i> , 2011, 41, 89-98.	1.3	74
1474	Graphical simulation environments for modelling and simulation of integrative physiology. <i>Computer Methods and Programs in Biomedicine</i> , 2011, 102, 295-304.	2.6	10
1475	TC-VGC: A Tumor Classification System using Variations in Genes™ Correlation. <i>Computer Methods and Programs in Biomedicine</i> , 2011, 104, e87-e101.	2.6	8
1476	The physiological, transcriptional and genetic responses of an ozone-sensitive and an ozone tolerant poplar and selected extremes of their F2 progeny. <i>Environmental Pollution</i> , 2011, 159, 45-54.	3.7	32
1477	Directing human embryonic stem cell differentiation by non-viral delivery of siRNA in 3D culture. <i>Biomaterials</i> , 2011, 32, 7793-7800.	5.7	42
1478	The influence of scaffold elasticity on germ layer specification of human embryonic stem cells. <i>Biomaterials</i> , 2011, 32, 9612-9621.	5.7	130
1479	A METHODOLOGY BASED ON MOLECULAR INTERACTIONS AND PATHWAYS TO FIND CANDIDATE GENES ASSOCIATED TO DISEASES: ITS APPLICATION TO SCHIZOPHRENIA AND ALZHEIMER'S DISEASE. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 541-557.	0.3	5

#	ARTICLE	IF	CITATIONS
1480	Lessons Learned from Molecular Scaffold Analysis. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 1742-1753.	2.5	82
1481	Mapping the Protein Interaction Network in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Proteome Research</i> , 2011, 10, 1139-1150.	1.8	55
1482	Software for systems biology: from tools to integrated platforms. <i>Nature Reviews Genetics</i> , 2011, 12, 821-832.	7.7	228
1483	NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop structures of biological networks. <i>Bioinformatics</i> , 2011, 27, 2767-2768.	1.8	29
1484	Proteomic Analysis of Virus-Host Interactions in an Infectious Context Using Recombinant Viruses. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.007443.	2.5	45
1485	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011, 5, 1262-1278.	4.4	206
1486	Biochemical investigation and gene expression analysis of the immunostimulatory functions of an edible <i>Salacia</i> extract in rat small intestine. <i>BioFactors</i> , 2011, 37, 31-39.	2.6	13
1487	A Directed Protein Interaction Network for Investigating Intracellular Signal Transduction. <i>Science Signaling</i> , 2011, 4, rs8.	1.6	313
1488	Visualizing Gene-Set Enrichment Results Using the Cytoscape Plug-in Enrichment Map. <i>Methods in Molecular Biology</i> , 2011, 781, 257-277.	0.4	68
1489	Protein-protein interaction and pathway databases, a graphical review. <i>Briefings in Bioinformatics</i> , 2011, 12, 702-713.	3.2	63
1490	Comparing bioassay response and similarity ensemble approaches to probing protein pharmacology. <i>Bioinformatics</i> , 2011, 27, 3044-3049.	1.8	12
1491	Cytoscape 2.8: new features for data integration and network visualization. <i>Bioinformatics</i> , 2011, 27, 431-432.	1.8	4,228
1492	A Heuristic Algorithm for Detecting Intercellular Interactions. , 2011, , .		0
1493	Embryonic stem cells: protein interaction networks. <i>Biomolecular Concepts</i> , 2011, 2, 13-25.	1.0	12
1494	Networks in Plant Epidemiology: From Genes to Landscapes, Countries, and Continents. <i>Phytopathology</i> , 2011, 101, 392-403.	1.1	81
1495	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65
1496	Metabolomics in pesticide research and development: review and future perspectives. <i>Metabolomics</i> , 2011, 7, 35-53.	1.4	106
1497	Genome-wide gene expression profiles in response to plastid division perturbations. <i>Planta</i> , 2011, 234, 1055-1063.	1.6	4



#	ARTICLE	IF	CITATIONS
1498	Integrative computational biology for cancer research. <i>Human Genetics</i> , 2011, 130, 465-481.	1.8	28
1499	Proteome analysis of microtubule-associated proteins and their interacting partners from mammalian brain. <i>Amino Acids</i> , 2011, 41, 363-385.	1.2	16
1500	The semantic organization of the animal category: evidence from semantic verbal fluency and network theory. <i>Cognitive Processing</i> , 2011, 12, 183-196.	0.7	87
1501	The developmental aging and origins of health and disease hypotheses explained by different protein networks. <i>Biogerontology</i> , 2011, 12, 293-308.	2.0	25
1502	Increasing phosphoproteome coverage and identification of phosphorylation motifs through combination of different HPLC fractionation methods. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2011, 879, 25-34.	1.2	33
1503	Using views of Systems Biology Cloud: application for model building. <i>Theory in Biosciences</i> , 2011, 130, 45-54.	0.6	2
1504	Interactomic study on interaction between lipid droplets and mitochondria. <i>Protein and Cell</i> , 2011, 2, 487-496.	4.8	144
1505	Cross experimental analysis of microarray gene expression data from volatile organic compounds treated targets. <i>Molecular and Cellular Toxicology</i> , 2011, 7, 233-241.	0.8	11
1506	Potential synergistic and multitarget effect of herbal pair Chuanxiong Rhizome-Paeonia Albiflora Pall on osteoarthritis disease: A computational pharmacology approach. <i>Chinese Journal of Integrative Medicine</i> , 2011, 17, 698-703.	0.7	19
1507	Correlation between cold and hot pattern in traditional Chinese medicine and gene expression profiles in rheumatoid arthritis. <i>Frontiers of Medicine</i> , 2011, 5, 219-228.	1.5	42
1508	Ai2NU: A Cytoscape plugin for uniformization of biomolecular accession identifiers. <i>Journal of Shanghai University</i> , 2011, 15, 456-462.	0.1	0
1509	Effects of abiotic stress on plants: a systems biology perspective. <i>BMC Plant Biology</i> , 2011, 11, 163.	1.6	1,005
1510	Dengue-2 Structural Proteins Associate with Human Proteins to Produce a Coagulation and Innate Immune Response Biased Interactome. <i>BMC Infectious Diseases</i> , 2011, 11, 34.	1.3	23
1511	Construction of gene regulatory networks using biclustering and bayesian networks. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 39.	2.1	18
1512	Nonsynonymous substitution rate (Ka) is a relatively consistent parameter for defining fast-evolving and slow-evolving protein-coding genes. <i>Biology Direct</i> , 2011, 6, 13.	1.9	37
1513	Multi-membership gene regulation in pathway based microarray analysis. <i>Algorithms for Molecular Biology</i> , 2011, 6, 22.	0.3	5
1514	Decreased expression of B cell related genes in leukocytes of women with Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2011, 6, 66.	4.4	23
1515	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. <i>Source Code for Biology and Medicine</i> , 2011, 6, 7.	1.7	120



#	ARTICLE	IF	CITATIONS
1516	A metabolic model of the mitochondrion and its use in modelling diseases of the tricarboxylic acid cycle. BMC Systems Biology, 2011, 5, 102.	3.0	62
1517	Simulating Quantitative Cellular Responses Using Asynchronous Threshold Boolean Network Ensembles. BMC Systems Biology, 2011, 5, 109.	3.0	27
1518	Exploring pathway interactions in insulin resistant mouse liver. BMC Systems Biology, 2011, 5, 127.	3.0	17
1519	Genomic phenotyping of the essential and non-essential yeast genome detects novel pathways for alkylation resistance. BMC Systems Biology, 2011, 5, 157.	3.0	22
1520	Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network. BMC Systems Biology, 2011, 5, 158.	3.0	20
1521	Identifying cancer biomarkers by network-constrained support vector machines. BMC Systems Biology, 2011, 5, 161.	3.0	76
1522	Initial characterization of the human central proteome. BMC Systems Biology, 2011, 5, 17.	3.0	66
1523	Genome-scale reconstruction and system level investigation of the metabolic network of <i>Methylobacterium extorquens</i> AM1. BMC Systems Biology, 2011, 5, 189.	3.0	111
1524	Dynamic proteomic profiling of a unicellular cyanobacterium <i>Cyanothece</i> ATCC51142 across light-dark diurnal cycles. BMC Systems Biology, 2011, 5, 194.	3.0	36
1525	Model-based clustering reveals vitamin D dependent multi-centrality hubs in a network of vitamin-related proteins. BMC Systems Biology, 2011, 5, 195.	3.0	15
1526	Regulatory coordination of clustered microRNAs based on microRNA-transcription factor regulatory network. BMC Systems Biology, 2011, 5, 199.	3.0	57
1527	Codon usage variability determines the correlation between proteome and transcriptome fold changes. BMC Systems Biology, 2011, 5, 33.	3.0	33
1528	Knowledge management for Systems Biology a general and visually driven framework applied to translational medicine. BMC Systems Biology, 2011, 5, 38.	3.0	52
1529	Predictive integration of gene functional similarity and co-expression defines treatment response of endothelial progenitor cells. BMC Systems Biology, 2011, 5, 46.	3.0	7
1530	Global network analysis of drug tolerance, mode of action and virulence in methicillin-resistant <i>S. aureus</i> . BMC Systems Biology, 2011, 5, 68.	3.0	36
1531	BiologicalNetworks - tools enabling the integration of multi-scale data for the host-pathogen studies. BMC Systems Biology, 2011, 5, 7.	3.0	18
1532	Using next generation transcriptome sequencing to predict an ectomycorrhizal metabolome. BMC Systems Biology, 2011, 5, 70.	3.0	60
1533	Understanding and predicting synthetic lethal genetic interactions in <i>Saccharomyces cerevisiae</i> using domain genetic interactions. BMC Systems Biology, 2011, 5, 73.	3.0	12

#	ARTICLE	IF	CITATIONS
1534	Large-scale analysis of expression signatures reveals hidden links among diverse cellular processes. BMC Systems Biology, 2011, 5, 87.	3.0	7
1535	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. BMC Systems Biology, 2011, 5, 93.	3.0	4
1536	Proteomic patterns of cervical cancer cell lines, a network perspective. BMC Systems Biology, 2011, 5, 96.	3.0	52
1537	State Space Model with hidden variables for reconstruction of gene regulatory networks. BMC Systems Biology, 2011, 5, S3.	3.0	24
1538	A network-based biomarker approach for molecular investigation and diagnosis of lung cancer. BMC Medical Genomics, 2011, 4, 2.	0.7	75
1539	CDCOCA: A statistical method to define complexity dependence of co-occurring chromosomal aberrations. BMC Medical Genomics, 2011, 4, 21.	0.7	7
1540	Cell cycle and aging, morphogenesis, and response to stimuli genes are individualized biomarkers of glioblastoma progression and survival. BMC Medical Genomics, 2011, 4, 49.	0.7	86
1541	Transforming growth factor $\beta$ 2 receptor 1 is a new candidate prognostic biomarker after acute myocardial infarction. BMC Medical Genomics, 2011, 4, 83.	0.7	32
1542	Using graph theory to analyze biological networks. BioData Mining, 2011, 4, 10.	2.2	547
1543	The Regulatory Network of Pseudomonas aeruginosa. Microbial Informatics and Experimentation, 2011, 1, 3.	7.6	72
1544	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. Microbial Informatics and Experimentation, 2011, 1, 4.	7.6	93
1545	The PathOlogist: an automated tool for pathway-centric analysis. BMC Bioinformatics, 2011, 12, 133.	1.2	33
1546	CASCADE_SCAN: mining signal transduction network from high-throughput data based on steepest descent method. BMC Bioinformatics, 2011, 12, 164.	1.2	13
1547	Web-based metabolic network visualization with a zooming user interface. BMC Bioinformatics, 2011, 12, 176.	1.2	30
1548	Context-dependent transcriptional regulations between signal transduction pathways. BMC Bioinformatics, 2011, 12, 19.	1.2	8
1549	Mapping the distribution of packing topologies within protein interiors shows predominant preference for specific packing motifs. BMC Bioinformatics, 2011, 12, 195.	1.2	26
1550	GraphCrunch 2: Software tool for network modeling, alignment and clustering. BMC Bioinformatics, 2011, 12, 24.	1.2	63
1551	Bio::Homology::InterologWalk - A Perl module to build putative protein-protein interaction networks through interolog mapping. BMC Bioinformatics, 2011, 12, 289.	1.2	16

#	ARTICLE	IF	CITATIONS
1552	GPS-Prot: A web-based visualization platform for integrating host-pathogen interaction data. BMC Bioinformatics, 2011, 12, 298.	1.2	73
1553	NETGEM: Network Embedded Temporal Generative Model for gene expression data. BMC Bioinformatics, 2011, 12, 327.	1.2	8
1554	Quantitative utilization of prior biological knowledge in the Bayesian network modeling of gene expression data. BMC Bioinformatics, 2011, 12, 359.	1.2	23
1555	iCTNet: A Cytoscape plugin to produce and analyze integrative complex traits networks. BMC Bioinformatics, 2011, 12, 380.	1.2	36
1556	iRefScape. A Cytoscape plug-in for visualization and data mining of protein interaction data from iRefIndex. BMC Bioinformatics, 2011, 12, 388.	1.2	13
1557	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541
1558	Network based transcription factor analysis of regenerating axolotl limbs. BMC Bioinformatics, 2011, 12, 80.	1.2	25
1559	Network-based functional enrichment. BMC Bioinformatics, 2011, 12, S14.	1.2	12
1560	SNP and gene networks construction and analysis from classification of copy number variations data. BMC Bioinformatics, 2011, 12, S4.	1.2	13
1562	Functional specialization in nucleotide sugar transporters occurred through differentiation of the gene cluster EamA (DUF6) before the radiation of Viridiplantae. BMC Evolutionary Biology, 2011, 11, 123.	3.2	37
1563	Molecular evolution of the vertebrate TLR1 gene family - a complex history of gene duplication, gene conversion, positive selection and co-evolution. BMC Evolutionary Biology, 2011, 11, 149.	3.2	66
1564	Genetic adaptation of the antibacterial human innate immunity network. BMC Evolutionary Biology, 2011, 11, 202.	3.2	23
1565	Visualization and Exploration of Conserved Regulatory Modules Using ReXSpecies 2. BMC Evolutionary Biology, 2011, 11, 267.	3.2	3
1566	Comparative tissue transcriptomics reveal prompt inter-organ communication in response to local bacterial kidney infection. BMC Genomics, 2011, 12, 123.	1.2	16
1567	Common and unique elements of the ABA-regulated transcriptome of Arabidopsis guard cells. BMC Genomics, 2011, 12, 216.	1.2	189
1568	MicroRNA genes preferentially expressed in dendritic cells contain sites for conserved transcription factor binding motifs in their promoters. BMC Genomics, 2011, 12, 330.	1.2	26
1569	Drosophila selenophosphate synthetase 1 regulates vitamin B6 metabolism: prediction and confirmation. BMC Genomics, 2011, 12, 426.	1.2	18
1570	Functional annotation of the transcriptome of Sorghum bicolor in response to osmotic stress and abscisic acid. BMC Genomics, 2011, 12, 514.	1.2	197

#	ARTICLE	IF	CITATIONS
1571	Comparative analysis and assessment of <i>M. tuberculosis</i> H37Rv protein-protein interaction datasets. <i>BMC Genomics</i> , 2011, 12, S20.	1.2	29
1572	Predicting sequence and structural specificities of RNA binding regions recognized by splicing factor SRSF1. <i>BMC Genomics</i> , 2011, 12, S8.	1.2	26
1573	Ontology-based <i>Brucella</i> vaccine literature indexing and systematic analysis of gene-vaccine association network. <i>BMC Immunology</i> , 2011, 12, 49.	0.9	34
1574	Caries induced cytokine network in the odontoblast layer of human teeth. <i>BMC Immunology</i> , 2011, 12, 9.	0.9	88
1575	Identification of functional motions in the adenylate kinase (ADK) protein family by computational hybrid approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1662-1671.	1.5	17
1576	The evolution of function in strictosidine synthase-like proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3082-3098.	1.5	43
1577	Combining peptide recognition specificity and context information for the prediction of the 14â€³â€³-mediated interactome in <i>S. cerevisiae</i> and <i>H. sapiens</i> . <i>Proteomics</i> , 2011, 11, 128-143.	1.3	34
1578	The Protein Information and Property Explorer 2: Goggle-like exploration of biological proteomic data within one webpage. <i>Proteomics</i> , 2011, 11, 154-158.	1.3	9
1579	Four-dimensional visualisation and analysis of protein-protein interaction networks. <i>Proteomics</i> , 2011, 11, 2672-2682.	1.3	16
1580	An expanded protein-protein interaction network in <i>Bacillus subtilis</i> reveals a group of hubs: Exploration by an integrative approach. <i>Proteomics</i> , 2011, 11, 2981-2991.	1.3	57
1581	Reactome pathway analysis to enrich biological discovery in proteomics data sets. <i>Proteomics</i> , 2011, 11, 3598-3613.	1.3	89
1582	Quantitative proteomics of microbes: Principles and applications to virulence. <i>Proteomics</i> , 2011, 11, 2947-2956.	1.3	24
1583	Advances in analysis of transcriptional regulatory networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 21-35.	6.6	29
1584	Adaptation of cells to new environments. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 544-561.	6.6	148
1585	Associating Drugs, Targets and Clinical Outcomes into an Integrated Network Affords a New Platform for Computer-Aided Drug Repurposing. <i>Molecular Informatics</i> , 2011, 30, 100-111.	1.4	100
1586	Rule-Based Classification of Chemical Structures by Scaffold. <i>Molecular Informatics</i> , 2011, 30, 646-664.	1.4	25
1587	A Microarray Tool Provides Pathway and GO Term Analysis. <i>Molecular Informatics</i> , 2011, 30, 918-921.	1.4	2
1588	Linking the proteinsâ€”Elucidation of proteome-scale networks using mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2011, 30, 268-297.	2.8	23

#	ARTICLE	IF	CITATIONS
1589	The Forkhead factor FoxQ1 influences epithelial differentiation. <i>Journal of Cellular Physiology</i> , 2011, 226, 710-719.	2.0	55
1591	Systems biology: Leading the revolution in ecotoxicology. <i>Environmental Toxicology and Chemistry</i> , 2011, 30, 265-273.	2.2	83
1592	Analysis of pathway mutation profiles highlights collaboration between cancer-associated superpathways. <i>Human Mutation</i> , 2011, 32, 1028-1035.	1.1	15
1593	Science mapping software tools: Review, analysis, and cooperative study among tools. <i>Journal of the Association for Information Science and Technology</i> , 2011, 62, 1382-1402.	2.6	1,536
1594	An application programming interface for CellNetAnalyzer. <i>BioSystems</i> , 2011, 105, 162-168.	0.9	63
1595	CADLIVE Converter for constructing a biochemical network map. <i>Biochemical Engineering Journal</i> , 2011, 54, 200-206.	1.8	3
1596	Popeye strikes again: The deep proteome of spinach leaves. <i>Journal of Proteomics</i> , 2011, 74, 127-136.	1.2	45
1597	Gene expression profiles induced by Salmonella infection in resistant and susceptible mice. <i>Microbes and Infection</i> , 2011, 13, 383-393.	1.0	6
1598	Proteomics – The key to understanding systems biology of Arabidopsis trichomes. <i>Phytochemistry</i> , 2011, 72, 1061-1070.	1.4	10
1599	Gene set assembly for quantitative prediction of developmental toxicity in the embryonic stem cell test. <i>Toxicology</i> , 2011, 284, 63-71.	2.0	33
1600	Membranous Expression of Ectodomain Isoforms of the Epidermal Growth Factor Receptor Predicts Outcome after Chemoradiotherapy of Lymph Node–Negative Cervical Cancer. <i>Clinical Cancer Research</i> , 2011, 17, 5501-5512.	3.2	15
1601	A Systems Pharmacology Analysis of Major Chemotherapy Combination Regimens Used in Gastric Cancer Treatment: Predicting Potential New Protein Targets and Drugs. <i>Current Cancer Drug Targets</i> , 2011, 11, 849-869.	0.8	16
1602	Sensitive detection of pathway perturbations in cancers. , 2011, , .		0
1603	DDN: a caBIG® analytical tool for differential network analysis. <i>Bioinformatics</i> , 2011, 27, 1036-1038.	1.8	39
1604	Can syntactic networks indicate morphological complexity of a language?. <i>Europhysics Letters</i> , 2011, 93, 28005.	0.7	39
1605	Public security. , 2011, , .		3
1606	Network for Activation of Human Endothelial Cells by Oxidized Phospholipids. <i>Circulation Research</i> , 2011, 109, e27-41.	2.0	117
1607	The Proteome Folding Project: Proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011, 21, 1981-1994.	2.4	40

#	ARTICLE	IF	CITATIONS
1608	Generation and Comprehensive Analysis of an Influenza Virus Polymerase Cellular Interaction Network. <i>Journal of Virology</i> , 2011, 85, 13010-13018.	1.5	69
1609	Transcriptome Data Analysis for Cell Culture Processes. , 2011, 127, 27-70.		2
1610	The effect of narrow bandwidth infrared radiation on the growth of Escherichia coli. <i>Applied Physics Letters</i> , 2011, 99, 163704.	1.5	8
1611	Exploring agent-based simulations using temporal graphs. , 2011, , .		0
1612	Protein Interaction Network Prediction and Pathways Analyses Related Atherosclerosis. , 2011, , .		0
1613	Reconstruction of gene regulatory networks using state space model. , 2011, , .		0
1614	Visual Exploration across Biomedical Databases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 536-550.	1.9	7
1615	Toward an understanding of the protein interaction network of the human liver. <i>Molecular Systems Biology</i> , 2011, 7, 536.	3.2	194
1616	Using Biological Networks in Protein Function Prediction and Gene Expression Analysis. <i>Internet Mathematics</i> , 2011, 7, 274-298.	0.7	3
1617	A flexible visualization tool for interaction. , 2011, , .		0
1618	Node-attribute Graph Layout for Small-World Networks. , 2011, , .		3
1619	Protein protein interaction visualization using VisANT. , 2011, , .		0
1620	AtCAST, a Tool for Exploring Gene Expression Similarities among DNA Microarray Experiments Using Networks. <i>Plant and Cell Physiology</i> , 2011, 52, 169-180.	1.5	21
1621	INOH: ontology-based highly structured database of signal transduction pathways. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar052-bar052.	1.4	57
1622	Genomic Analysis of Circadian Clock-, Light-, and Growth-Correlated Genes Reveals PHYTOCHROME-INTERACTING FACTOR5 as a Modulator of Auxin Signaling in Arabidopsis. <i>Plant Physiology</i> , 2011, 156, 357-372.	2.3	136
1623	NetSlim: high-confidence curated signaling maps. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar032-bar032.	1.4	29
1624	PROMISCUOUS: a database for network-based drug-repositioning. <i>Nucleic Acids Research</i> , 2011, 39, D1060-D1066.	6.5	203
1625	A distinct adipose tissue gene expression response to caloric restriction predicts 6-mo weight maintenance in obese subjects. <i>American Journal of Clinical Nutrition</i> , 2011, 94, 1399-1409.	2.2	54

#	ARTICLE	IF	CITATIONS
1626	Paraoxonase-2 Modulates Stress Response of Endothelial Cells to Oxidized Phospholipids and a Bacterial Quorum-Sensing Molecule. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2011, 31, 2624-2633.	1.1	35
1627	Integrative gene network construction for predicting a set of complementary prostate cancer genes. <i>Bioinformatics</i> , 2011, 27, 1846-1853.	1.8	34
1628	A Physical Interaction Network of Dengue Virus and Human Proteins. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012187.	2.5	153
1629	PRINCIPLE: a tool for associating genes with diseases via network propagation. <i>Bioinformatics</i> , 2011, 27, 3325-3326.	1.8	42
1630	PiNGO: a Cytoscape plugin to find candidate genes in biological networks. <i>Bioinformatics</i> , 2011, 27, 1030-1031.	1.8	41
1631	Tools and collaborative environments for bioinformatics research. <i>Briefings in Bioinformatics</i> , 2011, 12, 549-561.	3.2	58
1632	Constraint-based, Homology Model of the Extracellular Domain of the Epithelial Na <sup>+</sup> Channel $\beta$ Subunit Reveals a Mechanism of Channel Activation by Proteases. <i>Journal of Biological Chemistry</i> , 2011, 286, 649-660.	1.6	66
1633	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. <i>Bioinformatics</i> , 2011, 27, 326-333.	1.8	36
1634	Mindbomb 1, an E3 ubiquitin ligase, forms a complex with RYK to activate Wnt/ $\beta$ -catenin signaling. <i>Journal of Cell Biology</i> , 2011, 194, 737-750.	2.3	90
1635	A systems biology approach sheds new light on <i>Escherichia coli</i> acid resistance. <i>Nucleic Acids Research</i> , 2011, 39, 7512-7528.	6.5	86
1636	VISTA, a novel mouse Ig superfamily ligand that negatively regulates T cell responses. <i>Journal of Experimental Medicine</i> , 2011, 208, 577-592.	4.2	539
1637	Coordinated Activation of Cellulose and Repression of Lignin Biosynthesis Pathways in Rice $\beta$ . <i>Plant Physiology</i> , 2011, 155, 916-931.	2.3	198
1638	Targets of the Tumor Suppressor <i>miR-200</i> in Regulation of the Epithelial-Mesenchymal Transition in Cancer. <i>Cancer Research</i> , 2011, 71, 7670-7682.	0.4	126
1639	Computational reconstruction of primordial prototypes of elementary functional loops in modern proteins. <i>Bioinformatics</i> , 2011, 27, 2368-2375.	1.8	17
1640	GProX, a User-Friendly Platform for Bioinformatics Analysis and Visualization of Quantitative Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O110.007450.	2.5	150
1641	ChIP-Array: combinatory analysis of ChIP-seq/chip and microarray gene expression data to discover direct/indirect targets of a transcription factor. <i>Nucleic Acids Research</i> , 2011, 39, W430-W436.	6.5	49
1642	Lipid transport function is the main target of oral oleoylethanolamide to reduce adiposity in high-fat-fed mice. <i>Journal of Lipid Research</i> , 2011, 52, 1373-1382.	2.0	34
1643	An integrative functional genomics approach for discovering biomarkers in schizophrenia. <i>Briefings in Functional Genomics</i> , 2011, 10, 387-399.	1.3	19



#	ARTICLE	IF	CITATIONS
1644	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011, 39, D793-D799.	6.5	74
1645	Unraveling regulation and new components of human P-bodies through a protein interaction framework and experimental validation. <i>Rna</i> , 2011, 17, 1619-1634.	1.6	38
1646	Review of Weighted Gene Coexpression Network Analysis. , 2011, , 369-388.		19
1647	Modeling Human Endometrial Decidualization from the Interaction between Proteome and Secretome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2011, 96, 706-716.	1.8	53
1648	The Reconstruction of Transcriptional Networks Reveals Critical Genes with Implications for Clinical Outcome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2011, 17, 7402-7412.	3.2	65
1649	BioGRID REST Service, BiogridPlugin2 and BioGRID WebGraph: new tools for access to interaction data at BioGRID. <i>Bioinformatics</i> , 2011, 27, 1043-1044.	1.8	26
1650	CytoModeler: a tool for bridging large-scale network analysis and dynamic quantitative modeling. <i>Bioinformatics</i> , 2011, 27, 1578-1580.	1.8	2
1651	Functional genomic screen and network analysis reveal novel modifiers of tauopathy dissociated from tau phosphorylation. <i>Human Molecular Genetics</i> , 2011, 20, 4947-4977.	1.4	110
1652	ATTED-II Updates: Condition-Specific Gene Coexpression to Extend Coexpression Analyses and Applications to a Broad Range of Flowering Plants. <i>Plant and Cell Physiology</i> , 2011, 52, 213-219.	1.5	141
1653	Building Protein-Protein Interaction Networks with Proteomics and Informatics Tools. <i>Journal of Biological Chemistry</i> , 2011, 286, 23645-23651.	1.6	56
1654	Absence of Tec Family Kinases Interleukin-2 Inducible T cell Kinase (Itk) and Bruton's Tyrosine Kinase (Btk) Severely Impairs Fc $\mu$ RI-dependent Mast Cell Responses. <i>Journal of Biological Chemistry</i> , 2011, 286, 9503-9513.	1.6	41
1655	A set of miRNAs that involve in the pathways of drug resistance and leukemic stem-cell differentiation is associated with the risk of relapse and glucocorticoid response in childhood ALL. <i>Human Molecular Genetics</i> , 2011, 20, 4903-4915.	1.4	110
1656	Molecular Characterization of Propolis-Induced Cell Death in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2011, 10, 398-411.	3.4	49
1657	CyClus3D: a Cytoscape plugin for clustering network motifs in integrated networks. <i>Bioinformatics</i> , 2011, 27, 1587-1588.	1.8	13
1658	RING: networking interacting residues, evolutionary information and energetics in protein structures. <i>Bioinformatics</i> , 2011, 27, 2003-2005.	1.8	116
1659	A Tool for Biomarker Discovery in the Urinary Proteome: A Manually Curated Human and Animal Urine Protein Biomarker Database. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010975.	2.5	85
1660	A Systems Biology Approach for the Investigation of the Heparin/Heparan Sulfate Interactome. <i>Journal of Biological Chemistry</i> , 2011, 286, 19892-19904.	1.6	203
1661	OrthoNets: simultaneous visual analysis of orthologs and their interaction neighborhoods across different organisms. <i>Bioinformatics</i> , 2011, 27, 883-884.	1.8	4



#	ARTICLE	IF	CITATIONS
1662	The local protein-protein interactional feature can be caught by machine-learning method. , 2011, , .		0
1663	Next-Generation Sequencing Reveals HIV-1-Mediated Suppression of T Cell Activation and RNA Processing and Regulation of Noncoding RNA Expression in a CD4 <sup>+</sup> T Cell Line. MBio, 2011, 2, .	1.8	67
1664	Protein-network modeling of prostate cancer gene signatures reveals essential pathways in disease recurrence. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 392-402.	2.2	27
1665	Comparing Signaling Networks between Normal and Transformed Hepatocytes Using Discrete Logical Models. Cancer Research, 2011, 71, 5400-5411.	0.4	132
1666	Mitotic Substrates of the Kinase Aurora with Roles in Chromatin Regulation Identified Through Quantitative Phosphoproteomics of Fission Yeast. Science Signaling, 2011, 4, rs6.	1.6	105
1667	Customizable views on semantically integrated networks for systems biology. Bioinformatics, 2011, 27, 1299-1306.	1.8	9
1668	Interorgan Coordination of the Murine Adaptive Response to Fasting. Journal of Biological Chemistry, 2011, 286, 16332-16343.	1.6	50
1669	AKAP Signaling in Reinstated Cocaine Seeking Revealed by iTRAQ Proteomic Analysis. Journal of Neuroscience, 2011, 31, 5648-5658.	1.7	41
1670	Extending Biochemical Databases by Metabolomic Surveys. Journal of Biological Chemistry, 2011, 286, 23637-23643.	1.6	67
1671	Interdomain communication revealed in the diabetes drug target mitoNEET. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5266-5271.	3.3	25
1672	TVNViewer: An interactive visualization tool for exploring networks that change over time or space. Bioinformatics, 2011, 27, 1880-1881.	1.8	17
1673	Genomic Analyses of the RNA-binding Protein Hu Antigen R (HuR) Identify a Complex Network of Target Genes and Novel Characteristics of Its Binding Sites. Journal of Biological Chemistry, 2011, 286, 37063-37066.	1.6	68
1674	Proteomics approach to study the functions of <i>Drosophila</i> myosin VI through identification of multiple cargo-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5566-5571.	3.3	28
1675	Comparison of an expanded ataxia interactome with patient medical records reveals a relationship between macular degeneration and ataxia. Human Molecular Genetics, 2011, 20, 510-527.	1.4	45
1676	BioAssay Ontology Annotations Facilitate Cross-Analysis of Diverse High-Throughput Screening Data Sets. Journal of Biomolecular Screening, 2011, 16, 415-426.	2.6	42
1677	Translational Analysis of Mouse and Human Placental Protein and mRNA Reveals Distinct Molecular Pathologies in Human Preeclampsia. Molecular and Cellular Proteomics, 2011, 10, M111.012526.	2.5	44
1679	Missense Mutation in APOC3 within the C-terminal Lipid Binding Domain of Human ApoC-III Results in Impaired Assembly and Secretion of Triacylglycerol-rich Very Low Density Lipoproteins. Journal of Biological Chemistry, 2011, 286, 27769-27780.	1.6	91
1681	Systems biology of the autophagy-lysosomal pathway. Autophagy, 2011, 7, 477-489.	4.3	116

#	ARTICLE	IF	CITATIONS
1682	Identification by Gene Coregulation Mapping of Novel Genes Involved in Embryonic Stem Cell Differentiation. <i>Stem Cells and Development</i> , 2011, 20, 115-126.	1.1	10
1683	CLC and IFNAR1 are differentially expressed and a global immunity score is distinct between early- and late-onset colorectal cancer. <i>Genes and Immunity</i> , 2011, 12, 653-662.	2.2	40
1684	Resolution of infection promotes a state of dormancy and long survival of CD4 memory T cells. <i>Immunology and Cell Biology</i> , 2011, 89, 870-881.	1.0	22
1685	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	9.0	48
1686	Novel Visualisation and Analysis of Natural and Complex Systems Using Systemic Computation. <i>Information Visualization</i> , 2011, 10, 1-31.	1.2	2
1687	Î²-Catenin Causes Renal Dysplasia via Upregulation of Tgfb2 and Dkk1. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 718-731.	3.0	35
1688	Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression. <i>Genome Research</i> , 2011, 21, 645-657.	2.4	277
1689	Bioinformatics approaches in the discovery and understanding of reproduction-related biomarkers. <i>Expert Review of Proteomics</i> , 2011, 8, 187-195.	1.3	4
1691	Cobweb: a Java applet for network exploration and visualisation. <i>Bioinformatics</i> , 2011, 27, 1725-1726.	1.8	8
1692	Modular analysis of the probabilistic genetic interaction network. <i>Bioinformatics</i> , 2011, 27, 853-859.	1.8	10
1693	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar021-bar021.	1.4	39
1694	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	6.5	980
1695	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. <i>PLoS Computational Biology</i> , 2011, 7, e1002126.	1.5	83
1696	Mapping Protein Interactions between Dengue Virus and Its Human and Insect Hosts. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e954.	1.3	93
1697	Navigating the Human Metabolome for Biomarker Identification and Design of Pharmaceutical Molecules. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-19.	3.0	33
1698	The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. <i>PLoS Computational Biology</i> , 2011, 7, e1002318.	1.5	48
1699	Multiple Means to the Same End: The Genetic Basis of Acquired Stress Resistance in Yeast. <i>PLoS Genetics</i> , 2011, 7, e1002353.	1.5	91
1700	Human Cytomegalovirus IE1 Protein Elicits a Type II Interferon-Like Host Cell Response That Depends on Activated STAT1 but Not Interferon-Î³. <i>PLoS Pathogens</i> , 2011, 7, e1002016.	2.1	60

#	ARTICLE	IF	CITATIONS
1701	Prognostic transcriptional association networks: a new supervised approach based on regression trees. <i>Bioinformatics</i> , 2011, 27, 252-258.	1.8	12
1702	TREEGL: reverse engineering tree-evolving gene networks underlying developing biological lineages. <i>Bioinformatics</i> , 2011, 27, i196-i204.	1.8	27
1703	CytoscapeRPC: a plugin to create, modify and query Cytoscape networks from scripting languages. <i>Bioinformatics</i> , 2011, 27, 2451-2452.	1.8	7
1704	Network Archaeology: Uncovering Ancient Networks from Present-Day Interactions. <i>PLoS Computational Biology</i> , 2011, 7, e1001119.	1.5	64
1705	A Computational Approach to Finding Novel Targets for Existing Drugs. <i>PLoS Computational Biology</i> , 2011, 7, e1002139.	1.5	107
1706	Chemical Basis of Metabolic Network Organization. <i>PLoS Computational Biology</i> , 2011, 7, e1002214.	1.5	12
1707	The Epithelial-Mesenchymal Transition Mediator S100A4 Maintains Cancer-Initiating Cells in Head and Neck Cancers. <i>Cancer Research</i> , 2011, 71, 1912-1923.	0.4	123
1708	The Reactome BioMart. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar031-bar031.	1.4	32
1709	Reliability-Oriented bioinformatic networks visualization. <i>Bioinformatics</i> , 2011, 27, 1583-1584.	1.8	1
1710	Signaling gateway molecule pagesâ€”a data model perspective. <i>Bioinformatics</i> , 2011, 27, 1736-1738.	1.8	33
1711	Visualization and quality assessment of de novo genome assemblies. <i>Bioinformatics</i> , 2011, 27, 3425-3426.	1.8	9
1712	Evolutionary design principles and functional characteristics based on kingdom-specific network motifs. <i>Bioinformatics</i> , 2011, 27, 245-251.	1.8	17
1713	Capture of MicroRNAâ€”Bound mRNAs Identifies the Tumor Suppressor miR-34a as a Regulator of Growth Factor Signaling. <i>PLoS Genetics</i> , 2011, 7, e1002363.	1.5	222
1714	Kinesthetic pathways. , 2011, , .		38
1715	Interactive sensemaking in authorship networks. , 2011, , .		1
1716	Interactive, multiscale navigation of large and complicated biological networks. <i>Bioinformatics</i> , 2011, 27, 1121-1127.	1.8	10
1717	The Biomolecular Interaction Network Database in PSI-MI 2.5. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq037.	1.4	95
1718	Protein Complexes are Central in the Yeast Genetic Landscape. <i>PLoS Computational Biology</i> , 2011, 7, e1001092.	1.5	57

#	ARTICLE	IF	CITATIONS
1719	Transcriptional profiling and network analysis of the murine angiotensin II-induced abdominal aortic aneurysm. <i>Physiological Genomics</i> , 2011, 43, 993-1003.	1.0	67
1720	ConsensusPathDB: toward a more complete picture of cell biology. <i>Nucleic Acids Research</i> , 2011, 39, D712-D717.	6.5	537
1721	Heat Shock Partially Dissociates the Overlapping Modules of the Yeast Protein-Protein Interaction Network: A Systems Level Model of Adaptation. <i>PLoS Computational Biology</i> , 2011, 7, e1002187.	1.5	52
1722	Introduction to Network Analysis in Systems Biology. <i>Science Signaling</i> , 2011, 4, tr5.	1.6	108
1723	Mapping the Hsp90 Genetic Interaction Network in <i>Candida albicans</i> Reveals Environmental Contingency and Rewired Circuitry. <i>PLoS Genetics</i> , 2012, 8, e1002562.	1.5	98
1724	Visual Analysis of Transcriptome Data in the Context of Anatomical Structures and Biological Networks. <i>Frontiers in Plant Science</i> , 2012, 3, 252.	1.7	6
1725	Semi-automatic drawing of metabolic networks. <i>Information Visualization</i> , 2012, 11, 171-187.	1.2	2
1726	Transcriptome network analysis reveals candidate genes for renal cell carcinoma. <i>Journal of Cancer Research and Therapeutics</i> , 2012, 8, 28.	0.3	3
1727	Network-Based Gene Expression Biomarkers for Cold and Heat Patterns of Rheumatoid Arthritis in Traditional Chinese Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-17.	0.5	43
1728	Network Analysis of the Focal Adhesion to Invadopodia Transition Identifies a PI3K-PKC $\pm$ Invasive Signaling Axis. <i>Science Signaling</i> , 2012, 5, ra66.	1.6	69
1729	Identification of functional CNV region networks using a CNV-gene mapping algorithm in a genome-wide scale. <i>Bioinformatics</i> , 2012, 28, 2045-2051.	1.8	5
1730	Understanding the Molecular Mechanism of Interventions in Treating Rheumatoid Arthritis Patients with Corresponding Traditional Chinese Medicine Patterns Based on Bioinformatics Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-11.	0.5	18
1731	Mining and visualization of microarray and metabolomic data reveal extensive cell wall remodeling during winter hardening in Sitka spruce ( <i>Picea sitchensis</i> ). <i>Frontiers in Plant Science</i> , 2012, 3, 241.	1.7	11
1732	Networks of Neuronal Genes Affected by Common and Rare Variants in Autism Spectrum Disorders. <i>PLoS Genetics</i> , 2012, 8, e1002556.	1.5	139
1733	A Global Comparison of the Human and <i>T. brucei</i> Degradomes Gives Insights about Possible Parasite Drug Targets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1942.	1.3	3
1734	Automatic Filtering and Substantiation of Drug Safety Signals. <i>PLoS Computational Biology</i> , 2012, 8, e1002457.	1.5	34
1735	Proteome Sampling by the HLA Class I Antigen Processing Pathway. <i>PLoS Computational Biology</i> , 2012, 8, e1002517.	1.5	41
1736	Multiple Genetic Interaction Experiments Provide Complementary Information Useful for Gene Function Prediction. <i>PLoS Computational Biology</i> , 2012, 8, e1002559.	1.5	17

#	ARTICLE	IF	CITATIONS
1737	Suppressed Expression of T-Box Transcription Factors Is Involved in Senescence in Chronic Obstructive Pulmonary Disease. <i>PLoS Computational Biology</i> , 2012, 8, e1002597.	1.5	18
1738	Genome-Wide Functional Profiling Identifies Genes and Processes Important for Zinc-Limited Growth of <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002699.	1.5	57
1739	Disruption of Mouse <i>Cenpj</i> , a Regulator of Centriole Biogenesis, Phenocopies Seckel Syndrome. <i>PLoS Genetics</i> , 2012, 8, e1003022.	1.5	84
1740	<i>Tcf7</i> Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. <i>PLoS Genetics</i> , 2012, 8, e1002565.	1.5	88
1741	State of the Art in Silico Tools for the Study of Signaling Pathways in Cancer. <i>International Journal of Molecular Sciences</i> , 2012, 13, 6561-6581.	1.8	4
1742	CytoSEED: a Cytoscape plugin for viewing, manipulating and analyzing metabolic models created by the Model SEED. <i>Bioinformatics</i> , 2012, 28, 891-892.	1.8	12
1743	Evolution and Architecture of the Inner Membrane Complex in Asexual and Sexual Stages of the Malaria Parasite. <i>Molecular Biology and Evolution</i> , 2012, 29, 2113-2132.	3.5	135
1744	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. <i>PLoS Genetics</i> , 2012, 8, e1003100.	1.5	266
1745	Correlation networks visualization. <i>Frontiers in Plant Science</i> , 2012, 3, 240.	1.7	24
1746	Allelic Variation and Differential Expression of the mSIN3A Histone Deacetylase Complex Gene <i>Arid4b</i> Promote Mammary Tumor Growth and Metastasis. <i>PLoS Genetics</i> , 2012, 8, e1002735.	1.5	45
1747	Assessing Drug Target Association Using Semantic Linked Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002574.	1.5	128
1748	Systems Genetic Analysis of Osteoblast-Lineage Cells. <i>PLoS Genetics</i> , 2012, 8, e1003150.	1.5	48
1749	Revealing the Anti-Tumor Effect of Artificial miRNA p-27-5p on Human Breast Carcinoma Cell Line T-47D. <i>International Journal of Molecular Sciences</i> , 2012, 13, 6352-6369.	1.8	5
1750	Fast Inference for the Latent Space Network Model Using a Case-Control Approximate Likelihood. <i>Journal of Computational and Graphical Statistics</i> , 2012, 21, 901-919.	0.9	93
1751	Predictive networks: a flexible, open source, web application for integration and analysis of human gene networks. <i>Nucleic Acids Research</i> , 2012, 40, D866-D875.	6.5	28
1752	Screening the banana biodiversity for drought tolerance: can an in vitro growth model and proteomics be used as a tool to discover tolerant varieties and understand homeostasis. <i>Frontiers in Plant Science</i> , 2012, 3, 176.	1.7	96
1753	Induced Pluripotent Stem Cells Show Metabolomic Differences to Embryonic Stem Cells in Polyunsaturated Phosphatidylcholines and Primary Metabolism. <i>PLoS ONE</i> , 2012, 7, e46770.	1.1	68
1754	A Systems Biology Starter Kit for Arenaviruses. <i>Viruses</i> , 2012, 4, 3625-3646.	1.5	0

#	ARTICLE	IF	CITATIONS
1755	GIRAF: a method for fast search and flexible alignment of ligand binding interfaces in proteins at atomic resolution. <i>Biophysics (Nagoya-shi, Japan)</i> , 2012, 8, 79-94.	0.4	4
1756	Transcriptomic Characterization of Temperature Stress Responses in Larval Zebrafish. <i>PLoS ONE</i> , 2012, 7, e37209.	1.1	171
1757	Computing graphlet signatures of network nodes and motifs in Cytoscape with GraphletCounter. <i>Bioinformatics</i> , 2012, 28, 290-291.	1.8	9
1758	Proteome-Wide Discovery of Evolutionary Conserved Sequences in Disordered Regions. <i>Science Signaling</i> , 2012, 5, rs1.	1.6	109
1759	How well do the substrates KISS the enzyme? Molecular docking program selection for feruloyl esterases. <i>Scientific Reports</i> , 2012, 2, 323.	1.6	25
1760	An integer linear programming approach for finding deregulated subgraphs in regulatory networks. <i>Nucleic Acids Research</i> , 2012, 40, e43-e43.	6.5	84
1761	Proteomic Cornerstones of Hematopoietic Stem Cell Differentiation: Distinct Signatures of Multipotent Progenitors and Myeloid Committed Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 286-302.	2.5	60
1762	ArrayExpress update—trends in database growth and links to data analysis tools. <i>Nucleic Acids Research</i> , 2012, 41, D987-D990.	6.5	340
1763	CentiLib: comprehensive analysis and exploration of network centralities. <i>Bioinformatics</i> , 2012, 28, 1178-1179.	1.8	24
1764	Coiled-coil networking shapes cell molecular machinery. <i>Molecular Biology of the Cell</i> , 2012, 23, 3911-3922.	0.9	69
1765	Optimal structural inference of signaling pathways from unordered and overlapping gene sets. <i>Bioinformatics</i> , 2012, 28, 546-556.	1.8	8
1766	Nucleolar Protein Trafficking in Response to HIV-1 Tat: Rewiring the Nucleolus. <i>PLoS ONE</i> , 2012, 7, e48702.	1.1	56
1767	Human Family with Sequence Similarity 60 Member A (FAM60A) Protein: a New Subunit of the Sin3 Deacetylase Complex. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1815-1828.	2.5	47
1768	Reshaping of the maize transcriptome by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11878-11883.	3.3	154
1769	Deregulation of a Hox Protein Regulatory Network Spanning Prostate Cancer Initiation and Progression. <i>Clinical Cancer Research</i> , 2012, 18, 4291-4302.	3.2	61
1770	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012, 40, D76-D83.	6.5	167
1771	Enabling Computational Proteomics by Public and Local Data Management Systems. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 266-266.	5.1	1
1772	Guiding the interactive exploration of metabolic pathway interconnections. <i>Information Visualization</i> , 2012, 11, 136-150.	1.2	18

#	ARTICLE	IF	CITATIONS
1773	Identification of Differentially Expressed Proteins in Direct Expressed Prostatic Secretions of Men with Organ-confined Versus Extracapsular Prostate Cancer. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1870-1884.	2.5	71
1774	Interaction Proteomics Identify NEURL4 and the HECT E3 Ligase HERC2 as Novel Modulators of Centrosome Architecture. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014233.	2.5	57
1775	Transcriptome and Coexpression Network Analysis of the Human Glioma Cell Line Hs683 Exposed to Cadoxin. <i>Journal of International Medical Research</i> , 2012, 40, 887-898.	0.4	6
1776	Metabolic Modeling and Simulation Analysis of Thyroid Disorder Pathway. <i>Journal of Computer Science and Systems Biology</i> , 2012, 05, .	0.0	11
1777	Exploring Tomato Gene Functions Based on Coexpression Modules Using Graph Clustering and Differential Coexpression Approaches. <i>Plant Physiology</i> , 2012, 158, 1487-1502.	2.3	63
1778	A Systems Biology Perspective on Rational Design of Peptide Vaccine Against Virus Infections. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1310-1319.	1.0	14
1779	A Systematic Approach for Analysis of Peptide Array Kinome Data. <i>Science Signaling</i> , 2012, 5, pl2.	1.6	53
1780	High-quality sequence clustering guided by network topology and multiple alignment likelihood. <i>Bioinformatics</i> , 2012, 28, 1078-1085.	1.8	39
1781	GraphTrail. , 2012, , .		83
1782	TopicNets. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2012, 3, 1-26.	2.9	90
1783	QSEAfor fuzzy subgraph querying of KEGG pathways. , 2012, , .		2
1784	A syntactic rule-based method for automatic pathway information extraction from biomedical literature. , 2012, , .		1
1785	Identification of SRC as a Potent Drug Target for Asthma, Using an Integrative Approach of Protein Interactome Analysis and In Silico Drug Discovery. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 513-526.	1.0	15
1786	Systrip: A Visual Environment for the Investigation of Time-series Data in the Context of Metabolic Networks. , 2012, , .		1
1787	Potential blood biomarkers for stroke. <i>Expert Review of Proteomics</i> , 2012, 9, 437-449.	1.3	28
1788	ON SOME RECENT ADVANCES IN COMPLEX SOFTWARE NETWORKS: MODELING, ANALYSIS, EVOLUTION AND APPLICATIONS. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2012, 22, 1250024.	0.7	7
1789	Protein Disulfide Isomerase Is Required for Platelet-derived Growth Factor-induced Vascular Smooth Muscle Cell Migration, Nox1 NADPH Oxidase Expression, and RhoGTPase Activation. <i>Journal of Biological Chemistry</i> , 2012, 287, 29290-29300.	1.6	65
1790	Simple algorithms for network visualization: A tutorial. <i>Tsinghua Science and Technology</i> , 2012, 17, 383-398.	4.1	29



#	ARTICLE	IF	CITATIONS
1791	Viruses and Interactomes in Translation. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014738-1-M111.014738-12.	2.5	44
1792	Simultaneous supervised clustering and feature selection over a graph. <i>Biometrika</i> , 2012, 99, 899-914.	1.3	28
1793	A Novel 4EHP-GIGYF2 Translational Repressor Complex Is Essential for Mammalian Development. <i>Molecular and Cellular Biology</i> , 2012, 32, 3585-3593.	1.1	164
1794	Influenza A Virus Infection of Human Respiratory Cells Induces Primary MicroRNA Expression. <i>Journal of Biological Chemistry</i> , 2012, 287, 31027-31040.	1.6	114
1795	Strand swapping regulates the iron-sulfur cluster in the diabetes drug target mitoNEET. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1955-1960.	3.3	19
1796	Ketoamide Resistance and Hepatitis C Virus Fitness in Val55 Variants of the NS3 Serine Protease. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1907-1915.	1.4	32
1797	System Response of Metabolic Networks in <i>Chlamydomonas reinhardtii</i> to Total Available Ammonium. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 973-988.	2.5	93
1798	Clinical Proteomics. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 377-377.	5.1	4
1799	Functionalization of a protosynaptic gene expression network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10612-10618.	3.3	55
1800	A network clustering algorithm for detection of protein families. , 2012, 2012, 6329-32.		1
1801	Linkage of gut microbiome with cognition in hepatic encephalopathy. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, G168-G175.	1.6	448
1802	Genome-Wide Determination of a Broad ESRP-Regulated Posttranscriptional Network by High-Throughput Sequencing. <i>Molecular and Cellular Biology</i> , 2012, 32, 1468-1482.	1.1	127
1803	Quantitative typological analysis of Romance languages. <i>Poznan Studies in Contemporary Linguistics</i> , 2012, 48, .	0.1	9
1804	Plant Metabolic Pathways: Databases and Pipeline for Stoichiometric Analysis. , 2012, , 345-366.		3
1805	Application of Data Mining and Visualization Techniques for the Prediction of Drug-Induced Nausea in Man. <i>Toxicological Sciences</i> , 2012, 126, 275-284.	1.4	20
1806	BioNetwork Bench: Database and Software for Storage, Query, and Analysis of Gene and Protein Networks. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9728.	1.0	0
1807	Biomarker Identification Using Text Mining. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-4.	0.7	6
1808	Repertoire of Protein Kinases Encoded in the Genome of <i>Takifugu rubripes</i> . <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-12.	2.0	3



#	ARTICLE	IF	CITATIONS
1809	Investigating the Relationship between Topology and Evolution in a Dynamic Nematode Odor Genetic Network. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-8.	1.0	2
1810	The Autoimmune Tautology: An In Silico Approach. <i>Autoimmune Diseases</i> , 2012, 2012, 1-10.	2.7	5
1811	Proteomic and Bioinformatics Analyses of Mouse Liver Microsomes. <i>International Journal of Proteomics</i> , 2012, 2012, 1-24.	2.0	11
1812	Virtual Interactomics of Proteins from Biochemical Standpoint. <i>Molecular Biology International</i> , 2012, 2012, 1-22.	1.7	5
1813	Whole Transcriptome RNA-Seq Analysis of Breast Cancer Recurrence Risk Using Formalin-Fixed Paraffin-Embedded Tumor Tissue. <i>PLoS ONE</i> , 2012, 7, e40092.	1.1	70
1814	GENIES: gene network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2012, 40, W162-W167.	6.5	39
1815	ApoptoProteomics, an Integrated Database for Analysis of Proteomics Data Obtained from Apoptotic Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010447.	2.5	30
1816	Evolutionary Dynamics of Small RNAs in 27 <i>Escherichia coli</i> and <i>Shigella</i> Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 330-345.	1.1	43
1817	<i>Streptococcus pyogenes</i> in Human Plasma. <i>Journal of Biological Chemistry</i> , 2012, 287, 1415-1425.	1.6	35
1818	Integrin $\alpha 21$ Mediates Vaccinia Virus Entry through Activation of PI3K/Akt Signaling. <i>Journal of Virology</i> , 2012, 86, 6677-6687.	1.5	86
1819	Protein Data Bank Japan (PDBj): maintaining a structural data archive and resource description framework format. <i>Nucleic Acids Research</i> , 2012, 40, D453-D460.	6.5	126
1820	The disease and gene annotations (DGA): an annotation resource for human disease. <i>Nucleic Acids Research</i> , 2012, 41, D553-D560.	6.5	53
1821	ModuLand plug-in for Cytoscape: determination of hierarchical layers of overlapping network modules and community centrality. <i>Bioinformatics</i> , 2012, 28, 2202-2204.	1.8	91
1822	CySBML: a Cytoscape plugin for SBML. <i>Bioinformatics</i> , 2012, 28, 2402-2403.	1.8	49
1823	Quantitative proteomics profiling of the poly(ADP-ribose)-related response to genotoxic stress. <i>Nucleic Acids Research</i> , 2012, 40, 7788-7805.	6.5	138
1824	A Wnt-Bmp Feedback Circuit Controls Intertissue Signaling Dynamics in Tooth Organogenesis. <i>Science Signaling</i> , 2012, 5, ra4.	1.6	93
1825	Using systems and structure biology tools to dissect cellular phenotypes. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 171-175.	2.2	6
1826	Translating Mendelian and complex inheritance of Alzheimer's disease genes for predicting unique personal genome variants. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 306-316.	2.2	18

#	ARTICLE	IF	CITATIONS
1827	DroPNet: a web portal for integrated analysis of Drosophila protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012, 40, W134-W139.	6.5	5
1828	Predicting Adaptive Phenotypes From Multilocus Genotypes in Sitka Spruce ( <i>Picea sitchensis</i> ) Using Random Forest. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1085-1093.	0.8	59
1829	Managing biological complexity across orthologs with a visual knowledgebase of documented biomolecular interactions. <i>Scientific Reports</i> , 2012, 2, 1011.	1.6	6
1830	Transcriptional profiling of <i>Saccharomyces cerevisiae</i> exposed to propolis. <i>BMC Complementary and Alternative Medicine</i> , 2012, 12, 194.	3.7	19
1831	Mining PeptideAtlas for Biomarkers and Therapeutics in Human Disease. <i>Current Pharmaceutical Design</i> , 2012, 18, 748-754.	0.9	2
1832	Synergizing Genomic Analysis With Biological Knowledge to Identify and Validate Novel Genes in Pancreatic Development. <i>Pancreas</i> , 2012, 41, 962-969.	0.5	7
1833	In the critically ill patient, diabetes predicts mortality independent of statin therapy but is not associated with acute lung injury. <i>Critical Care Medicine</i> , 2012, 40, 1835-1843.	0.4	27
1834	Network systems biology for targeted cancer therapies. <i>Chinese Journal of Cancer</i> , 2012, 31, 134-141.	4.9	24
1835	Gene-centric gene-gene interaction: A model-based kernel machine method. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	43
1836	Large-scale mapping of human protein interactome using structural complexes. <i>EMBO Reports</i> , 2012, 13, 266-271.	2.0	43
1837	Genome-wide transcriptome analysis of rice genes responsive to chilling stress. <i>Canadian Journal of Plant Science</i> , 2012, 92, 447-460.	0.3	13
1838	Employing functional interactions for characterisation and detection of sparse complexes from yeast PPI networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2012, 8, 286.	0.1	29
1840	Genes with a spike expression are clustered in chromosome (sub)bands and spike (sub)bands have a powerful prognostic value in patients with multiple myeloma. <i>Haematologica</i> , 2012, 97, 622-630.	1.7	44
1841	NetView: A High-Definition Network-Visualization Approach to Detect Fine-Scale Population Structures from Genome-Wide Patterns of Variation. <i>PLoS ONE</i> , 2012, 7, e48375.	1.1	113
1842	A systematic analysis of heart transcriptome highlights divergent cardiovascular disease pathways between animal models and humans. <i>Molecular BioSystems</i> , 2012, 8, 504-510.	2.9	15
1843	In Silico Implementation of Synthetic Gene Networks. <i>Methods in Molecular Biology</i> , 2012, 813, 3-21.	0.4	7
1844	Mind the gap: diversity and reactivity relationships among multihaem cytochromes of the MtrA/DmsE family. <i>Biochemical Society Transactions</i> , 2012, 40, 1268-1273.	1.6	15
1845	A Systems Biology View of Responses to Lignin Biosynthesis Perturbations in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 3506-3529.	3.1	321

#	ARTICLE	IF	CITATIONS
1846	A travel guide to Cytoscape plugins. <i>Nature Methods</i> , 2012, 9, 1069-1076.	9.0	1,289
1847	Identification of retinoblastoma related genes with shortest path in a protein-protein interaction network. <i>Biochimie</i> , 2012, 94, 1910-1917.	1.3	28
1848	Integrating Biomolecular and Clinical Data for Cancer Research: Concepts and Challenges. , 2012, , 159-172.		0
1849	Targeted Quantitative Phosphoproteomics Approach for the Detection of Phospho-tyrosine Signaling in Plants. <i>Journal of Proteome Research</i> , 2012, 11, 438-448.	1.8	44
1850	Cheminformatics-Driven Discovery of Selective, Nanomolar Inhibitors for Staphylococcal Pyruvate Kinase. <i>ACS Chemical Biology</i> , 2012, 7, 350-359.	1.6	23
1851	Conserved Noncoding Sequences Highlight Shared Components of Regulatory Networks in Dicotyledonous Plants. <i>Plant Cell</i> , 2012, 24, 3949-3965.	3.1	64
1852	Protein Phosphatase 1± Interacting Proteins in the Human Brain. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 3-17.	1.0	36
1853	Using the NeAT Toolbox to Compare Networks to Networks, Clusters to Clusters, and Network to Clusters. <i>Methods in Molecular Biology</i> , 2012, 804, 327-342.	0.4	6
1854	Network Reconstruction and Systems Analysis of Cardiac Myocyte Hypertrophy Signaling. <i>Journal of Biological Chemistry</i> , 2012, 287, 42259-42268.	1.6	82
1855	Towards an integrated molecular model of plant-virus interactions. <i>Current Opinion in Virology</i> , 2012, 2, 719-724.	2.6	54
1856	Metscape 2 bioinformatics tool for the analysis and visualization of metabolomics and gene expression data. <i>Bioinformatics</i> , 2012, 28, 373-380.	1.8	392
1857	TranscriptomeBrowser 3.0: introducing a new compendium of molecular interactions and a new visualization tool for the study of gene regulatory networks. <i>BMC Bioinformatics</i> , 2012, 13, 19.	1.2	30
1858	Alkylation Sensitivity Screens Reveal a Conserved Cross-species Functionome. <i>Molecular Cancer Research</i> , 2012, 10, 1580-1596.	1.5	35
1859	BioTapestry: A Tool to Visualize the Dynamic Properties of Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2012, 786, 359-394.	0.4	60
1860	A System-Level Transcriptomic Analysis of Schizophrenia Using Postmortem Brain Tissue Samples. <i>Archives of General Psychiatry</i> , 2012, 69, 1205.	13.8	94
1861	Systems Biology, Bioinformatics, and Biomarkers in Neuropsychiatry. <i>Frontiers in Neuroscience</i> , 2012, 6, 187.	1.4	41
1862	Mining Functional Gene Modules Linked with Rheumatoid Arthritis Using a SNP-SNP Network. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 23-34.	3.0	13
1863	The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. <i>Breast Cancer Research</i> , 2012, 14, R113.	2.2	49

#	ARTICLE	IF	CITATIONS
1864	Microbiome dynamics of human epidermis following skin barrier disruption. <i>Genome Biology</i> , 2012, 13, R101.	13.9	201
1865	Mediation of <i>Drosophila</i> autosomal dosage effects and compensation by network interactions. <i>Genome Biology</i> , 2012, 13, R28.	13.9	98
1866	CIDeR: multifactorial interaction networks in human diseases. <i>Genome Biology</i> , 2012, 13, R62.	13.9	28
1867	A network-based gene-weighting approach for pathway analysis. <i>Cell Research</i> , 2012, 22, 565-580.	5.7	46
1868	Autoimmunoreactive <sc>I</sc><sc>G</sc>s from patients with postural orthostatic tachycardia syndrome. <i>Proteomics - Clinical Applications</i> , 2012, 6, 615-625.	0.8	30
1869	Integration of biological networks and pathways with genetic association studies. <i>Human Genetics</i> , 2012, 131, 1677-1686.	1.8	40
1870	<i>Brachypodium distachyon</i> as a model for defining the allergen potential of non-prolamin proteins. <i>Functional and Integrative Genomics</i> , 2012, 12, 439-446.	1.4	4
1871	The Genomic Landscape and Evolutionary Resolution of Antagonistic Pleiotropy in Yeast. <i>Cell Reports</i> , 2012, 2, 1399-1410.	2.9	177
1872	Identification and quantification of newly synthesized proteins translationally regulated by YB-1 using a novel Clickâ€“SILAC approach. <i>Journal of Proteomics</i> , 2012, 77, e1-e10.	1.2	39
1873	Perspectives on Systems Biology Applications in Diabetic Kidney Disease. <i>Journal of Cardiovascular Translational Research</i> , 2012, 5, 491-508.	1.1	33
1874	Cross-experimental analysis of microarray gene expression datasets for in silico risk assessment of TiO2 nano-particles. <i>Molecular and Cellular Toxicology</i> , 2012, 8, 229-239.	0.8	8
1875	Syntactic trees and small-world networks: syntactic development as a dynamical process. <i>Adaptive Behavior</i> , 2012, 20, 427-442.	1.1	18
1876	Gene expression networks in COPD: microRNA and mRNA regulation. <i>Thorax</i> , 2012, 67, 122-131.	2.7	292
1877	Graph-based ontology analysis in the linked open data. , 2012, , .		10
1878	Transcriptional responses to loss of RNase H2 in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2012, 11, 933-941.	1.3	20
1879	A Critical Examination of Complex Network File Formats for Bioinformatics Data Sources. , 2012, , .		0
1880	Systematic Identification of Functional Plant Modules through the Integration of Complementary Data Sources Å Å. <i>Plant Physiology</i> , 2012, 159, 884-901.	2.3	108
1881	Compressed Adjacency Matrices: Untangling Gene Regulatory Networks. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2012, 18, 2457-2466.	2.9	44

#	ARTICLE	IF	CITATIONS
1882	An ecosystem of tools and methods for archeological research. , 2012, , .		4
1883	Synthetic lethality for linking the mycophenolate mofetil mode of action with molecular disease and drug profiles. <i>Molecular BioSystems</i> , 2012, 8, 3197.	2.9	4
1884	A Systems Biology Approach to Solving the Puzzle of Unknown Genomic Gene-Function Association Using Grid-Ready SVM Committee Machines. <i>IEEE Computational Intelligence Magazine</i> , 2012, 7, 46-54.	3.4	1
1885	Genetic screens for the control of influenza virus replication: from meta-analysis to drug discovery. <i>Molecular BioSystems</i> , 2012, 8, 1297.	2.9	30
1886	ANAP: An Integrated Knowledge Base for Arabidopsis Protein Interaction Network Analysis. <i>Plant Physiology</i> , 2012, 158, 1523-1533.	2.3	31
1887	SAMNet: a network-based approach to integrate multi-dimensional high throughput datasets. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 1415.	0.6	20
1888	Understanding the structural and energetic basis of inhibitor and substrate bound to the full-length NS3/4A: insights from molecular dynamics simulation, binding free energy calculation and network analysis. <i>Molecular BioSystems</i> , 2012, 8, 2753.	2.9	26
1889	Shaping Reactor Microbiomes to Produce the Fuel Precursor <i>n</i> -Butyrate from Pretreated Cellulosic Hydrolysates. <i>Environmental Science &amp; Technology</i> , 2012, 46, 10229-10238.	4.6	55
1890	Annotator: Postprocessing Software for Generating Function-based Signatures from Quantitative Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 1521-1536.	1.8	1
1891	Visualization of network data provenance. , 2012, , .		28
1892	Promiscuous domains: facilitating stability of the yeast protein-protein interaction network. <i>Molecular BioSystems</i> , 2012, 8, 766-771.	2.9	10
1893	Construction and analysis of human phosphorylation network. , 2012, , .		0
1894	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. <i>Blood</i> , 2012, 119, e22-e34.	0.6	84
1895	GSGS: A Computational Approach to Reconstruct Signaling Pathway Structures from Gene Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 438-450.	1.9	10
1896	enRoute: Dynamic path extraction from biological pathway maps for in-depth experimental data analysis. , 2012, , .		12
1897	Discovering link communities in complex networks by exploiting link dynamics. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2012, 2012, P10015.	0.9	18
1898	Collaboration visualization on large dataset for protein-protein interaction network. , 2012, , .		0
1899	Proteomic analysis of extracellular matrix from the hepatic stellate cell line LX-2 identifies CYR61 and Wnt-5a as novel constituents of fibrotic liver. <i>Journal of Proteome Research</i> , 2012, 11, 4052-4064.	1.8	66

#	ARTICLE	IF	CITATIONS
1900	Quantitative Proteome Analysis Reveals RNA Processing Factors As Modulators of Ionizing Radiation-Induced Apoptosis in the <i>C. elegans</i> Germline.. Journal of Proteome Research, 2012, 11, 4277-4288.	1.8	9
1901	XGDBench: A benchmarking platform for graph stores in exascale clouds. , 2012, , .		18
1902	The Protein Interaction Network of Extracellular Vesicles Derived from Human Colorectal Cancer Cells. Journal of Proteome Research, 2012, 11, 1144-1151.	1.8	66
1903	CytoMCL: A Cytoscape plugin for fast clustering of protein interaction networks. , 2012, , .		1
1904	Construction of large signaling pathways using an adaptive perturbation approach with phosphoproteomic data. Molecular BioSystems, 2012, 8, 1571.	2.9	15
1905	Genome-Wide Networks of Amino Acid Covariances Are Common among Viruses. Journal of Virology, 2012, 86, 3050-3063.	1.5	17
1906	Characterization of a Highly Conserved Histone Related Protein, Ydl156w, and Its Functional Associations Using Quantitative Proteomic Analyses. Molecular and Cellular Proteomics, 2012, 11, M111.011544.	2.5	28
1907	The Functional Network of the Arabidopsis Plastoglobule Proteome Based on Quantitative Proteomics and Genome-Wide Coexpression Analysis Å Å Å. Plant Physiology, 2012, 158, 1172-1192.	2.3	193
1908	The Arabidopsis thaliana SET-domain-containing protein ASHH1/SDG26 interacts with itself and with distinct histone lysine methyltransferases. Journal of Plant Research, 2012, 125, 679-692.	1.2	17
1909	Proteomic Profiling of Infiltrating Ductal Carcinoma Reveals Increased Cellular Interactions with Tissue Microenvironment. Journal of Proteome Research, 2012, 11, 2236-2246.	1.8	5
1910	A Multidimensional Matrix for Systems Biology Research and Its Application to Interaction Networks. Journal of Proteome Research, 2012, 11, 5204-5220.	1.8	5
1911	Proteomic Plasma Membrane Profiling Reveals an Essential Role for gp96 in the Cell Surface Expression of LDLR Family Members, Including the LDL Receptor and LRP6. Journal of Proteome Research, 2012, 11, 1475-1484.	1.8	68
1912	Identification of microRNA-regulated gene networks by expression analysis of target genes. Genome Research, 2012, 22, 1163-1172.	2.4	165
1913	Identification of Differentially Expressed Proteins in Curcumin-Treated Prostate Cancer Cell Lines. OMICS A Journal of Integrative Biology, 2012, 16, 289-300.	1.0	41
1914	Deciphering plantâ€“pathogen interactions applying metabolomics: principles and applications. Canadian Journal of Plant Pathology, 2012, 34, 29-33.	0.8	20
1915	Detection of allosteric signal transmission by informationâ€“theoretic analysis of protein dynamics. FASEB Journal, 2012, 26, 868-881.	0.2	97
1916	Identification of Core Components and Transient Interactors of the Peroxisomal Importomer by Dual-Track Stable Isotope Labeling with Amino Acids in Cell Culture Analysis. Journal of Proteome Research, 2012, 11, 2567-2580.	1.8	59
1917	Systematic Identification and Classification of Three-Dimensional Activity Cliffs. Journal of Chemical Information and Modeling, 2012, 52, 1490-1498.	2.5	26

#	ARTICLE	IF	CITATIONS
1918	C-Terminal Heat Shock Protein 90 Inhibitor Decreases Hyperglycemia-induced Oxidative Stress and Improves Mitochondrial Bioenergetics in Sensory Neurons. <i>Journal of Proteome Research</i> , 2012, 11, 2581-2593.	1.8	47
1919	Toxicogenomic Mechanisms of 6-HO-BDE-47, 6-MeO-BDE-47, and BDE-47 in <i>E. coli</i> . <i>Environmental Science &amp; Technology</i> , 2012, 46, 1185-1191.	4.6	39
1920	The Role and Impact of Research Agendas on the Comparative-Effectiveness Research Among Antihyperlipidemics. <i>Clinical Pharmacology and Therapeutics</i> , 2012, 91, 685-691.	2.3	10
1921	Triple SILAC to Determine Stimulus Specific Interactions in the Wnt Pathway. <i>Journal of Proteome Research</i> , 2012, 11, 982-994.	1.8	63
1922	An optimized gene set for transcriptomics based neurodevelopmental toxicity prediction in the neural embryonic stem cell test. <i>Toxicology</i> , 2012, 300, 158-167.	2.0	21
1923	Changes in the topology of gene expression networks by human immunodeficiency virus type 1 (HIV-1) integration in macrophages. <i>Virus Research</i> , 2012, 163, 91-97.	1.1	12
1924	Rising StARs: Behavioral, hormonal, and molecular responses to social challenge and opportunity. <i>Hormones and Behavior</i> , 2012, 61, 631-641.	1.0	52
1925	Hive plots—rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012, 13, 627-644.	3.2	187
1926	A meta-analysis of caloric restriction gene expression profiles to infer common signatures and regulatory mechanisms. <i>Molecular BioSystems</i> , 2012, 8, 1339.	2.9	80
1927	Merging experimental data and <i>in silico</i> analysis: a systems-level approach to autoimmune disease and cancer. <i>Expert Review of Clinical Immunology</i> , 2012, 8, 361-372.	1.3	8
1928	Exploration of 3D Activity Cliffs on the Basis of Compound Binding Modes and Comparison of 2D and 3D Cliffs. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 670-677.	2.5	23
1929	Dissecting ensemble networks in ES cell populations reveals micro-heterogeneity underlying pluripotency. <i>Molecular BioSystems</i> , 2012, 8, 744.	2.9	52
1930	Interfaces to PeptideAtlas: a case study of standard data access systems. <i>Briefings in Bioinformatics</i> , 2012, 13, 615-626.	3.2	1
1931	Predicting Metabolic Pathways by Sub-network Extraction. <i>Methods in Molecular Biology</i> , 2012, 804, 107-130.	0.4	8
1932	Growth of Ligand-Target Interaction Data in ChEMBL Is Associated with Increasing and Activity Measurement-Dependent Compound Promiscuity. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 2550-2558.	2.5	37
1933	Charting the Landscape of Tandem BRCT Domain-Mediated Protein Interactions. <i>Science Signaling</i> , 2012, 5, rs6.	1.6	88
1934	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. <i>Nature Biotechnology</i> , 2012, 30, 984-990.	9.4	234
1935	Pathway Based Microarray Analysis, Utilising Enzyme Compounds and Cascade Events. <i>Methods of Information in Medicine</i> , 2012, 51, 323-331.	0.7	1



#	ARTICLE	IF	CITATIONS
1936	CORNET 2.0: integrating plant coexpression, protein-protein interactions, regulatory interactions, gene associations and functional annotations. <i>New Phytologist</i> , 2012, 195, 707-720.	3.5	113
1937	New genes that extend <i>Caenorhabditis elegans</i> lifespan in response to reproductive signals. <i>Aging Cell</i> , 2012, 11, 192-202.	3.0	115
1938	Effects of Developmental Lead Exposure on the Hippocampal Transcriptome: Influences of Sex, Developmental Period, and Lead Exposure Level. <i>Toxicological Sciences</i> , 2012, 129, 108-125.	1.4	44
1939	Comprehensive Analysis of Host Cellular Interactions with Human Papillomavirus E6 Proteins Identifies New E6 Binding Partners and Reflects Viral Diversity. <i>Journal of Virology</i> , 2012, 86, 13174-13186.	1.5	178
1940	Topological analysis and interactive visualization of biological networks and protein structures. <i>Nature Protocols</i> , 2012, 7, 670-685.	5.5	445
1941	Identification of human protein complexes from local sub-graphs of protein-protein interaction network based on random forest with topological structure features. <i>Analytica Chimica Acta</i> , 2012, 718, 32-41.	2.6	14
1942	Gadd45 proteins: Relevance to aging, longevity and age-related pathologies. <i>Ageing Research Reviews</i> , 2012, 11, 51-66.	5.0	126
1943	A quick guide to biomolecular network studies: Construction, analysis, applications, and resources. <i>Biochemical and Biophysical Research Communications</i> , 2012, 424, 7-11.	1.0	11
1944	A network-based analysis of traditional Chinese medicine cold and hot patterns in rheumatoid arthritis. <i>Complementary Therapies in Medicine</i> , 2012, 20, 23-30.	1.3	54
1945	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
1946	Fumarate Is Cardioprotective via Activation of the Nrf2 Antioxidant Pathway. <i>Cell Metabolism</i> , 2012, 15, 361-371.	7.2	231
1947	PACAP interactions in the mouse brain: Implications for behavioral and other disorders. <i>Gene</i> , 2012, 491, 224-231.	1.0	15
1948	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
1949	Temporal- and Strain-Specific Host MicroRNA Molecular Signatures Associated with Swine-Origin H1N1 and Avian-Origin H7N7 Influenza A Virus Infection. <i>Journal of Virology</i> , 2012, 86, 6109-6122.	1.5	90
1950	Efficient key pathway mining: combining networks and OMICS data. <i>Integrative Biology (United Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 1</i>	0.6	54
1951	Proteomic profiling of high glucose primed monocytes identifies cyclophilin A as a potential secretory marker of inflammation in type 2 diabetes. <i>Proteomics</i> , 2012, 12, 2808-2821.	1.3	47
1952	Dopaminergic modulation of the hippocampal neuropil proteome identified by bioorthogonal noncanonical amino acid tagging (<sc>BONCAT</sc>). <i>Proteomics</i> , 2012, 12, 2464-2476.	1.3	58
1953	Theoretical and technological building blocks for an innovation accelerator. <i>European Physical Journal: Special Topics</i> , 2012, 214, 183-214.	1.2	12

#	ARTICLE	IF	CITATIONS
1954	The role of molecular chaperonins in warm ischemia and reperfusion injury in the steatotic liver: A proteomic study. <i>BMC Biochemistry</i> , 2012, 13, 17.	4.4	7
1955	OLSVis: an animated, interactive visual browser for bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 116.	1.2	20
1956	Genes2FANs: connecting genes through functional association networks. <i>BMC Bioinformatics</i> , 2012, 13, 156.	1.2	28
1957	Enabling dynamic network analysis through visualization in TVNViewer. <i>BMC Bioinformatics</i> , 2012, 13, 204.	1.2	0
1958	Network enrichment analysis: extension of gene-set enrichment analysis to gene networks. <i>BMC Bioinformatics</i> , 2012, 13, 226.	1.2	102
1959	Regulatory network operations in the Pathway Tools software. <i>BMC Bioinformatics</i> , 2012, 13, 243.	1.2	13
1960	MetNet Online: a novel integrated resource for plant systems biology. <i>BMC Bioinformatics</i> , 2012, 13, 267.	1.2	17
1961	Bioinformatics resource manager v2.3: an integrated software environment for systems biology with microRNA and cross-species analysis tools. <i>BMC Bioinformatics</i> , 2012, 13, 311.	1.2	21
1962	A Computational model for compressed sensing RNAi cellular screening. <i>BMC Bioinformatics</i> , 2012, 13, 337.	1.2	3
1963	miRTrail - a comprehensive webserver for analyzing gene and miRNA patterns to enhance the understanding of regulatory mechanisms in diseases. <i>BMC Bioinformatics</i> , 2012, 13, 36.	1.2	36
1964	Methods for visual mining of genomic and proteomic data atlases. <i>BMC Bioinformatics</i> , 2012, 13, 58.	1.2	8
1965	Quantitatively integrating molecular structure and bioactivity profile evidence into drug-target relationship analysis. <i>BMC Bioinformatics</i> , 2012, 13, 75.	1.2	6
1966	PHYLOViZ: phylogenetic inference and data visualization for sequence based typing methods. <i>BMC Bioinformatics</i> , 2012, 13, 87.	1.2	492
1967	MetaMapp: mapping and visualizing metabolomic data by integrating information from biochemical pathways and chemical and mass spectral similarity. <i>BMC Bioinformatics</i> , 2012, 13, 99.	1.2	203
1968	Sensitive detection of pathway perturbations in cancers. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	4
1969	Exploring the evolution of protein function in Archaea. <i>BMC Evolutionary Biology</i> , 2012, 12, 75.	3.2	13
1970	Target mimics: an embedded layer of microRNA-involved gene regulatory networks in plants. <i>BMC Genomics</i> , 2012, 13, 197.	1.2	76
1971	Transcriptome profiling of the demosponge <i>Amphimedon queenslandica</i> reveals genome-wide events that accompany major life cycle transitions. <i>BMC Genomics</i> , 2012, 13, 209.	1.2	47

#	ARTICLE	IF	CITATIONS
1972	atBioNetâ€“ an integrated network analysis tool for genomics and biomarker discovery. <i>BMC Genomics</i> , 2012, 13, 325.	1.2	33
1973	Remodeling of central metabolism in invasive breast cancer compared to normal breast tissue â€“ a GC-TOFMS based metabolomics study. <i>BMC Genomics</i> , 2012, 13, 334.	1.2	123
1974	The RosR transcription factor is required for gene expression dynamics in response to extreme oxidative stress in a hypersaline-adapted archaeon. <i>BMC Genomics</i> , 2012, 13, 351.	1.2	40
1975	RNA-seq and microarray complement each other in transcriptome profiling. <i>BMC Genomics</i> , 2012, 13, 629.	1.2	131
1976	Factors regulated by interferon gamma and hypoxia-inducible factor 1A contribute to responses that protect mice from <i>Coccidioides immitis</i> infection. <i>BMC Microbiology</i> , 2012, 12, 218.	1.3	17
1977	Genome-scale identification of cell-wall related genes in <i>Arabidopsis</i> based on co-expression network analysis. <i>BMC Plant Biology</i> , 2012, 12, 138.	1.6	56
1978	Co-expression analysis identifies putative targets for CBP60g and SARD1 regulation. <i>BMC Plant Biology</i> , 2012, 12, 216.	1.6	38
1979	Systems analysis of inflammatory bowel disease based on comprehensive gene information. <i>BMC Medical Genetics</i> , 2012, 13, 25.	2.1	8
1980	Changes in the gene expression programs of renal mesangial cells during diabetic nephropathy. <i>BMC Nephrology</i> , 2012, 13, 70.	0.8	48
1981	Global gene expression profiling displays a network of dysregulated genes in non-atherosclerotic arterial tissue from patients with type 2 diabetes. <i>Cardiovascular Diabetology</i> , 2012, 11, 15.	2.7	30
1982	Positive genetic interactors of HMG2 identify a new set of genetic perturbations for improving sesquiterpene production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 162.	1.9	48
1983	Logic modeling and the ridiculome under the rug. <i>BMC Biology</i> , 2012, 10, 92.	1.7	6
1984	Clarifying off-target effects for torcetrapib using network pharmacology and reverse docking approach. <i>BMC Systems Biology</i> , 2012, 6, 152.	3.0	32
1985	Network motif comparison rationalizes Sec1/Munc18-SNARE regulation mechanism in exocytosis. <i>BMC Systems Biology</i> , 2012, 6, 19.	3.0	3
1986	Predicting new molecular targets for rhein using network pharmacology. <i>BMC Systems Biology</i> , 2012, 6, 20.	3.0	38
1987	Creating and analyzing pathway and protein interaction compendia for modelling signal transduction networks. <i>BMC Systems Biology</i> , 2012, 6, 29.	3.0	71
1988	Simultaneous learning of instantaneous and time-delayed genetic interactions using novel information theoretic scoring technique. <i>BMC Systems Biology</i> , 2012, 6, 62.	3.0	17
1989	Cancer core modules identification through genomic and transcriptomic changes correlation detection at network level. <i>BMC Systems Biology</i> , 2012, 6, 64.	3.0	2

#	ARTICLE	IF	CITATIONS
1990	FAME, the Flux Analysis and Modeling Environment. <i>BMC Systems Biology</i> , 2012, 6, 8.	3.0	75
1991	MicroRNA expression signature in human abdominal aortic aneurysms. <i>BMC Medical Genomics</i> , 2012, 5, 25.	0.7	65
1992	Murine colon proteome and characterization of the protein pathways. <i>BioData Mining</i> , 2012, 5, 11.	2.2	36
1993	A multilevel layout algorithm for visualizing physical and genetic interaction networks, with emphasis on their modular organization. <i>BioData Mining</i> , 2012, 5, 2.	2.2	11
1994	CytoITMprobe: a network information flow plugin for Cytoscape. <i>BMC Research Notes</i> , 2012, 5, 237.	0.6	3
1995	LXtoo: an integrated live Linux distribution for the bioinformatics community. <i>BMC Research Notes</i> , 2012, 5, 360.	0.6	3
1996	Emerging trends in regenerative medicine: a scientometric analysis in <i>CiteSpace</i> . <i>Expert Opinion on Biological Therapy</i> , 2012, 12, 593-608.	1.4	860
1997	Diversity of Bifidobacteria within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	1.1	512
1998	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.	2.9	216
1999	A Consistent Phylogenetic Backbone for the Fungi. <i>Molecular Biology and Evolution</i> , 2012, 29, 1319-1334.	3.5	129
2000	Gene network analyses of first service conception in Brangus heifers: Use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors1. <i>Journal of Animal Science</i> , 2012, 90, 2894-2906.	0.2	66
2001	Distinct and diverse anaerobic bacterial communities in boreal lakes dominated by candidate division OD1. <i>ISME Journal</i> , 2012, 6, 1640-1652.	4.4	136
2002	Diverse epigenetic strategies interact to control epidermal differentiation. <i>Nature Cell Biology</i> , 2012, 14, 753-763.	4.6	139
2003	Identification of Essential Proteins Based on Edge Clustering Coefficient. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1070-1080.	1.9	254
2004	The proteomics of feather development in pied flycatchers ( <i>Ficedula hypoleuca</i> ) with different plumage coloration. <i>Molecular Ecology</i> , 2012, 21, 5762-5777.	2.0	13
2005	High Selectivity of the $\hat{1}^3$ -Aminobutyric Acid Transporter 2 (GAT-2, SLC6A13) Revealed by Structure-based Approach. <i>Journal of Biological Chemistry</i> , 2012, 287, 37745-37756.	1.6	49
2006	Complex Network Analysis in Microbial Systems: Theory and Examples. <i>Methods in Molecular Biology</i> , 2012, 881, 551-571.	0.4	2
2007	Comprehensive Phosphoproteome Analysis of INS-1 Pancreatic Beta-Cells using Various Digestion Strategies Coupled with Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 2206-2223.	1.8	22

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2008	Characterization of the <i>Mycobacterium tuberculosis</i> Proteome by Liquid Chromatography Mass Spectrometry-based Proteomics Techniques: A Comprehensive Resource for Tuberculosis Research. <i>Journal of Proteome Research</i> , 2012, 11, 119-130.	1.8	61
2009	Transcriptomics and systems biology analysis in identification of specific pathways involved in cacao resistance and susceptibility to witches' broom disease. <i>Molecular BioSystems</i> , 2012, 8, 1507.	2.9	23
2010	Analyzing Protein-Protein Interactions from Affinity Purification-Mass Spectrometry Data with SAINT. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.15.	25.8	114
2011	Spatial pedagogy: mapping meanings in the use of classroom space. <i>Cambridge Journal of Education</i> , 2012, 42, 235-251.	1.6	87
2012	Conceptus-Endometrium Crosstalk During Maternal Recognition of Pregnancy in Cattle1. <i>Biology of Reproduction</i> , 2012, 87, 6, 1-9.	1.2	56
2013	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. <i>Science Translational Medicine</i> , 2012, 4, 142ra94.	5.8	236
2014	An Enhanced Community Detection Method Based on Neighborhood Similarity. , 2012, , .		0
2015	A comparative analysis of protein targets of withdrawn cardiovascular drugs in human and mouse. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 10.	1.2	3
2016	Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements. <i>Methods in Cell Biology</i> , 2012, 110, 19-56.	0.5	17
2017	Soil bacterial community abundance and diversity in ice-free areas of Keller Peninsula, Antarctica. <i>Applied Soil Ecology</i> , 2012, 61, 7-15.	2.1	36
2018	Preliminary characterization of the murine membrane reticulocyte proteome. <i>Blood Cells, Molecules, and Diseases</i> , 2012, 49, 74-82.	0.6	15
2019	Vicious cycle in liver carcinogenesis: An epigenetic mirage. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2012, 36, 200-201.	0.7	0
2020	Opportunities in systems biology to discover mechanisms and repurpose drugs for CNS diseases. <i>Drug Discovery Today</i> , 2012, 17, 1208-1216.	3.2	23
2021	Gene regulatory network from microarray data of colon cancer patients using TSK-type recurrent neural fuzzy network. <i>Gene</i> , 2012, 506, 408-416.	1.0	13
2022	Computational prediction of the PolyQ and CAG repeat spinocerebellar ataxia network based on sequence identity to untranslated regions. <i>Gene</i> , 2012, 509, 273-281.	1.0	5
2023	Prediction of gene network models in limb muscle precursors. <i>Gene</i> , 2012, 509, 16-23.	1.0	8
2024	Transcriptome analysis of the human T lymphocyte cell line Jurkat and human peripheral blood mononuclear cells exposed to deoxynivalenol (DON): New mechanistic insights. <i>Toxicology and Applied Pharmacology</i> , 2012, 264, 51-64.	1.3	49
2025	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. <i>Neuroscience</i> , 2012, 226, 10-20.	1.1	4

#	ARTICLE	IF	CITATIONS
2026	Dairy fat blends high in $\hat{\iota}$ -linolenic acid are superior to n-3 fatty-acid-enriched palm oil blends for increasing DHA levels in the brains of young rats. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 1573-1582.	1.9	41
2027	Network analysis of temporal trends in scholarly research productivity. <i>Journal of Informetrics</i> , 2012, 6, 97-110.	1.4	12
2028	Gene Expression Profile of Adult Human Olfactory Bulb and Embryonic Neural Stem Cell Suggests Distinct Signaling Pathways and Epigenetic Control. <i>PLoS ONE</i> , 2012, 7, e33542.	1.1	38
2029	Drug repositioning through incomplete bi-cliques in an integrated drugâ€“targetâ€“disease network. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 778.	0.6	51
2031	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. <i>Methods in Molecular Biology</i> , 2012, 910, 279-296.	0.4	13
2032	Linking Variants from Genome-Wide Association Analysis to Function via Transcriptional Network Analysis. <i>Methods in Molecular Biology</i> , 2012, 910, 297-308.	0.4	0
2033	Characterization and Evolutionary Analysis of Proteinâ€“Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2012, 856, 363-380.	0.4	3
2034	The <i>Plasmodium falciparum</i> Schizont Phosphoproteome Reveals Extensive Phosphatidylinositol and cAMP-Protein Kinase A Signaling. <i>Journal of Proteome Research</i> , 2012, 11, 5323-5337.	1.8	128
2035	Next generation sequencing in clinical medicine: Challenges and lessons for pathology and biomedical informatics. <i>Journal of Pathology Informatics</i> , 2012, 3, 40.	0.8	128
2036	Genome-wide copy number variation study associates metabotropic glutamate receptor gene networks with attention deficit hyperactivity disorder. <i>Nature Genetics</i> , 2012, 44, 78-84.	9.4	334
2037	HYDROGEN BOND NETWORK OF 1-ALKYL-3-METHYLIMIDAZOLIUM IONIC LIQUIDS: A NETWORK THEORY ANALYSIS. <i>Journal of Theoretical and Computational Chemistry</i> , 2012, 11, 587-598.	1.8	6
2038	Phosphoproteomic Analysis of <i>Rhodospseudomonas palustris</i> Reveals the Role of Pyruvate Phosphate Dikinase Phosphorylation in Lipid Production. <i>Journal of Proteome Research</i> , 2012, 11, 5362-5375.	1.8	37
2039	Application of MapMan and RiceNet drives systematic analyses of the early heat stress transcriptome in rice seedlings. <i>Journal of Plant Biology</i> , 2012, 55, 436-449.	0.9	49
2040	Application of a systems approach to study developmental gene regulation. <i>Biophysical Reviews</i> , 2012, 4, 245-253.	1.5	2
2041	Symmetry Compression Method for Discovering Network Motifs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1776-1789.	1.9	14
2042	Matched Molecular Pair Analysis of Small Molecule Microarray Data Identifies Promiscuity Cliffs and Reveals Molecular Origins of Extreme Compound Promiscuity. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10220-10228.	2.9	41
2043	Causal reasoning on biological networks: interpreting transcriptional changes. <i>Bioinformatics</i> , 2012, 28, 1114-1121.	1.8	126
2044	A Genome-Wide Regulatorâ€“DNA Interaction Network in the Human Pathogen <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Proteome Research</i> , 2012, 11, 4682-4692.	1.8	19

#	ARTICLE	IF	CITATIONS
2045	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
2046	Proteome-wide selected reaction monitoring assays for the human pathogen <i>Streptococcus pyogenes</i> . <i>Nature Communications</i> , 2012, 3, 1301.	5.8	63
2047	Transcriptional network analysis of the tryptophan-accumulating rice mutant during grain filling. <i>Molecular Genetics and Genomics</i> , 2012, 287, 699-709.	1.0	1
2048	Integrating the Alzheimer's Disease Proteome and Transcriptome: A Comprehensive Network Model of a Complex Disease. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 37-49.	1.0	57
2049	A signal transduction score flow algorithm for cyclic cellular pathway analysis, which combines transcriptome and ChIP-seq data. <i>Molecular BioSystems</i> , 2012, 8, 3224.	2.9	11
2050	Proteomic Analysis Reveals Drug Accessible Cell Surface N-Glycoproteins of Primary and Established Glioblastoma Cell Lines. <i>Journal of Proteome Research</i> , 2012, 11, 4885-4893.	1.8	20
2051	The immune contexture in human tumours: impact on clinical outcome. <i>Nature Reviews Cancer</i> , 2012, 12, 298-306.	12.8	3,873
2052	Coherent dynamics and association networks among lake bacterioplankton taxa. <i>ISME Journal</i> , 2012, 6, 330-342.	4.4	449
2053	Combing the hairball with BioFabric: a new approach for visualization of large networks. <i>BMC Bioinformatics</i> , 2012, 13, 275.	1.2	34
2054	GSA-PCA: gene set generation by principal component analysis of the Laplacian matrix of a metabolic network. <i>BMC Bioinformatics</i> , 2012, 13, 197.	1.2	2
2055	Integration of interactive, multi-scale network navigation approach with Cytoscape for functional genomics in the big data era. <i>BMC Genomics</i> , 2012, 13, S24.	1.2	39
2056	A parallel genome-wide mRNA and microRNA profiling of the frontal cortex of HIV patients with and without HIV-associated dementia shows the role of axon guidance and downstream pathways in HIV-mediated neurodegeneration. <i>BMC Genomics</i> , 2012, 13, 677.	1.2	36
2057	Deep-sequencing transcriptome analysis of chilling tolerance mechanisms of a subnival alpine plant, <i>Chorispora bungeana</i> . <i>BMC Plant Biology</i> , 2012, 12, 222.	1.6	84
2058	Mining functional subgraphs from cancer protein-protein interaction networks. <i>BMC Systems Biology</i> , 2012, 6, S2.	3.0	10
2059	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. <i>BMC Systems Biology</i> , 2012, 6, S13.	3.0	36
2060	IntPath—an integrated pathway gene relationship database for model organisms and important pathogens. <i>BMC Systems Biology</i> , 2012, 6, S2.	3.0	41
2061	VANTED v2: a framework for systems biology applications. <i>BMC Systems Biology</i> , 2012, 6, 139.	3.0	158
2062	A new therapy for drug-resistant malaria using <i>Plasmodium</i> synthetic lethality inference. <i>Malaria Journal</i> , 2012, 11, .	0.8	0



#	ARTICLE	IF	CITATIONS
2063	Characterization of Breast Cancer Interstitial Fluids by TmT Labeling, LTQ-Orbitrap Velos Mass Spectrometry, and Pathway Analysis. <i>Journal of Proteome Research</i> , 2012, 11, 3199-3210.	1.8	40
2064	Visualising associations between paired omics™ data sets. <i>BioData Mining</i> , 2012, 5, 19.	2.2	261
2065	A network module-based method for identifying cancer prognostic signatures. <i>Genome Biology</i> , 2012, 13, R112.	13.9	141
2066	Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets. <i>Genome Medicine</i> , 2012, 4, 41.	3.6	136
2067	Systems-level analysis of age-related macular degeneration reveals global biomarkers and phenotype-specific functional networks. <i>Genome Medicine</i> , 2012, 4, 16.	3.6	234
2068	Genetic Interactions between Chromosomes 11 and 18 Contribute to Airway Hyperresponsiveness in Mice. <i>PLoS ONE</i> , 2012, 7, e29579.	1.1	8
2069	Analysis and Practical Guideline of Constraint-Based Boolean Method in Genetic Network Inference. <i>PLoS ONE</i> , 2012, 7, e30232.	1.1	6
2070	Computational Identification of Phospho-Tyrosine Sub-Networks Related to Acanthocyte Generation in Neuroacanthocytosis. <i>PLoS ONE</i> , 2012, 7, e31015.	1.1	19
2071	Mechanisms of Loss of Functions of Human Angiogenin Variants Implicated in Amyotrophic Lateral Sclerosis. <i>PLoS ONE</i> , 2012, 7, e32479.	1.1	47
2072	Charting the NF- $\kappa$ B Pathway Interactome Map. <i>PLoS ONE</i> , 2012, 7, e32678.	1.1	68
2073	Genetic Dissection of Acute Ethanol Responsive Gene Networks in Prefrontal Cortex: Functional and Mechanistic Implications. <i>PLoS ONE</i> , 2012, 7, e33575.	1.1	109
2074	Combinatorial Expression Rules of Ion Channel Genes in Juvenile Rat ( <i>Rattus norvegicus</i> ) Neocortical Neurons. <i>PLoS ONE</i> , 2012, 7, e34786.	1.1	14
2075	Application of Approximate Pattern Matching in Two Dimensional Spaces to Grid Layout for Biochemical Network Maps. <i>PLoS ONE</i> , 2012, 7, e37739.	1.1	9
2076	Predicting Candidate Genes Based on Combined Network Topological Features: A Case Study in Coronary Artery Disease. <i>PLoS ONE</i> , 2012, 7, e39542.	1.1	45
2077	miRNA-mRNA Correlation-Network Modules in Human Prostate Cancer and the Differences between Primary and Metastatic Tumor Subtypes. <i>PLoS ONE</i> , 2012, 7, e40130.	1.1	38
2078	Developmental Changes in the Metabolic Network of Snapdragon Flowers. <i>PLoS ONE</i> , 2012, 7, e40381.	1.1	72
2079	Cancer Association Study of Aminoacyl-tRNA Synthetase Signaling Network in Glioblastoma. <i>PLoS ONE</i> , 2012, 7, e40960.	1.1	26
2080	The Transcription Profile of Tax-3 Is More Similar to Tax-1 than Tax-2: Insights into HTLV-3 Potential Leukemogenic Properties. <i>PLoS ONE</i> , 2012, 7, e41003.	1.1	28

#	ARTICLE	IF	CITATIONS
2081	The Protein Architecture of Human Secretory Vesicles Reveals Differential Regulation of Signaling Molecule Secretion by Protein Kinases. PLoS ONE, 2012, 7, e41134.	1.1	11
2082	Prediction and Analysis of the Protein Interactome in Pseudomonas aeruginosa to Enable Network-Based Drug Target Selection. PLoS ONE, 2012, 7, e41202.	1.1	33
2083	NEXCADE: Perturbation Analysis for Complex Networks. PLoS ONE, 2012, 7, e41827.	1.1	22
2084	PATHLOGIC-S: A Scalable Boolean Framework for Modelling Cellular Signalling. PLoS ONE, 2012, 7, e41977.	1.1	6
2085	Comparative Transcriptome Analysis of Two Olive Cultivars in Response to NaCl-Stress. PLoS ONE, 2012, 7, e42931.	1.1	39
2086	Distinct and Competitive Regulatory Patterns of Tumor Suppressor Genes and Oncogenes in Ovarian Cancer. PLoS ONE, 2012, 7, e44175.	1.1	27
2087	Recruitment of Rpd3 to the Telomere Depends on the Protein Arginine Methyltransferase Hmt1. PLoS ONE, 2012, 7, e44656.	1.1	4
2088	Porcine Tissue-Specific Regulatory Networks Derived from Meta-Analysis of the Transcriptome. PLoS ONE, 2012, 7, e46159.	1.1	23
2089	Expression Profiling of Human Immune Cell Subsets Identifies miRNA-mRNA Regulatory Relationships Correlated with Cell Type Specific Expression. PLoS ONE, 2012, 7, e29979.	1.1	180
2090	The Surname Space of the Czech Republic: Examining Population Structure by Network Analysis of Spatial Co-Occurrence of Surnames. PLoS ONE, 2012, 7, e48568.	1.1	17
2091	Wiki-Pi: A Web-Server of Annotated Human Protein-Protein Interactions to Aid in Discovery of Protein Function. PLoS ONE, 2012, 7, e49029.	1.1	67
2092	Protein Interaction Network of Arabidopsis thaliana Female Gametophyte Development Identifies Novel Proteins and Relations. PLoS ONE, 2012, 7, e49931.	1.1	36
2093	Computational Prediction of Protein-Protein Interactions in Leishmania Predicted Proteomes. PLoS ONE, 2012, 7, e51304.	1.1	32
2094	Gene Expression Profiling Combined with Bioinformatics Analysis Identify Biomarkers for Parkinson Disease. PLoS ONE, 2012, 7, e52319.	1.1	20
2095	The Vineyard Yeast Microbiome, a Mixed Model Microbial Map. PLoS ONE, 2012, 7, e52609.	1.1	176
2096	Using Multiple Phenotype Assays and Epistasis Testing to Enhance the Reliability of RNAi Screening and Identify Regulators of Muscle Protein Degradation. Genes, 2012, 3, 686-701.	1.0	5
2097	The Effect of Curcumin on Human Bronchial Epithelial Cells Exposed to Fine Particulate Matter: A Predictive Analysis. Molecules, 2012, 17, 12406-12426.	1.7	11
2098	Systems Biology Approach to Identify Gene Network Signatures for Colorectal Cancer. Frontiers in Genetics, 2012, 3, 80.	1.1	16

#	ARTICLE	IF	CITATIONS
2099	Genetic Background Specific Hypoxia Resistance in Rat is Correlated with Balanced Activation of a Cross-Chromosomal Genetic Network Centering on Physiological Homeostasis. <i>Frontiers in Genetics</i> , 2012, 3, 208.	1.1	4
2100	Distribution, Abundance, and Diversity Patterns of the Thermoacidophilic "Deep-Sea Hydrothermal Vent Euryarchaeota". <i>Frontiers in Microbiology</i> , 2012, 3, 47.	1.5	32
2101	Tuning the Orchestra: Transcriptional Pathways Controlling Axon Regeneration. <i>Frontiers in Molecular Neuroscience</i> , 2011, 4, 60.	1.4	68
2102	Centralities Based Analysis of Complex Networks. , 0, , .		44
2103	Current Advances in Computational Strategies for Drug Discovery in Leishmaniasis. , 0, , .		1
2104	Analysis of Gene Expression Data Using Biclustering Algorithms. , 0, , .		1
2105	Systemic Approach to the Genome Integration Process of Human Lentivirus. , 2012, , .		1
2106	Potential Candidate Genes for Alveolar Hypoxia Identified by Transcriptome Network Analysis. <i>Medicina (Lithuania)</i> , 2012, 48, 84.	0.8	1
2107	Protein-Protein Interactions and Disease. , 0, , .		1
2108	In silico analysis strategies and resources for psychiatric genetics research. , 0, , 34-48.		0
2109	Computational methods for the analysis of tag sequences in metagenomics studies. <i>Frontiers in Bioscience - Scholar</i> , 2012, S4, 1333-1343.	0.8	2
2110	Interactive state-transition diagrams for visualization of multimodal annotation. <i>Intelligent Data Analysis</i> , 2012, 16, 683-702.	0.4	4
2111	'Omics' Approaches to Understanding Interstitial Cystitis/Painful Bladder Syndrome/Bladder Pain Syndrome. <i>International Neurourology Journal</i> , 2012, 16, 159.	0.5	19
2112	Exploring and linking biomedical resources through multidimensional semantic spaces. <i>BMC Bioinformatics</i> , 2012, 13, S6.	1.2	12
2113	Mining proteomic data for biomedical research. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 1-13.	4.6	11
2114	Computational structural analysis of protein interactions and networks. <i>Proteomics</i> , 2012, 12, 1697-1705.	1.3	14
2115	Toward a systems level view of the ECM and related proteins: A framework for the systematic definition and analysis of biological systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1522-1544.	1.5	26
2116	Review of statistical network analysis: models, algorithms, and software. <i>Statistical Analysis and Data Mining</i> , 2012, 5, 243-264.	1.4	97

#	ARTICLE	IF	CITATIONS
2117	PTMScan Direct: Identification and Quantification of Peptides from Critical Signaling Proteins by Immunoaffinity Enrichment Coupled with LC-MS/MS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 187-201.	2.5	119
2118	Analyzing Proteinâ€“Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 2014-2031.	1.8	145
2119	PhosphoSiteAnalyzer: A Bioinformatic Platform for Deciphering Phospho Proteomes Using Kinase Predictions Retrieved from NetworkKIN. <i>Journal of Proteome Research</i> , 2012, 11, 3480-3486.	1.8	19
2120	Systematic identification of genomic markers of drug sensitivity in cancer cells. <i>Nature</i> , 2012, 483, 570-575.	13.7	2,173
2121	Expression2Kinases: mRNA profiling linked to multiple upstream regulatory layers. <i>Bioinformatics</i> , 2012, 28, 105-111.	1.8	137
2122	Detecting overlapping protein complexes in protein-protein interaction networks. <i>Nature Methods</i> , 2012, 9, 471-472.	9.0	1,129
2123	COVAIn: a toolbox for uni- and multivariate statistics, time-series and correlation network analysis and inverse estimation of the differential Jacobian from metabolomics covariance data. <i>Metabolomics</i> , 2012, 8, 81-93.	1.4	168
2124	MicroRNA and transcription factor co-regulatory network analysis reveals miR-19 inhibits CYLD in T-cell acute lymphoblastic leukemia. <i>Nucleic Acids Research</i> , 2012, 40, 5201-5214.	6.5	119
2125	Prediction of chemicalâ€“protein interactions: multitarget-QSAR versus computational chemogenomic methods. <i>Molecular BioSystems</i> , 2012, 8, 2373.	2.9	100
2126	Effect of supplementation with an 80:20 <i>cis</i> : <i>trans</i> 11 conjugated linoleic acid blend on the human platelet proteome. <i>Molecular Nutrition and Food Research</i> , 2012, 56, 1148-1159.	1.5	14
2127	Alperujo extract, hydroxytyrosol, and 3,4-dihydroxyphenylglycol are bioavailable and have antioxidant properties in vitamin E-deficient ratsâ€“a proteomics and network analysis approach. <i>Molecular Nutrition and Food Research</i> , 2012, 56, 1131-1147.	1.5	31
2128	Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. <i>Human Mutation</i> , 2012, 33, 1566-1575.	1.1	26
2129	Systematic analysis of genotypeâ€“specific drug responses in cancer. <i>International Journal of Cancer</i> , 2012, 131, 2456-2464.	2.3	28
2130	SMILE silencing and PMA activation gene networks in hela cells: Comparison with kidney transplantation gene networks. <i>Journal of Cellular Biochemistry</i> , 2012, 113, 1820-1832.	1.2	14
2131	Systematic identification of interactions between host cell proteins and E7 oncoproteins from diverse human papillomaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E260-7.	3.3	182
2132	Determination of Protein Interactome of Transcription Factor Sox2 in Embryonic Stem Cells Engineered for Inducible Expression of Four Reprogramming Factors. <i>Journal of Biological Chemistry</i> , 2012, 287, 11384-11397.	1.6	63
2133	Analyzing Biological Data Using R: Methods for Graphs and Networks. <i>Methods in Molecular Biology</i> , 2012, 804, 343-373.	0.4	16
2134	MicroRNA expression changes after lung cancer resection. <i>RNA Biology</i> , 2012, 9, 900-910.	1.5	30

#	ARTICLE	IF	CITATIONS
2135	Integrated cross-species transcriptional network analysis of metastatic susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3184-3189.	3.3	50
2136	<scp>SciMAT</scp>: A new science mapping analysis software tool. Journal of the Association for Information Science and Technology, 2012, 63, 1609-1630.	2.6	692
2137	Expression, Circulation, and Excretion Profile of MicroRNA-21, -155, and -18a Following Acute Kidney Injury. Toxicological Sciences, 2012, 129, 256-267.	1.4	173
2138	Mass spectral molecular networking of living microbial colonies. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1743-52.	3.3	804
2139	Gene Set Enrichment Analysis Identifies LIF as a Negative Regulator of Human Th2 Cell Differentiation. Scientific Reports, 2012, 2, 464.	1.6	8
2140	Public Domain Databases for Medicinal Chemistry. Journal of Medicinal Chemistry, 2012, 55, 6987-7002.	2.9	81
2141	Predicting drug targets based on protein domains. Molecular BioSystems, 2012, 8, 1528.	2.9	31
2142	Browsing Metabolic and Regulatory Networks with BioCyc. Methods in Molecular Biology, 2012, 804, 197-216.	0.4	27
2143	Computational tools for prioritizing candidate genes: boosting disease gene discovery. Nature Reviews Genetics, 2012, 13, 523-536.	7.7	387
2144	Surface Interactome in Streptococcus pyogenes. Molecular and Cellular Proteomics, 2012, 11, M111.015206.	2.5	9
2145	Identification of salt treated proteins in sorghum using gene ontology linkage. Physiology and Molecular Biology of Plants, 2012, 18, 209-216.	1.4	7
2146	Bayesian mapping of multiple traits in maize: the importance of pleiotropic effects in studying the inheritance of quantitative traits. Theoretical and Applied Genetics, 2012, 125, 479-493.	1.8	13
2147	A longitudinal systems biology analysis of lactulose withdrawal in hepatic encephalopathy. Metabolic Brain Disease, 2012, 27, 205-215.	1.4	88
2148	Computational kinetic studies of pyruvate metabolism in Carboxydotherrmus hydrogenoformans Z-2901 for improved hydrogen production. Biotechnology and Bioprocess Engineering, 2012, 17, 565-575.	1.4	2
2149	Global profiling of ultraviolet-induced metabolic disruption in Melissa officinalis by using gas chromatography-mass spectrometry. Analytical and Bioanalytical Chemistry, 2012, 404, 553-562.	1.9	24
2150	Prioritization of SNPs for Genome-Wide Association Studies Using an Interaction Model of Genetic Variation, Gene Expression, and Trait Variation. Molecules and Cells, 2012, 33, 351-362.	1.0	2
2151	A subcellular localization compendium of hydrogen peroxide-induced proteins. Plant, Cell and Environment, 2012, 35, 308-320.	2.8	86
2152	The SCO2 protein disulphide isomerase is required for thylakoid biogenesis and interacts with LCHB1 chlorophyll a/b binding proteins which affects chlorophyll biosynthesis in Arabidopsis seedlings. Plant Journal, 2012, 69, 743-754.	2.8	64

#	ARTICLE	IF	CITATIONS
2153	GPEC: A Cytoscape plug-in for random walk-based gene prioritization and biomedical evidence collection. <i>Computational Biology and Chemistry</i> , 2012, 37, 17-23.	1.1	50
2154	Combining imaging and pathway profiling: an alternative approach to cancer drug discovery. <i>Drug Discovery Today</i> , 2012, 17, 203-214.	3.2	18
2155	Seasonal variability in airborne bacterial communities at a high-elevation site. <i>Atmospheric Environment</i> , 2012, 50, 41-49.	1.9	226
2156	Automatic generation of causal networks linking growth factor stimuli to functional cell state changes. <i>FEBS Journal</i> , 2012, 279, 3462-3474.	2.2	7
2157	Star-like auto-configurable layouts of variable radius for visualizing and exploring RDF/S ontologies. <i>Journal of Visual Languages and Computing</i> , 2012, 23, 137-153.	1.8	4
2158	Identification of potential host proteins for influenza A virus based on topological and biological characteristics by proteome-wide network approach. <i>Journal of Proteomics</i> , 2012, 75, 2500-2513.	1.2	10
2159	Meta-analysis of genetic and environmental Parkinson's disease models reveals a common role of mitochondrial protection pathways. <i>Neurobiology of Disease</i> , 2012, 45, 1018-1030.	2.1	34
2160	In utero exposure to benzo(a)pyrene predisposes offspring to cardiovascular dysfunction in later-life. <i>Toxicology</i> , 2012, 295, 56-67.	2.0	36
2161	Computational tools for metabolic engineering. <i>Metabolic Engineering</i> , 2012, 14, 270-280.	3.6	93
2162	A proteomics approach reveals divergent molecular responses to salinity in populations of European whitefish ( <i>Coregonus lavaretus</i> ). <i>Molecular Ecology</i> , 2012, 21, 3516-3530.	2.0	54
2163	Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor <i>SIERF6</i> plays an important role in ripening and carotenoid accumulation. <i>Plant Journal</i> , 2012, 70, 191-204.	2.8	268
2164	Dissection of genotype-phenotype associations in rice grains using metabolome quantitative trait loci analysis. <i>Plant Journal</i> , 2012, 70, 624-636.	2.8	173
2165	Deciphering energy-associated gene networks operating in the response of Arabidopsis plants to stress and nutritional cues. <i>Plant Journal</i> , 2012, 70, 954-966.	2.8	29
2166	A stress-specific calcium signature regulating an ozone-responsive gene expression network in Arabidopsis. <i>Plant Journal</i> , 2012, 71, 948-961.	2.8	52
2167	Export diversification in a transitioning economy. <i>Economics of Transition</i> , 2012, 20, 339-367.	0.7	7
2168	Prediction of protein-protein interactions between viruses and human by an SVM model. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	83
2169	RuleBender: integrated modeling, simulation and visualization for rule-based intracellular biochemistry. <i>BMC Bioinformatics</i> , 2012, 13, S3.	1.2	56
2170	Prediction and characterization of protein-protein interaction networks in swine. <i>Proteome Science</i> , 2012, 10, 2.	0.7	33

#	ARTICLE	IF	CITATIONS
2171	Alterations in tumor necrosis factor signaling pathways are associated with cytotoxicity and resistance to taxanes: a study in isogenic resistant tumor cells. <i>Breast Cancer Research</i> , 2012, 14, R2.	2.2	45
2172	Tools for protein-protein interaction network analysis in cancer research. <i>Clinical and Translational Oncology</i> , 2012, 14, 3-14.	1.2	35
2173	Genome-Wide Analysis of Genes Induced by <i>Fusarium graminearum</i> Infection in Resistant and Susceptible Wheat Cultivars. <i>Journal of Plant Biology</i> , 2012, 55, 64-72.	0.9	11
2174	Cold and heat pattern of rheumatoid arthritis in traditional Chinese medicine: distinct molecular signatures indentified by microarray expression profiles in CD4-positive T cell. <i>Rheumatology International</i> , 2012, 32, 61-68.	1.5	74
2175	Of possible cheminformatics futures. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 107-112.	1.3	10
2176	The application of gene co-expression network reconstruction based on CNVs and gene expression microarray data in breast cancer. <i>Molecular Biology Reports</i> , 2012, 39, 1627-1637.	1.0	16
2177	Tea Tree Oilâ€”Induced Transcriptional Alterations in <i>Staphylococcus aureus</i> . <i>Phytotherapy Research</i> , 2013, 27, 390-396.	2.8	32
2178	Comparison of a simulated $\beta$ Cro dimer conformational ensemble to its NMR models. <i>International Journal of Quantum Chemistry</i> , 2013, 113, 518-524.	1.0	4
2179	Angiogenin induces modifications in the astrocyte secretome: Relevance to amyotrophic lateral sclerosis. <i>Journal of Proteomics</i> , 2013, 91, 274-285.	1.2	40
2180	Interactions between specific phytoplankton and bacteria affect lake bacterial community succession. <i>Environmental Microbiology</i> , 2013, 15, 2489-2504.	1.8	94
2181	What google maps can do for biomedical data dissemination: examples and a design study. <i>BMC Research Notes</i> , 2013, 6, 179.	0.6	6
2183	Data-Independent Microbial Metabolomics with Ambient Ionization Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1167-1176.	1.2	22
2184	A human skeletal muscle interactome centered on proteins involved in muscular dystrophies: LGMD interactome. <i>Skeletal Muscle</i> , 2013, 3, 3.	1.9	36
2185	Hepatitis C virus/human interactome identifies SMURF2 and the viral protease as critical elements for the control of TGF $\beta$ signaling. <i>FASEB Journal</i> , 2013, 27, 4027-4040.	0.2	16
2186	Metabolomics Reveals Differential Levels of Oral Metabolites in HIV-Infected Patients: Toward Novel Diagnostic Targets. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 5-15.	1.0	46
2187	In silico identification of Gram-negative bacterial secreted proteins from primary sequence. <i>Computers in Biology and Medicine</i> , 2013, 43, 1177-1181.	3.9	14
2188	Microarray gene expression profiling analysis combined with bioinformatics in multiple sclerosis. <i>Molecular Biology Reports</i> , 2013, 40, 3731-3737.	1.0	14
2189	Coexpression patterns indicate that GPI-anchored non-specific lipid transfer proteins are involved in accumulation of cuticular wax, suberin and sporopollenin. <i>Plant Molecular Biology</i> , 2013, 83, 625-649.	2.0	70



#	ARTICLE	IF	CITATIONS
2190	Systems approaches and polypharmacology for drug discovery from herbal medicines: An example using licorice. <i>Journal of Ethnopharmacology</i> , 2013, 146, 773-793.	2.0	290
2191	Differential seminal plasma proteome according to semen retrieval in men with spinal cord injury. <i>Fertility and Sterility</i> , 2013, 100, 959-969.e3.	0.5	27
2192	Previously unknown and highly divergent ssDNA viruses populate the oceans. <i>ISME Journal</i> , 2013, 7, 2169-2177.	4.4	160
2193	Structurally distinct polycyclic aromatic hydrocarbons induce differential transcriptional responses in developing zebrafish. <i>Toxicology and Applied Pharmacology</i> , 2013, 272, 656-670.	1.3	73
2194	Sexual dimorphic floral development in dioecious plants revealed by transcriptome, phytohormone, and DNA methylation analysis in <i>Populus tomentosa</i> . <i>Plant Molecular Biology</i> , 2013, 83, 559-576.	2.0	66
2195	Temporal variability and coherence of euphotic zone bacterial communities over a decade in the Southern California Bight. <i>ISME Journal</i> , 2013, 7, 2259-2273.	4.4	162
2196	Lack of correlation between predicted and actual off-target effects of short-interfering RNAs targeting the human papillomavirus type 16 E7 oncogene. <i>British Journal of Cancer</i> , 2013, 108, 450-460.	2.9	16
2197	Efficiency of siRNA delivery by lipid nanoparticles is limited by endocytic recycling. <i>Nature Biotechnology</i> , 2013, 31, 653-658.	9.4	660
2198	Recent advances in cardiovascular proteomics. <i>Journal of Proteomics</i> , 2013, 81, 3-14.	1.2	30
2199	Mapping the functional yeast ABC transporter interactome. <i>Nature Chemical Biology</i> , 2013, 9, 565-572.	3.9	93
2200	A tripartite transcription factor network regulates primordial germ cell specification in mice. <i>Nature Cell Biology</i> , 2013, 15, 905-915.	4.6	240
2201	A Miniaturized Chemical Proteomic Approach for Target Profiling of Clinical Kinase Inhibitors in Tumor Biopsies. <i>Journal of Proteome Research</i> , 2013, 12, 4005-4017.	1.8	15
2202	Putative cobalt- and nickel-binding proteins and motifs in <i>Streptococcus pneumoniae</i> . <i>Metallomics</i> , 2013, 5, 928.	1.0	37
2203	Reconstruction of regulatory networks through temporal enrichment profiling and its application to H1N1 influenza viral infection. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	11
2204	Discovery and analysis of consistent active sub-networks in cancers. <i>BMC Bioinformatics</i> , 2013, 14, S7.	1.2	12
2205	bioWeb3D: an online WebGL 3D data visualisation tool. <i>BMC Bioinformatics</i> , 2013, 14, 185.	1.2	15
2206	Active subnetwork recovery with a mechanism-dependent scoring function; with application to angiogenesis and organogenesis studies. <i>BMC Bioinformatics</i> , 2013, 14, 59.	1.2	4
2207	Predicting PDZ domain mediated protein interactions from structure. <i>BMC Bioinformatics</i> , 2013, 14, 27.	1.2	32

#	ARTICLE	IF	CITATIONS
2208	CySBGN: A Cytoscape plug-in to integrate SBGN maps. BMC Bioinformatics, 2013, 14, 17.	1.2	35
2209	Visualization of protein interaction networks: problems and solutions. BMC Bioinformatics, 2013, 14, S1.	1.2	70
2210	A knowledge-based decision support system in bioinformatics: an application to protein complex extraction. BMC Bioinformatics, 2013, 14, S5.	1.2	15
2211	A system-level, molecular evolutionary analysis of mammalian phototransduction. BMC Evolutionary Biology, 2013, 13, 52.	3.2	21
2212	Multiscale modeling of the causal functional roles of nsSNPs in a genome-wide association study: application to hypoxia. BMC Genomics, 2013, 14, S9.	1.2	6
2213	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. BMC Genomics, 2013, 14, 449.	1.2	118
2214	An integrative "omics" approach identifies new candidate genes to impact aroma volatiles in peach fruit. BMC Genomics, 2013, 14, 343.	1.2	48
2215	ContigScape: a Cytoscape plugin facilitating microbial genome gap closing. BMC Genomics, 2013, 14, 289.	1.2	34
2216	Comparative genomics and functional study of lipid metabolic genes in <i>Caenorhabditis elegans</i> . BMC Genomics, 2013, 14, 164.	1.2	84
2217	Expanding the boundaries of local similarity analysis. BMC Genomics, 2013, 14, S3.	1.2	34
2218	From desk to bed: Computational simulations provide indication for rheumatoid arthritis clinical trials. BMC Systems Biology, 2013, 7, 10.	3.0	10
2219	Signalink 2 " a signaling pathway resource with multi-layered regulatory networks. BMC Systems Biology, 2013, 7, 7.	3.0	169
2220	Integrative analysis of congenital muscular torticollis: from gene expression to clinical significance. BMC Medical Genomics, 2013, 6, S10.	0.7	17
2221	Phosphoproteomics Study on the Activated PKC $\gamma$ -Induced Cell Death. Journal of Proteome Research, 2013, 12, 4280-4301.	1.8	8
2222	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome. World Journal of Microbiology and Biotechnology, 2013, 29, 223-233.	1.7	40
2223	Global Phosphoproteomic Analysis Reveals Diverse Functions of Serine/Threonine/Tyrosine Phosphorylation in the Model Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. Journal of Proteome Research, 2013, 12, 1909-1923.	1.8	72
2224	Databases as instruments for analysis of large-scale data sets of interactions between molecular biological objects. Biology Bulletin, 2013, 40, 233-242.	0.1	2
2225	Complex Adaptive Systems Modeling: A multidisciplinary Roadmap. Complex Adaptive Systems Modeling, 2013, 1, .	1.6	45

#	ARTICLE	IF	CITATIONS
2226	Network motifs in the transcriptional regulation network of cervical carcinoma cells respond to EGF. Archives of Gynecology and Obstetrics, 2013, 287, 771-777.	0.8	12
2227	Personal genomes, quantitative dynamic omics and personalized medicine. Quantitative Biology, 2013, 1, 71-90.	0.3	29
2228	Proteomic Identification Network Analysis of Haptoglobin as a Key Regulator Associated with Liver Fibrosis. Applied Biochemistry and Biotechnology, 2013, 169, 832-846.	1.4	12
2229	Identification of MFS proteins in sorghum using semantic similarity. Theory in Biosciences, 2013, 132, 105-113.	0.6	5
2230	Gene expression analysis distinguishes tissue-specific and gender-related functions among adult Ascaris suum tissues. Molecular Genetics and Genomics, 2013, 288, 243-260.	1.0	9
2231	Time-dependent network analysis reveals molecular targets underlying the development of diet-induced obesity and non-alcoholic steatohepatitis. Genes and Nutrition, 2013, 8, 301-316.	1.2	13
2232	Screening of osteoprotegerin-related feature genes in osteoporosis and functional analysis with DNA microarray. European Journal of Medical Research, 2013, 18, 15.	0.9	4
2233	LGR5 is a Proneural Factor and is Regulated by OLIG2 in Glioma Stem-Like Cells. Cellular and Molecular Neurobiology, 2013, 33, 851-865.	1.7	15
2234	Construction of small RNA-mediated gene regulatory networks in the roots of rice (Oryza sativa). BMC Genomics, 2013, 14, 510.	1.2	22
2235	Fast prediction of deleterious angiogenin mutations causing amyotrophic lateral sclerosis. FEBS Letters, 2013, 587, 1762-1766.	1.3	14
2236	Prediction of Functional Loss of Human Angiogenin Mutants Associated with ALS by Molecular Dynamics Simulations. Scientific Reports, 2013, 3, 1225.	1.6	43
2237	Network-based target ranking for polypharmacological therapies. Journal of Biomedical Informatics, 2013, 46, 876-881.	2.5	39
2238	Information content and scalability in signal transduction network reconstruction formats. Molecular BioSystems, 2013, 9, 1993.	2.9	15
2239	Transcription Factor Binding in Human Cells Occurs in Dense Clusters Formed around Cohesin Anchor Sites. Cell, 2013, 154, 801-813.	13.5	327
2240	Interpreting the Omics "era"™ Data. Smart Innovation, Systems and Technologies, 2013, , 79-100.	0.5	7
2241	Capturing the population structure of microparasites: using ITS "sequence data and a pooled DNA approach. Molecular Ecology Resources, 2013, 13, 918-928.	2.2	7
2242	5' Regulatory region of ubiquitin 2 gene from Porteresia coarctata makes efficient promoters for transgene expression in monocots and dicots. Plant Cell Reports, 2013, 32, 1199-1210.	2.8	28
2243	Sequencing of Sitka spruce (Picea sitchensis) cDNA libraries constructed from autumn buds and foliage reveals autumn-specific spruce transcripts. Tree Genetics and Genomes, 2013, 9, 683-691.	0.6	6

#	ARTICLE	IF	CITATIONS
2244	Computational annotation of plant metabolomics profiles via a novel network-assisted approach. <i>Metabolomics</i> , 2013, 9, 904-918.	1.4	17
2245	Epigenetic regulation of cholinergic receptor M1 (CHRM1) by histone H3K9me3 impairs Ca <sup>2+</sup> signaling in Huntington's disease. <i>Acta Neuropathologica</i> , 2013, 125, 727-739.	3.9	48
2246	Proposal for a new therapy for drug-resistant malaria using Plasmodium synthetic lethality inference. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2013, 3, 119-128.	1.4	10
2247	Hierarchical approaches for systems modeling in cardiac development. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 289-305.	6.6	8
2248	Qualitative Modelling of Metabolic Networks. <i>Advances in Botanical Research</i> , 2013, 67, 557-591.	0.5	0
2249	Deciphering the host-pathogen protein interface in chikungunya virus-mediated sickness. <i>Archives of Virology</i> , 2013, 158, 1159-1172.	0.9	14
2250	The CRTC1-SIK1 Pathway Regulates Entrainment of the Circadian Clock. <i>Cell</i> , 2013, 154, 1100-1111.	13.5	175
2251	Sewage reflects the distribution of human faecal <i>Achnospiraceae</i> . <i>Environmental Microbiology</i> , 2013, 15, 2213-2227.	1.8	88
2252	Reconstruction and visualization of carbohydrate, N-glycosylation pathways in <i>Pichia pastoris</i> CBS7435 using computational and system biology approaches. <i>Systems and Synthetic Biology</i> , 2013, 7, 7-22.	1.0	9
2253	The sarcoplasmic fish proteome: Pathways, metabolic networks and potential bioactive peptides for nutritional inferences. <i>Journal of Proteomics</i> , 2013, 78, 211-220.	1.2	43
2254	Gene coexpression network analysis identifies genes and biological processes shared among anterior pituitary and brain areas that affect estrous behavior in dairy cows. <i>Journal of Dairy Science</i> , 2013, 96, 2583-2595.	1.4	15
2255	Phoenix 2: A locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. <i>Journal of Biotechnology</i> , 2013, 167, 393-403.	1.9	53
2256	High-level colonisation of the human gut by Verrucomicrobia following broad-spectrum antibiotic treatment. <i>International Journal of Antimicrobial Agents</i> , 2013, 41, 149-155.	1.1	186
2257	A UV-Induced Genetic Network Links the RSC Complex to Nucleotide Excision Repair and Shows Dose-Dependent Rewiring. <i>Cell Reports</i> , 2013, 5, 1714-1724.	2.9	18
2258	Whole-blood gene expression profiling in ankylosing spondylitis identifies novel candidate genes that may contribute to the inflammatory and tissue-destructive disease aspects. <i>Cellular Immunology</i> , 2013, 286, 59-64.	1.4	6
2259	A comprehensive machine-readable view of the mammalian cholesterol biosynthesis pathway. <i>Biochemical Pharmacology</i> , 2013, 86, 56-66.	2.0	64
2260	On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks. , 2013, , .		1
2261	Identifying Spurious Interactions and Predicting Missing Interactions in the Protein-Protein Interaction Networks via a Generative Network Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 219-225.	1.9	16

#	ARTICLE	IF	CITATIONS
2262	Proteomics study on the hepatoprotective effects of traditional Chinese medicine formulae Yin-Chen-Hao-Tang by a combination of two-dimensional polyacrylamide gel electrophoresis and matrix-assisted laser desorption/ionization-time of flight mass spectrometry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2013, 75, 173-179.	1.4	48
2263	Polygalacturonases from <i>Moniliophthora perniciosa</i> are regulated by fermentable carbon sources and possible post-translational modifications. <i>Fungal Genetics and Biology</i> , 2013, 60, 110-121.	0.9	7
2264	A survey of two-dimensional graph layout techniques for information visualisation. <i>Information Visualization</i> , 2013, 12, 324-357.	1.2	123
2265	Predicting the host protein interactors of Chandipura virus using a structural similarity-based approach. <i>Pathogens and Disease</i> , 2013, 69, n/a-n/a.	0.8	14
2266	A proteomic approach of pediatric astrocytomas: MiRNAs and network insight. <i>Journal of Proteomics</i> , 2013, 94, 162-175.	1.2	20
2268	Image-based transcriptomics in thousands of single human cells at single-molecule resolution. <i>Nature Methods</i> , 2013, 10, 1127-1133.	9.0	253
2269	Impact of TGF- $\beta$ on breast cancer from a quantitative proteomic analysis. <i>Computers in Biology and Medicine</i> , 2013, 43, 2096-2102.	3.9	4
2270	Impaired tissue regeneration corresponds with altered expression of developmental genes that persists in the metabolic memory state of diabetic zebrafish. <i>Wound Repair and Regeneration</i> , 2013, 21, 320-328.	1.5	27
2271	Spatiotemporal Dynamics of Intratumoral Immune Cells Reveal the Immune Landscape in Human Cancer. <i>Immunity</i> , 2013, 39, 782-795.	6.6	2,983
2272	Comparative Proteomics Reveal Diverse Functions and Dynamic Changes of <i>Bombyx mori</i> Silk Proteins Spun from Different Development Stages. <i>Journal of Proteome Research</i> , 2013, 12, 5213-5222.	1.8	75
2273	Encore: Genetic Association Interaction Network Centrality Pipeline and Application to SLE Exome Data. <i>Genetic Epidemiology</i> , 2013, 37, 614-621.	0.6	25
2274	Functional Classification of Immune Regulatory Proteins. <i>Structure</i> , 2013, 21, 766-776.	1.6	23
2275	Transcriptome alterations in zebrafish embryos after exposure to environmental estrogens and anti-androgens can reveal endocrine disruption. <i>Reproductive Toxicology</i> , 2013, 42, 210-223.	1.3	56
2276	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. <i>Human Molecular Genetics</i> , 2013, 22, 4194-4205.	1.4	81
2277	Adaptation response of <i>Arabidopsis thaliana</i> to random positioning. <i>Advances in Space Research</i> , 2013, 52, 1320-1331.	1.2	6
2278	Phylogenomic Network and Comparative Genomics Reveal a Diverged Member of the $\Phi$ KZ-Related Group, Marine <i>Vibrio</i> Phage $\Phi$ JM-2012. <i>Journal of Virology</i> , 2013, 87, 12866-12878.	1.5	38
2279	SIRT1 is a Highly Networked Protein That Mediates the Adaptation to Chronic Physiological Stress. <i>Genes and Cancer</i> , 2013, 4, 125-134.	0.6	50
2280	A Spatio-Temporal Understanding of Growth Regulation during the Salt Stress Response in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 2132-2154.	3.1	351

#	ARTICLE	IF	CITATIONS
2281	Transcriptomic analysis of UV-treated rice leaves reveals UV-induced phytoalexin biosynthetic pathways and their regulatory networks in rice. <i>Phytochemistry</i> , 2013, 96, 57-71.	1.4	65
2282	OCSANA: optimal combinations of interventions from network analysis. <i>Bioinformatics</i> , 2013, 29, 1571-1573.	1.8	28
2283	Molecular characterization of two small heat shock protein genes in rice: their expression patterns, localizations, networks, and heterogeneous overexpressions. <i>Molecular Biology Reports</i> , 2013, 40, 6709-6720.	1.0	26
2284	Proteomic, Cellular, and Network Analyses Reveal New DUSP3 Interactions with Nucleolar Proteins in HeLa Cells. <i>Journal of Proteome Research</i> , 2013, 12, 5851-5866.	1.8	23
2285	Protein Interaction Network of the Mammalian Hippo Pathway Reveals Mechanisms of Kinase-Phosphatase Interactions. <i>Science Signaling</i> , 2013, 6, rs15.	1.6	411
2286	Network2Canvas: network visualization on a canvas with enrichment analysis. <i>Bioinformatics</i> , 2013, 29, 1872-1878.	1.8	34
2287	Transcriptional profiling technology for studying vaccine responses: An untapped goldmine. <i>Methods</i> , 2013, 60, 269-274.	1.9	10
2288	Artificial Selection on Brain-Expressed Genes during the Domestication of Dog. <i>Molecular Biology and Evolution</i> , 2013, 30, 1867-1876.	3.5	74
2289	Network cluster analysis of protein-protein interaction network identified biomarker for early onset colorectal cancer. <i>Molecular Biology Reports</i> , 2013, 40, 6561-6568.	1.0	29
2290	Circulating miRNA profile in HCV infected serum: novel insight into pathogenesis. <i>Scientific Reports</i> , 2013, 3, 1555.	1.6	77
2291	Bioinformatics analysis of protein interaction networks: Statistics, topologies, and meeting the standards of experimental biologists. <i>Biochemistry (Moscow)</i> , 2013, 78, 1098-1103.	0.7	6
2292	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. <i>Bioinformatics</i> , 2013, 29, 1206-1207.	1.8	17
2293	Drafting the CLN3 Protein Interactome in SH-SY5Y Human Neuroblastoma Cells: A Label-free Quantitative Proteomics Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2101-2115.	1.8	42
2294	Identification and comparative analysis of hepatitis C virus-host cell protein interactions. <i>Molecular BioSystems</i> , 2013, 9, 3199.	2.9	46
2295	Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. <i>Bioinformatics</i> , 2013, 29, 2826-2834.	1.8	29
2296	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
2297	A system biology approach to identify regulatory pathways underlying the neuroendocrine control of female puberty in rats and nonhuman primates. <i>Hormones and Behavior</i> , 2013, 64, 175-186.	1.0	43
2298	SPNConverter: a new link between static and dynamic complex network analysis. <i>Bioinformatics</i> , 2013, 29, 2507-2508.	1.8	1

#	ARTICLE	IF	CITATIONS
2299	SubNet: a Java application for subnetwork extraction. <i>Bioinformatics</i> , 2013, 29, 2509-2511.	1.8	18
2300	Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. <i>Bioinformatics</i> , 2013, 29, 2892-2899.	1.8	108
2301	Analysis of mass spectrometry data from the secretome of an explant model of articular cartilage exposed to pro-inflammatory and anti-inflammatory stimuli using machine learning. <i>BMC Musculoskeletal Disorders</i> , 2013, 14, 349.	0.8	18
2302	Biosynthesis of Antinutritional Alkaloids in Solanaceous Crops Is Mediated by Clustered Genes. <i>Science</i> , 2013, 341, 175-179.	6.0	464
2303	The gut microbiota of a patient with resistant tuberculosis is more comprehensively studied by culturomics than by metagenomics. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013, 32, 637-645.	1.3	123
2304	Pclust: protein network visualization highlighting experimental data. <i>Bioinformatics</i> , 2013, 29, 2647-2648.	1.8	7
2305	Gene expression patterns combined with bioinformatics analysis identify genes associated with cholangiocarcinoma. <i>Computational Biology and Chemistry</i> , 2013, 47, 192-197.	1.1	19
2306	SHANK3 overexpression causes manic-like behaviour with unique pharmacogenetic properties. <i>Nature</i> , 2013, 503, 72-77.	13.7	323
2307	Transcriptome signatures in <i>Helicobacter pylori</i> -infected mucosa identifies acidic mammalian chitinase loss as a corpus atrophy marker. <i>BMC Medical Genomics</i> , 2013, 6, 41.	0.7	52
2308	RMaNI: Regulatory Module Network Inference framework. <i>BMC Bioinformatics</i> , 2013, 14, S14.	1.2	6
2309	Understanding cooperativity of microRNAs via microRNA association networks. <i>BMC Genomics</i> , 2013, 14, S17.	1.2	31
2310	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , 2013, 7, 100.	3.0	52
2311	Applications of the InChI in cheminformatics with the CDK and Bioclipse. <i>Journal of Cheminformatics</i> , 2013, 5, 14.	2.8	8
2312	Inferring Boolean network states from partial information. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2013, 2013, 11.	1.4	8
2313	Single nucleotide polymorphisms and haplotypes associated with feed efficiency in beef cattle. <i>BMC Genetics</i> , 2013, 14, 94.	2.7	52
2314	Proteomic analysis of mismatch repair-mediated alkylating agent-induced DNA damage response. <i>Cell and Bioscience</i> , 2013, 3, 37.	2.1	4
2315	Assessing the translatability of In vivo cardiotoxicity mechanisms to In vitro models using causal reasoning. <i>BMC Pharmacology &amp; Toxicology</i> , 2013, 14, 46.	1.0	10
2316	Transcriptomic characterization of cold acclimation in larval zebrafish. <i>BMC Genomics</i> , 2013, 14, 612.	1.2	174



#	ARTICLE	IF	CITATIONS
2317	RCytoscape: tools for exploratory network analysis. BMC Bioinformatics, 2013, 14, 217.	1.2	105
2319	Research prioritization through prediction of future impact on biomedical science: a position paper on inference-analytics. GigaScience, 2013, 2, 11.	3.3	6
2320	Complex Network Structure of Flocks in the Standard Vicsek Model. Journal of Statistical Physics, 2013, 153, 270-288.	0.5	11
2321	Arabidopsis Polycomb Repressive Complex 2 binding sites contain putative GAGA factor binding motifs within coding regions of genes. BMC Genomics, 2013, 14, 593.	1.2	94
2322	WholeCellViz: data visualization for whole-cell models. BMC Bioinformatics, 2013, 14, 253.	1.2	23
2323	Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (Brassica) Tj ETQq1 1 0.784314 rgBT /Overbo 1.2 172	1.2	172
2324	Interspecies protein-protein interaction network construction for characterization of host-pathogen interactions: a Candida albicans-zebrafish interaction study. BMC Systems Biology, 2013, 7, 79.	3.0	32
2325	SLiMScape: a protein short linear motif analysis plugin for Cytoscape. BMC Bioinformatics, 2013, 14, 224.	1.2	19
2326	Label-free mass spectrometry proteome quantification of human embryonic kidney cells following 24 hours of sialic acid overproduction. Proteome Science, 2013, 11, 38.	0.7	13
2327	Investigation of the hub genes and related mechanism in ovarian cancer via bioinformatics analysis. Journal of Ovarian Research, 2013, 6, 92.	1.3	16
2328	The drug:H <sup>+</sup> antiporters of family 2 (DHA2), siderophore transporters (ARN) and glutathione:H <sup>+</sup> antiporters (GEX) have a common evolutionary origin in hemiascomycete yeasts. BMC Genomics, 2013, 14, 901.	1.2	36
2329	Metabolite profiling and network analysis reveal coordinated changes in grapevine water stress response. BMC Plant Biology, 2013, 13, 184.	1.6	158
2330	Computational drug repositioning through heterogeneous network clustering. BMC Systems Biology, 2013, 7, S6.	3.0	111
2331	Comparative secretome analysis of Trichoderma asperellum S4F8 and Trichoderma reesei Rut C30 during solid-state fermentation on sugarcane bagasse. Biotechnology for Biofuels, 2013, 6, 172.	6.2	88
2332	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. BMC Genomics, 2013, 14, 798.	1.2	76
2333	Transcriptome signatures of class I and III stress response deregulation in Lactobacillus plantarum reveal pleiotropic adaptation. Microbial Cell Factories, 2013, 12, 112.	1.9	21
2334	Transcription factors and genetic circuits orchestrating the complex, multilayered response of Clostridium acetobutylicum to butanol and butyrate stress. BMC Systems Biology, 2013, 7, 120.	3.0	65
2335	Species Diversity and Temporal Variation of the Orchid-Bee Fauna (Hymenoptera, Apidae) in a Conservation Gradient of a Rocky Field Area in the Espinha�so Range, State of Minas Gerais, Southeastern Brazil. Neotropical Entomology, 2013, 42, 565-575.	0.5	18

#	ARTICLE	IF	CITATIONS
2336	Integrative genomics identifies candidate microRNAs for pathogenesis of experimental biliary atresia. BMC Systems Biology, 2013, 7, 104.	3.0	25
2337	A Comprehensive Metabolic Modeling of Thyroid Pathway in Relation to Thyroid Pathophysiology and Therapeutics. OMICS A Journal of Integrative Biology, 2013, 17, 584-593.	1.0	13
2338	Integrative approaches for finding modular structure in biological networks. Nature Reviews Genetics, 2013, 14, 719-732.	7.7	512
2340	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
2341	Protein Phosphatase 1 <sup>β</sup> Isoforms Linked Interactions in the Brain. Journal of Molecular Neuroscience, 2013, 50, 179-197.	1.1	16
2342	Screening of differentially expressed miRNAs related to muscle strain and their target gene. Molecular Biology, 2013, 47, 758-764.	0.4	1
2343	Provenance Capture and Use in a Satellite Data Processing Pipeline. IEEE Transactions on Geoscience and Remote Sensing, 2013, 51, 5090-5097.	2.7	26
2344	Predicting drug-target interactions through integrative analysis of chemogenetic assays in yeast. Molecular BioSystems, 2013, 9, 768.	2.9	6
2345	Exploring agent-based simulations in political science using Aggregate Temporal Graphs. , 2013, , .		1
2346	Combining small molecules for cell reprogramming through an interatomic analysis. Molecular BioSystems, 2013, 9, 2741.	2.9	2
2347	Identification of complex relationship between protein kinases and substrates during the cell cycle of <sc>H</sc><sc>L</sc>a cells by phosphoproteomic analysis. Proteomics, 2013, 13, 1233-1246.	1.3	2
2348	Visual Analysis of Biological Activity Data with Scaffold Hunter. Molecular Informatics, 2013, 32, 964-975.	1.4	18
2349	Molecular Differences between Chronic and Aggressive Periodontitis. Journal of Dental Research, 2013, 92, 1081-1088.	2.5	77
2350	Integrating semantic transcriptomic data analysis and knowledge extraction from biological literature. , 2013, , .		0
2351	Visualizing multidimensional cancer genomics data. Genome Medicine, 2013, 5, 9.	3.6	79
2352	Construction of human tissue-specific phosphorylation networks with protein expression data. , 2013, , .		0
2353	A system based approach to construct a Kaposi sarcoma-associated herpesvirus (KSHV) specific pathway crosstalk network. , 2013, , .		0
2354	PodNet, a protein-protein interaction network of the podocyte. Kidney International, 2013, 84, 104-115.	2.6	19

#	ARTICLE	IF	CITATIONS
2355	Aerobic deconstruction of cellulosic biomass by an insect-associated <i>Streptomyces</i> . <i>Scientific Reports</i> , 2013, 3, 1030.	1.6	107
2356	Hummod browser: An exploratory visualization tool for the analysis of whole-body physiology simulation data. , 2013, , .		5
2357	A tool for comparing multirelational networks from biology. , 2013, , .		0
2358	Network analysis for gene discovery in plant-specific specialized metabolism. <i>Plant, Cell and Environment</i> , 2013, 36, 1597-1606.	2.8	75
2359	A dictionary of behavioral motifs reveals clusters of genes affecting <i>Caenorhabditis elegans</i> locomotion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 791-796.	3.3	196
2360	Exploring the Molecular Mechanism of Cross-Resistance to HIV-1 Integrase Strand Transfer Inhibitors by Molecular Dynamics Simulation and Residue Interaction Network Analysis. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 210-222.	2.5	75
2361	E pluribus unum: isolation, structure determination, network analysis and DFT studies of a single metastable structure from a shapeshifting mixture of 852 bullvalene structural isomers. <i>Organic and Biomolecular Chemistry</i> , 2013, 11, 1306-1317.	1.5	23
2362	Developmental Arrest and Mouse Antral Not-Surrounded Nucleolus Oocytes1. <i>Biology of Reproduction</i> , 2013, 88, 2.	1.2	56
2363	Identification of transcription regulatory relationships in rheumatoid arthritis and osteoarthritis. <i>Clinical Rheumatology</i> , 2013, 32, 609-615.	1.0	21
2364	Lineage-Specific Responses of Microbial Communities to Environmental Change. <i>Applied and Environmental Microbiology</i> , 2013, 79, 39-47.	1.4	20
2365	Systematic genetic interaction screens uncover cell polarity regulators and functional redundancy. <i>Nature Cell Biology</i> , 2013, 15, 103-112.	4.6	84
2366	Molecular evolutionary and population genomic analysis of the nine-spined stickleback using a modified restriction-site-associated DNA tag approach. <i>Molecular Ecology</i> , 2013, 22, 565-582.	2.0	85
2367	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. <i>Genome Research</i> , 2013, 23, 217-227.	2.4	139
2368	Linking the signaling cascades and dynamic regulatory networks controlling stress responses. <i>Genome Research</i> , 2013, 23, 365-376.	2.4	71
2369	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. <i>Archives of Toxicology</i> , 2013, 87, 123-143.	1.9	222
2370	Transcriptional regulation of tocopherol biosynthesis in tomato. <i>Plant Molecular Biology</i> , 2013, 81, 309-325.	2.0	83
2371	Metabolomic and elemental profiling of melon fruit quality as affected by genotype and environment. <i>Metabolomics</i> , 2013, 9, 57-77.	1.4	74
2372	Gene Regulatory Networks. , 2013, , 65-88.		4

#	ARTICLE	IF	CITATIONS
2373	Bioinformatics and systems biology analysis of genes network involved in OLP (Oral Lichen Planus) pathogenesis. <i>Archives of Oral Biology</i> , 2013, 58, 664-673.	0.8	39
2374	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. <i>Nature Chemical Biology</i> , 2013, 9, 184-191.	3.9	160
2375	The integration of proteomics and systems approaches to map regulatory mechanisms underpinning platelet function. <i>Proteomics - Clinical Applications</i> , 2013, 7, 144-154.	0.8	9
2376	S-linked protein homocysteinylation: identifying targets based on structural, physicochemical and protein-protein interactions of homocysteinylation. <i>Amino Acids</i> , 2013, 44, 1307-1316.	1.2	7
2377	Activation of protein kinase C delta by Î³RACK peptide promotes embryonic stem cell proliferation through ERK 1/2. <i>Journal of Proteomics</i> , 2013, 94, 497-512.	1.2	7
2378	Identification of Immunity-related Genes in Arabidopsis and Cassava Using Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 345-353.	3.0	8
2379	Progress in Detecting Genetic Alterations and Their Association with Human Disease. <i>Journal of Molecular Biology</i> , 2013, 425, 3914-3918.	2.0	7
2380	Polyphenol tri-vanillic ester 13c inhibits P-JAK2V617F and Bcr-Abl oncokininase expression in correlation with STAT3/STAT5 inactivation and apoptosis induction in human leukemia cells. <i>Cancer Letters</i> , 2013, 340, 30-42.	3.2	6
2381	iBIG: An Integrative Network Tool for Supporting Human Disease Mechanism Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 166-171.	3.0	7
2382	Functional genomics of pain in analgesic drug development and therapy. , 2013, 139, 60-70.		61
2383	Prediction and characterization of protein-protein interaction network in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>Research in Microbiology</i> , 2013, 164, 1035-1044.	1.0	12
2384	Transcriptome Analysis Identifies Regulators of Hematopoietic Stem and Progenitor Cells. <i>Stem Cell Reports</i> , 2013, 1, 266-280.	2.3	100
2385	Bcl2-associated Athanogene 3 Interactome Analysis Reveals a New Role in Modulating Proteasome Activity. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2804-2819.	2.5	62
2386	Pou5f1 Transcription Factor Controls Zygotic Gene Activation In Vertebrates. <i>Science</i> , 2013, 341, 1005-1009.	6.0	217
2387	Candidate Blood Proteome Markers of Alzheimer's Disease Onset and Progression: A Systematic Review and Replication Study. <i>Journal of Alzheimer's Disease</i> , 2013, 38, 515-531.	1.2	160
2388	Identification of Lysine Succinylation Substrates and the Succinylation Regulatory Enzyme CobB in <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3509-3520.	2.5	236
2389	Human Milk Secretory Immunoglobulin A and Lactoferrin N-Glycans Are Altered in Women with Gestational Diabetes Mellitus. <i>Journal of Nutrition</i> , 2013, 143, 1906-1912.	1.3	75
2390	Clust&See: A Cytoscape plugin for the identification, visualization and manipulation of network clusters. <i>BioSystems</i> , 2013, 113, 91-95.	0.9	37

#	ARTICLE	IF	CITATIONS
2391	Characterization of the Drosophila Atlastin Interactome Reveals VCP as a Functionally Related Interactor. <i>Journal of Genetics and Genomics</i> , 2013, 40, 297-306.	1.7	11
2392	Metabolic rates associated with membrane fatty acids in mice selected for increased maximal metabolic rate. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2013, 165, 70-78.	0.8	17
2393	TreeVis: A MATLAB-based tool for tree visualization. <i>Computer Methods and Programs in Biomedicine</i> , 2013, 109, 74-76.	2.6	6
2394	Autoimmunoreactive IgGs against cardiac lipid raft-associated proteins in patients with postural orthostatic tachycardia syndrome. <i>Translational Research</i> , 2013, 162, 34-44.	2.2	34
2395	Dysfunctional co-expression network analysis of familial hypercholesterolemia. <i>Journal of Cardiology</i> , 2013, 62, 58-62.	0.8	2
2396	Deciphering the combination principles of Traditional Chinese Medicine from a systems pharmacology perspective based on Ma-huang Decoction. <i>Journal of Ethnopharmacology</i> , 2013, 150, 619-638.	2.0	95
2397	Differential lysine acetylation profiles of <i>Erwinia amylovora</i> strains revealed by proteomics. <i>Journal of Proteomics</i> , 2013, 79, 60-71.	1.2	78
2398	Assessment of the usefulness of the murine cytotoxic T cell line CTLL-2 for immunotoxicity screening by transcriptomics. <i>Toxicology Letters</i> , 2013, 217, 1-13.	0.4	16
2399	Natural variation of the root morphological response to nitrate supply in <i>Arabidopsis thaliana</i> . <i>Mechanisms of Development</i> , 2013, 130, 45-53.	1.7	55
2400	The Impact of Network Medicine in Gastroenterology and Hepatology. <i>Clinical Gastroenterology and Hepatology</i> , 2013, 11, 1240-1244.	2.4	13
2401	Identification of susceptibility modules for coronary artery disease using a genome wide integrated network analysis. <i>Gene</i> , 2013, 531, 347-354.	1.0	17
2402	Untangling the Chemistry of Port Wine Aging with the Use of GC-FID, Multivariate Statistics, and Network Reconstruction. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 2513-2521.	2.4	17
2403	Identification of candidate effector genes in the transcriptome of the rice root knot nematode <i>Meloidogyne graminicola</i> . <i>Molecular Plant Pathology</i> , 2013, 14, 379-390.	2.0	69
2404	Defining the extracellular matrix using proteomics. <i>International Journal of Experimental Pathology</i> , 2013, 94, 75-92.	0.6	137
2405	Transcriptional regulatory network for psoriasis. <i>Journal of Dermatology</i> , 2013, 40, 48-53.	0.6	22
2406	Chemogenomic Profiling. , 2013, , 153-176.		3
2407	Short-term observations of marine bacterial and viral communities: patterns, connections and resilience. <i>ISME Journal</i> , 2013, 7, 1274-1285.	4.4	144
2408	A Versatile Mass Spectrometry-Based Method to Both Identify Kinase Client-Relationships and Characterize Signaling Network Topology. <i>Journal of Proteome Research</i> , 2013, 12, 937-948.	1.8	25

#	ARTICLE	IF	CITATIONS
2409	Current trends in modeling host-pathogen interactions. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2013, 3, 109-128.	4.6	8
2410	A global approach to analysis and interpretation of metabolic data for plant natural product discovery. <i>Natural Product Reports</i> , 2013, 30, 565.	5.2	104
2411	MosaicFinder: identification of fused gene families in sequence similarity networks. <i>Bioinformatics</i> , 2013, 29, 837-844.	1.8	29
2412	More than Cell Dust: Microparticles Isolated from Cerebrospinal Fluid of Brain Injured Patients Are Messengers Carrying mRNAs, miRNAs, and Proteins. <i>Journal of Neurotrauma</i> , 2013, 30, 1232-1242.	1.7	74
2413	A Role for the Nucleoporin Nup170p in Chromatin Structure and Gene Silencing. <i>Cell</i> , 2013, 152, 969-983.	13.5	141
2414	Immunofluorescence and fluorescent-protein tagging show high correlation for protein localization in mammalian cells. <i>Nature Methods</i> , 2013, 10, 315-323.	9.0	209
2415	A multi-omic systems approach to elucidating <i>Yersinia</i> virulence mechanisms. <i>Molecular BioSystems</i> , 2013, 9, 44-54.	2.9	29
2416	Cell Death Proteomics Database: Consolidating Proteomics Data on Cell Death. <i>Journal of Proteome Research</i> , 2013, 12, 2206-2213.	1.8	21
2417	Oligomerisation status and evolutionary conservation of interfaces of protein structural domain superfamilies. <i>Molecular BioSystems</i> , 2013, 9, 1652.	2.9	72
2418	Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346.	7.7	288
2419	Gene Regulatory Networks Governing Pancreas Development. <i>Developmental Cell</i> , 2013, 25, 5-13.	3.1	148
2420	<i>Salmonella</i> modulates metabolism during growth under conditions that induce expression of virulence genes. <i>Molecular BioSystems</i> , 2013, 9, 1522.	2.9	49
2421	Discovery of microRNA Regulatory Networks by Integrating Multidimensional High-Throughput Data. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 251-266.	0.8	5
2422	Tracking Individuals Shows Spatial Fidelity Is a Key Regulator of Ant Social Organization. <i>Science</i> , 2013, 340, 1090-1093.	6.0	335
2423	CSC Technology: Selective Labeling of Glycoproteins by Mild Oxidation to Phenotype Cells. <i>Methods in Molecular Biology</i> , 2013, 951, 33-43.	0.4	11
2424	Profiling of Ubiquitin-like Modifications Reveals Features of Mitotic Control. <i>Cell</i> , 2013, 152, 1160-1172.	13.5	91
2425	Links Reconstruction Attack. , 2013, , 181-196.		13
2426	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. <i>Proteomics</i> , 2013, 13, 2786-2804.	1.3	46

#	ARTICLE	IF	CITATIONS
2427	Two algorithms for biospecimen comparison and differentiation using SNP genotypes. <i>Pharmacogenomics</i> , 2013, 14, 379-390.	0.6	4
2428	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, p1.	1.6	11,344
2429	Effects of Multiple Electron Acceptors on Microbial Interactions in a Hydrogen-Based Biofilm. <i>Environmental Science &amp; Technology</i> , 2013, 47, 7396-7403.	4.6	48
2430	Human Corneal Epithelial Subpopulations: Oxygen Dependent <i>Ex Vivo</i> Expansion and Transcriptional Profiling. <i>Acta Ophthalmologica</i> , 2013, 91, 1-34.	0.6	7
2431	PKC signaling prevents irradiation-induced apoptosis of primary human fibroblasts. <i>Cell Death and Disease</i> , 2013, 4, e498-e498.	2.7	40
2432	Apple gene function and gene family database: an integrated bioinformatics database for apple research. <i>Plant Growth Regulation</i> , 2013, 70, 199-206.	1.8	15
2433	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	13.5	311
2434	Identification of eight candidate target genes of the recurrent 3p12p14 loss in cervical cancer by integrative genomic profiling. <i>Journal of Pathology</i> , 2013, 230, 59-69.	2.1	37
2435	Graphical Identification of Cancer-Associated Gene Subnetworks Based on Small Proteomics Data Sets. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 393-397.	1.0	1
2436	Integration of Genomic Information with Biological Networks Using Cytoscape. <i>Methods in Molecular Biology</i> , 2013, 1021, 37-61.	0.4	50
2437	Identification of Key Nodes of Type 2 Diabetes Mellitus Protein Interactome and Study of their Interactions with Phloridzin. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 302-317.	1.0	14
2438	Proteomic analysis of balding and non-balding mesenchyme-derived dermal papilla cells from androgenetic alopecia patients using on-line two-dimensional reversed phase-reversed phase LC-MS/MS. <i>Journal of Proteomics</i> , 2013, 85, 174-191.	1.2	13
2439	Boolean modeling of biological regulatory networks: A methodology tutorial. <i>Methods</i> , 2013, 62, 3-12.	1.9	121
2441	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 291-315.	0.8	6
2442	SLC Classification: An Update. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 94, 19-23.	2.3	74
2443	The gene vitellogenin affects microRNA regulation in honey bee ( <i>Apis mellifera</i> ) fat body and brain. <i>Journal of Experimental Biology</i> , 2013, 216, 3724-32.	0.8	54
2444	Fungal networks in yield-invigorating and -debilitating soils induced by prolonged potato monoculture. <i>Soil Biology and Biochemistry</i> , 2013, 65, 186-194.	4.2	197
2445	Association Weight Matrix: A Network-Based Approach Towards Functional Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2013, 1019, 437-447.	0.4	19



#	ARTICLE	IF	CITATIONS
2446	Parallel evolution of tumour subclones mimics diversity between tumours. <i>Journal of Pathology</i> , 2013, 230, 356-364.	2.1	79
2447	Bacterial infection activates the immune system response and dysregulates microRNA expression in honey bees. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 474-482.	1.2	55
2448	Genome-wide association mapping of natural variation in odour-guided behaviour in <i>Drosophila</i> . <i>Genes, Brain and Behavior</i> , 2013, 12, 503-515.	1.1	28
2449	Genome-wide expression analysis of rice aquaporin genes and development of a functional gene network mediated by aquaporin expression in roots. <i>Planta</i> , 2013, 238, 669-681.	1.6	76
2450	Overcoming chemotherapy resistance of ovarian cancer cells by liposomal cisplatin: Molecular mechanisms unveiled by gene expression profiling. <i>Biochemical Pharmacology</i> , 2013, 85, 1077-1090.	2.0	36
2451	An Extracellular Interactome of Immunoglobulin and LRR Proteins Reveals Receptor-Ligand Networks. <i>Cell</i> , 2013, 154, 228-239.	13.5	207
2452	A Guide to CORNET for the Construction of Coexpression and Protein-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2013, 1011, 327-343.	0.4	4
2453	TFEB controls cellular lipid metabolism through a starvation-induced autoregulatory loop. <i>Nature Cell Biology</i> , 2013, 15, 647-658.	4.6	796
2456	Glycocapture-Assisted Global Quantitative Proteomics (gagQP) Reveals Multiorgan Responses in Serum Toxicoproteome. <i>Journal of Proteome Research</i> , 2013, 12, 2034-2044.	1.8	17
2457	Culturomics identified 11 new bacterial species from a single anorexia nervosa stool sample. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013, 32, 1471-1481.	1.3	150
2458	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. <i>Nature Genetics</i> , 2013, 45, 670-675.	9.4	339
2459	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. <i>American Journal of Human Genetics</i> , 2013, 92, 854-865.	2.6	164
2460	MicroRNA-mRNA interaction network using TSK-type recurrent neural fuzzy network. <i>Gene</i> , 2013, 515, 385-390.	1.0	11
2461	Network pharmacology-based prediction of the active ingredients and potential targets of Chinese herbal <i>Radix Curcumae</i> formula for application to cardiovascular disease. <i>Journal of Ethnopharmacology</i> , 2013, 145, 1-10.	2.0	502
2463	Fully automated protein complex prediction based on topological similarity and community structure. <i>Proteome Science</i> , 2013, 11, S9.	0.7	1
2464	Identifying common and specific microRNAs expressed in peripheral blood mononuclear cell of type 1, type 2, and gestational diabetes mellitus patients. <i>BMC Research Notes</i> , 2013, 6, 491.	0.6	132
2465	Transcriptomic analysis of genetically defined autism candidate genes reveals common mechanisms of action. <i>Molecular Autism</i> , 2013, 4, 45.	2.6	43
2466	Comparative analysis of differential network modularity in tissue specific normal and cancer protein interaction networks. <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 19.	1.2	18

#	ARTICLE	IF	CITATIONS
2467	Identification of biomarkers for hepatocellular carcinoma using network-based bioinformatics methods. <i>European Journal of Medical Research</i> , 2013, 18, 35.	0.9	11
2468	Systematic Identification of Scaffolds Representing Compounds Active against Individual Targets and Single or Multiple Target Families. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 312-326.	2.5	23
2469	Shotgun Protein Profile of Human Adipose Tissue and Its Changes in Relation to Systemic Amyloidoses. <i>Journal of Proteome Research</i> , 2013, 12, 5642-5655.	1.8	45
2470	Comparative Proteomics Reveals a Role for Seed Storage Protein AmA1 in Cellular Growth, Development, and Nutrient Accumulation. <i>Journal of Proteome Research</i> , 2013, 12, 4904-4930.	1.8	35
2471	Novel biomarkers discovery for HBV and HCV monitoring through protein interaction networks analysis. , 2013, , .		1
2472	Subcellular Proteomics Reveals a Role for Nucleo-cytoplasmic Trafficking at the DNA Replication Origin Activation Checkpoint. <i>Journal of Proteome Research</i> , 2013, 12, 1436-1453.	1.8	14
2473	Tools for the functional interpretation of metabolomic experiments. <i>Briefings in Bioinformatics</i> , 2013, 14, 737-744.	3.2	56
2475	Discovering gene-environment interactions in Glioblastoma through a comprehensive data integration bioinformatics method. <i>NeuroToxicology</i> , 2013, 35, 1-14.	1.4	16
2476	A Transcriptomic Network Underlies Microstructural and Physiological Responses to Cadmium in <i>Populus</i> – <i>canescens</i> . <i>Plant Physiology</i> , 2013, 162, 424-439.	2.3	187
2477	Application of omics technologies to biomarker discovery in inflammatory lung diseases. <i>European Respiratory Journal</i> , 2013, 42, 802-825.	3.1	234
2478	Integrated gene co-expression network analysis in the growth phase of <i>Mycobacterium tuberculosis</i> reveals new potential drug targets. <i>Molecular BioSystems</i> , 2013, 9, 2798.	2.9	22
2479	Comprehensive Analysis of the Rice RING E3 Ligase Family Reveals Their Functional Diversity in Response to Abiotic stress. <i>DNA Research</i> , 2013, 20, 299-314.	1.5	46
2480	Complex expression dynamics and robustness in <i>C. elegans</i> insulin networks. <i>Genome Research</i> , 2013, 23, 954-965.	2.4	87
2481	Network Clusters Analysis Based on Protein-Protein Interaction Network Constructed in Phosgene-Induced Acute Lung Injury. <i>Lung</i> , 2013, 191, 545-551.	1.4	0
2482	Quantitative Proteomic and Functional Analysis of Liver Mitochondria from High Fat Diet (HFD) Diabetic Mice. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3744-3758.	2.5	62
2483	Unraveling toxicological mechanisms and predicting toxicity classes with gene dysregulation networks. <i>Journal of Applied Toxicology</i> , 2013, 33, 1407-1415.	1.4	6
2484	Fold or hold: experimental evolution <i>in vitro</i> . <i>Journal of Evolutionary Biology</i> , 2013, 26, 2123-2134.	0.8	0
2485	Visualization of biomolecular networks' comparison on cytoscape. <i>Tsinghua Science and Technology</i> , 2013, 18, 515-521.	4.1	6

#	ARTICLE	IF	CITATIONS
2486	Multi-focus and multi-level techniques for visualization and analysis of networks with thematic data. Proceedings of SPIE, 2013, , .	0.8	3
2487	An information-gain approach to detecting three-way epistatic interactions in genetic association studies. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 630-636.	2.2	69
2488	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. Nucleic Acids Research, 2013, 41, 8853-8871.	6.5	45
2489	From -omics to personalized medicine in nephrology: integration is the key. Nephrology Dialysis Transplantation, 2013, 28, 24-28.	0.4	29
2490	System-Wide Hypersensitive Response-Associated Transcriptome and Metabolome Reprogramming in Tomato . Plant Physiology, 2013, 162, 1599-1617.	2.3	41
2491	Next-Generation Sequencing of Small RNAs from HIV-Infected Cells Identifies Phased microRNA Expression Patterns and Candidate Novel microRNAs Differentially Expressed upon Infection. MBio, 2013, 4, e00549-12.	1.8	48
2492	Microarray analysis of active cardiac remodeling genes in a familial hypertrophic cardiomyopathy mouse model rescued by a phospholamban knockout. Physiological Genomics, 2013, 45, 764-773.	1.0	8
2493	A Kinetic Analysis of the Auxin Transcriptome Reveals Cell Wall Remodeling Proteins That Modulate Lateral Root Development in <i>Arabidopsis</i> . Plant Cell, 2013, 25, 3329-3346.	3.1	147
2494	Toward a visual interface for brain connectivity analysis. , 2013, , .		0
2495	Regulation of constitutive and alternative splicing by PRMT5 reveals a role for <i>Mdm4</i> pre-mRNA in sensing defects in the spliceosomal machinery. Genes and Development, 2013, 27, 1903-1916.	2.7	213
2496	Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. Neurosurgical Focus, 2013, 35, E3.	1.0	28
2497	Coevolution Reveals a Network of Human Proteins Originating with Multicellularity. Molecular Biology and Evolution, 2013, 30, 332-346.	3.5	21
2498	The Genetic Architecture of Alopecia Areata. Journal of Investigative Dermatology Symposium Proceedings, 2013, 16, S16-S22.	0.8	18
2499	A process-centric data mining and visual analytic tool for exploring complex social networks. , 2013, , .		1
2500	The CARLSBAD Database: A Confederated Database of Chemical Bioactivities. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat044.	1.4	30
2501	Bacterial Community Response to Petroleum Hydrocarbon Amendments in Freshwater, Marine, and Hypersaline Water-Containing Microcosms. Applied and Environmental Microbiology, 2013, 79, 5927-5935.	1.4	90
2502	RiceFRIEND: a platform for retrieving coexpressed gene networks in rice. Nucleic Acids Research, 2013, 41, D1214-D1221.	6.5	163
2503	Navigating Traditional Chinese Medicine Network Pharmacology and Computational Tools. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-23.	0.5	76

#	ARTICLE	IF	CITATIONS
2504	NetWeAvers: an <i>R</i> package for integrative biological network analysis with mass spectrometry data. <i>Bioinformatics</i> , 2013, 29, 2946-2947.	1.8	5
2505	Social network analysis of scientific collaborations across different subject fields. <i>Information Services and Use</i> , 2013, 33, 219-233.	0.1	9
2506	Discovery of Anthelmintic Drug Targets and Drugs Using Chokepoints in Nematode Metabolic Pathways. <i>PLoS Pathogens</i> , 2013, 9, e1003505.	2.1	69
2507	MicroRNA Expression Profile in Human Macrophages in Response to <i>Leishmania major</i> Infection. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2478.	1.3	125
2508	Rheumatoid Arthritis with Deficiency Pattern in Traditional Chinese Medicine Shows Correlation with Cold and Hot Patterns in Gene Expression Profiles. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-12.	0.5	17
2509	A Highly Redundant Gene Network Controls Assembly of the Outer Spore Wall in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2013, 9, e1003700.	1.5	52
2510	Protein Complex-Based Analysis Framework for High-Throughput Data Sets. <i>Science Signaling</i> , 2013, 6, rs5.	1.6	110
2511	Controllability in Cancer Metabolic Networks According to Drug Targets as Driver Nodes. <i>PLoS ONE</i> , 2013, 8, e79397.	1.1	57
2512	eFG: an electronic resource for <i>Fusarium graminearum</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat042-bat042.	1.4	5
2513	Characterization of Schizophrenia Adverse Drug Interactions through a Network Approach and Drug Classification. <i>BioMed Research International</i> , 2013, 2013, 1-10.	0.9	13
2514	Predicting the Drug Safety for Traditional Chinese Medicine through a Comparative Analysis of Withdrawn Drugs Using Pharmacological Network. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-11.	0.5	5
2515	A Network Study of Chinese Medicine Xuesaitong Injection to Elucidate a Complex Mode of Action with Multicompound, Multitarget, and Multipathway. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-8.	0.5	36
2516	The RAVEN Toolbox and Its Use for Generating a Genome-scale Metabolic Model for <i>Penicillium chrysogenum</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1002980.	1.5	364
2517	Towards Systematic Discovery of Signaling Networks in Budding Yeast Filamentous Growth Stress Response Using Interventional Phosphorylation Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003077.	1.5	15
2518	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. <i>Frontiers in Plant Science</i> , 2013, 4, 325.	1.7	124
2519	Dietary Restriction Induced Longevity Is Mediated by Nuclear Receptor NHR-62 in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013, 9, e1003651.	1.5	73
2520	Quantitative Profiling of DNA Damage and Apoptotic Pathways in UV Damaged Cells Using PTMScan Direct. <i>International Journal of Molecular Sciences</i> , 2013, 14, 286-307.	1.8	14
2521	GALANT: a Cytoscape plugin for visualizing data as functional landscapes projected onto biological networks. <i>Bioinformatics</i> , 2013, 29, 2505-2506.	1.8	5

#	ARTICLE	IF	CITATIONS
2522	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. PLoS Computational Biology, 2013, 9, e1003030.	1.5	62
2523	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. PLoS Genetics, 2013, 9, e1003202.	1.5	84
2524	Gene-Based Testing of Interactions in Association Studies of Quantitative Traits. PLoS Genetics, 2013, 9, e1003321.	1.5	89
2525	GSATools: analysis of allosteric communication and functional local motions using a structural alphabet. Bioinformatics, 2013, 29, 2053-2055.	1.8	44
2526	NetworkTrail—a web service for identifying and visualizing deregulated subnetworks. Bioinformatics, 2013, 29, 1702-1703.	1.8	14
2527	Comparison of the Microbial Community Structures of Untreated Wastewaters from Different Geographic Locales. Applied and Environmental Microbiology, 2013, 79, 2906-2913.	1.4	142
2528	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas062.	1.4	17
2529	Transcriptional Networks Controlling the Cell Cycle. G3: Genes, Genomes, Genetics, 2013, 3, 75-90.	0.8	22
2530	Systemic Cold Stress Adaptation of Chlamydomonas reinhardtii. Molecular and Cellular Proteomics, 2013, 12, 2032-2047.	2.5	122
2531	ProteoMirExpress: Inferring MicroRNA and Protein-centered Regulatory Networks from High-throughput Proteomic and mRNA Expression Data. Molecular and Cellular Proteomics, 2013, 12, 3379-3387.	2.5	5
2532	Estrogen Receptor-Mediated Effects of Isoflavone Supplementation Were Not Observed in Whole-Genome Gene Expression Profiles of Peripheral Blood Mononuclear Cells in Postmenopausal, Equol-Producing Women. Journal of Nutrition, 2013, 143, 774-780.	1.3	23
2533	N-Glycoprotein SRMAtlas. Molecular and Cellular Proteomics, 2013, 12, 1005-1016.	2.5	48
2534	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. Briefings in Functional Genomics, 2013, 12, 366-380.	1.3	57
2535	Proteomics of Genetically Engineered Mouse Mammary Tumors Identifies Fatty Acid Metabolism Members as Potential Predictive Markers for Cisplatin Resistance. Molecular and Cellular Proteomics, 2013, 12, 1319-1334.	2.5	24
2536	Systems Genetics of Environmental Response in the Mature Wheat Embryo. Genetics, 2013, 194, 265-277.	1.2	16
2537	HOMECAAT: consensus homologs mapping for interspecific knowledge transfer and functional genomic data integration. Bioinformatics, 2013, 29, 1574-1576.	1.8	3
2538	Genome-wide single-cell-level screen for protein abundance and localization changes in response to DNA damage in <i>S. cerevisiae</i> . Nucleic Acids Research, 2013, 41, 9310-9324.	6.5	40
2539	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. Bioinformatics, 2013, 29, 2216-2217.	1.8	4

#	ARTICLE	IF	CITATIONS
2540	The Comparative Toxicogenomics Database: update 2013. <i>Nucleic Acids Research</i> , 2013, 41, D1104-D1114.	6.5	371
2541	Reverse engineering and analysis of large genome-scale gene networks. <i>Nucleic Acids Research</i> , 2013, 41, e24-e24.	6.5	34
2542	Quality-based guidance for exploratory dimensionality reduction. <i>Information Visualization</i> , 2013, 12, 44-64.	1.2	18
2543	Microbial Ecology Dynamics during Rye and Wheat Sourdough Preparation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7827-7836.	1.4	183
2544	Metabolic profiling reveals coordinated switches in primary carbohydrate metabolism in grape berry ( <i>Vitis vinifera</i> L.), a non-climacteric fleshy fruit. <i>Journal of Experimental Botany</i> , 2013, 64, 1345-1355.	2.4	125
2545	Circ2Traits: a comprehensive database for circular RNA potentially associated with disease and traits. <i>Frontiers in Genetics</i> , 2013, 4, 283.	1.1	417
2546	Cytoscape App Store. <i>Bioinformatics</i> , 2013, 29, 1350-1351.	1.8	154
2547	Bacterial Communities Associated with Subsurface Geochemical Processes in Continental Serpentine Springs. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3906-3916.	1.4	111
2548	<i>BRANCHED1</i> Promotes Axillary Bud Dormancy in Response to Shade in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 834-850.	3.1	219
2549	Genetic circuitry of <i>Survival motor neuron</i> , the gene underlying spinal muscular atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2371-80.	3.3	37
2550	The Brassica rapa FLC homologue FLC2 is a key regulator of flowering time, identified through transcriptional co-expression networks. <i>Journal of Experimental Botany</i> , 2013, 64, 4503-4516.	2.4	113
2551	dTGS: Method for Effective Components Identification from Traditional Chinese Medicine Formula and Mechanism Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-9.	0.5	11
2552	Expanding the Marine Virosphere Using Metagenomics. <i>PLoS Genetics</i> , 2013, 9, e1003987.	1.5	259
2553	Target Prediction for an Open Access Set of Compounds Active against <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1003253.	1.5	51
2554	From manual curation to visualization of gene families and networks across Solanaceae plant species. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat028.	1.4	8
2555	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. <i>Genome Biology</i> , 2013, 14, r106.	13.9	102
2556	Unexpected Diversity during Community Succession in the Apple Flower Microbiome. <i>MBio</i> , 2013, 4, .	1.8	210
2557	Transcriptome-wide expansion of non-coding regulatory switches: evidence from co-occurrence of Alu exonization, antisense and editing. <i>Nucleic Acids Research</i> , 2013, 41, 2121-2137.	6.5	29



#	ARTICLE	IF	CITATIONS
2558	A new reference implementation of the PSICQUIC web service. <i>Nucleic Acids Research</i> , 2013, 41, W601-W606.	6.5	91
2559	MS/MS networking guided analysis of molecule and gene cluster families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2611-20.	3.3	250
2560	Systems approaches map regulatory networks downstream of the auxin receptor AFB3 in the nitrate response of <i>Arabidopsis thaliana</i> roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12840-12845.	3.3	191
2561	Comparative Proteomic Analysis of Supportive and Unsupportive Extracellular Matrix Substrates for Human Embryonic Stem Cell Maintenance. <i>Journal of Biological Chemistry</i> , 2013, 288, 18716-18731.	1.6	50
2562	Dissecting the Roles of Tyrosines 490 and 785 of TrkA Protein in the Induction of Downstream Protein Phosphorylation Using Chimeric Receptors. <i>Journal of Biological Chemistry</i> , 2013, 288, 16606-16618.	1.6	18
2563	Protein Kinase PKN1 Represses Wnt/ $\beta$ -Catenin Signaling in Human Melanoma Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 34658-34670.	1.6	29
2564	Annotated genes and nonannotated genomes: cross-species use of Gene Ontology in ecology and evolution research. <i>Molecular Ecology</i> , 2013, 22, 3216-3241.	2.0	77
2565	Release of Severe Acute Respiratory Syndrome Coronavirus Nuclear Import Block Enhances Host Transcription in Human Lung Cells. <i>Journal of Virology</i> , 2013, 87, 3885-3902.	1.5	140
2566	Metabolomic Dynamic Analysis of Hypoxia in MDA-MB-231 and the Comparison with Inferred Metabolites from Transcriptomics Data. <i>Cancers</i> , 2013, 5, 491-510.	1.7	14
2567	Construction of a Computable Network Model for DNA Damage, Autophagy, Cell Death, and Senescence. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S11154.	1.0	58
2568	Applications of Machine Learning in Genomics and Systems Biology. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-1.	0.7	16
2569	A network approach to controlling pathogenic inflammation. <i>Systems Biomedicine (Austin, Tex )</i> , 2013, 1, 35-46.	0.7	0
2570	PiHelper: an open source framework for drug-target and antibody-target data. <i>Bioinformatics</i> , 2013, 29, 2071-2072.	1.8	13
2571	Systems-Level Analysis of Genome-Wide Association Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 119-129.	0.8	55
2572	Conserved miRNAs Are Candidate Post-Transcriptional Regulators of Developmental Arrest in Free-Living and Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1246-1260.	1.1	31
2573	Core sediment bacteria drive community response to anthropogenic contamination over multiple environmental gradients. <i>Environmental Microbiology</i> , 2013, 15, 2517-2531.	1.8	206
2574	Visualization of Activity Landscapes and Chemogenomics Data. <i>Molecular Informatics</i> , 2013, 32, 954-963.	1.4	2
2575	Interaction proteome of human $\text{H}\beta$ signaling: modular control of the co-activator $\text{YAP}^1$ . <i>Molecular Systems Biology</i> , 2013, 9, 713.	3.2	82



#	ARTICLE	IF	CITATIONS
2576	Dmrt1 regulates proneural gene expression downstream of $Pax6$ in the mammalian telencephalon. <i>Genes To Cells</i> , 2013, 18, 636-649.	0.5	45
2577	A user centered approach to developing information visualization module for NEIMiner. , 2013, , .		1
2578	Entourage: Visualizing Relationships between Biological Pathways using Contextual Subsets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2013, 19, 2536-2545.	2.9	38
2579	ADraw: A novel social network visualization tool with attribute-based layout and coloring. , 2013, , .		6
2580	InnateDB: systems biology of innate immunity and beyondâ€”recent updates and continuing curation. <i>Nucleic Acids Research</i> , 2013, 41, D1228-D1233.	6.5	1,073
2581	Temporal succession of putative glycolate-utilizing bacterioplankton tracks changes in dissolved organic matter in a high-elevation lake. <i>FEMS Microbiology Ecology</i> , 2013, 83, 541-551.	1.3	8
2582	Exponential random graph models for networks with community structure. <i>Physical Review E</i> , 2013, 88, 032810.	0.8	19
2583	Metabolic reconstruction identifies strainâ€”specific regulation of virulence in <i>Toxoplasma gondii</i> . <i>Molecular Systems Biology</i> , 2013, 9, 708.	3.2	48
2584	Phosphoproteomicsâ€”based network medicine. <i>FEBS Journal</i> , 2013, 280, 5696-5704.	2.2	16
2585	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Journal of Computational Biology</i> , 2013, 20, 124-136.	0.8	108
2586	A genetic algorithm approach to active subnetwork search applied to GWAS data. , 2013, , .		0
2587	EINVis: A Visualization Tool for Analyzing and Exploring Genetic Interactions in Largeâ€”scale Association Studies. <i>Genetic Epidemiology</i> , 2013, 37, 675-685.	0.6	9
2588	ChIPBase: a database for decoding the transcriptional regulation of long non-coding RNA and microRNA genes from ChIP-Seq data. <i>Nucleic Acids Research</i> , 2013, 41, D177-D187.	6.5	293
2589	Visual Analysis of Complex Networks for Business Intelligence with Gephi. , 2013, , .		24
2590	Color distribution can accelerate network alignment. , 2013, , .		7
2591	Shrinking the FadE Proteome of <i>Mycobacterium tuberculosis</i> : Insights into Cholesterol Metabolism through Identification of an $\text{H}_2\text{O}_2$ Heterotetrameric Acyl Coenzyme A Dehydrogenase Family. <i>Journal of Bacteriology</i> , 2013, 195, 4331-4341.	1.0	59
2592	RECONN: A CYTOSCAPE PLUG-IN FOR EXPLORING AND VISUALIZING REACTOME. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350004.	0.3	5
2593	Concise Review: New Paradigms for Down Syndrome Research Using Induced Pluripotent Stem Cells: Tackling Complex Human Genetic Disease. <i>Stem Cells Translational Medicine</i> , 2013, 2, 175-184.	1.6	13

#	ARTICLE	IF	CITATIONS
2594	Succumbing to the laws of attraction. <i>Systems Biomedicine (Austin, Tex )</i> , 2013, 1, 179-194.	0.7	22
2597	A Network Approach to Wound Healing. <i>Advances in Wound Care</i> , 2013, 2, 499-509.	2.6	17
2598	siRNA screening identifies differences in the Fanconi anemia pathway in BALB/c-Trp53+/Δ <sup>+</sup> with susceptibility versus C57BL/6-Trp53+/Δ <sup>+</sup> mice with resistance to mammary tumors. <i>Oncogene</i> , 2013, 32, 5458-5470.	2.6	8
2599	Gene expression profiling by mRNA sequencing reveals increased expression of immune/inflammation-related genes in the hippocampus of individuals with schizophrenia. <i>Translational Psychiatry</i> , 2013, 3, e321-e321.	2.4	162
2600	miR-125b transcriptionally increased by Nrf2 inhibits AhR repressor, which protects kidney from cisplatin-induced injury. <i>Cell Death and Disease</i> , 2013, 4, e899-e899.	2.7	77
2601	Behavioural fever is a synergic signal amplifying the innate immune response. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131381.	1.2	104
2602	CluePedia Cytoscape plugin: pathway insights using integrated experimental and <i>in silico</i> data. <i>Bioinformatics</i> , 2013, 29, 661-663.	1.8	958
2603	Active transcriptomic and proteomic reprogramming in the <i>C. elegans</i> nucleotide excision repair mutant xpa-1. <i>Nucleic Acids Research</i> , 2013, 41, 5368-5381.	6.5	40
2604	Multi-dimensional Co-separation Analysis Reveals Protein-Protein Interactions Defining Plasma Lipoprotein Subspecies. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3123-3134.	2.5	62
2605	Phenotypic overlap in the contribution of individual genes to CNV pathogenicity revealed by cross-species computational analysis of single-gene mutations in humans, mice and zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2013, 6, 358-72.	1.2	43
2606	The two-faced T cell epitope. <i>Human Vaccines and Immunotherapeutics</i> , 2013, 9, 1577-1586.	1.4	88
2607	Investigation of Pokemon-Regulated Proteins in Hepatocellular Carcinoma Using Mass Spectrometry-Based Multiplex Quantitative Proteomics. <i>European Journal of Mass Spectrometry</i> , 2013, 19, 111-121.	0.5	3
2608	BREEDING AND GENETICS SYMPOSIUM: Networks and pathways to guide genomic selection1-3. <i>Journal of Animal Science</i> , 2013, 91, 537-552.	0.2	57
2609	Integrating Ontologies Using Ontology Learning Approach. <i>IEICE Transactions on Information and Systems</i> , 2013, E96.D, 40-50.	0.4	8
2610	SBEToolbox: A Matlab Toolbox for Biological Network Analysis. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12012.	0.6	40
2611	Identification of breast cancer patients based on human signaling network motifs. <i>Scientific Reports</i> , 2013, 3, 3368.	1.6	26
2612	Global expression profiling reveals genetic programs underlying the developmental divergence between mouse and human embryogenesis. <i>BMC Genomics</i> , 2013, 14, 568.	1.2	47
2613	Integrated transcriptomics and metabolomics decipher differences in the resistance of pedunculate oak to the herbivore <i>Tortrix viridana</i> L.. <i>BMC Genomics</i> , 2013, 14, 737.	1.2	35

#	ARTICLE	IF	CITATIONS
2615	Evidence for extensive heterotrophic metabolism, antioxidant action, and associated regulatory events during winter hardening in Sitka spruce. <i>BMC Plant Biology</i> , 2013, 13, 72.	1.6	7
2616	Functional analysis of microRNA and transcription factor synergistic regulatory network based on identifying regulatory motifs in non-small cell lung cancer. <i>BMC Systems Biology</i> , 2013, 7, 122.	3.0	24
2617	3Omics: a web-based systems biology tool for analysis, integration and visualization of human transcriptomic, proteomic and metabolomic data. <i>BMC Systems Biology</i> , 2013, 7, 64.	3.0	152
2618	Identification of microRNA-mRNA functional interactions in UVB-induced senescence of human diploid fibroblasts. <i>BMC Genomics</i> , 2013, 14, 224.	1.2	55
2619	miRNA Mediated Regulation of Rice ( <i>Oryza sativa</i> ) Genome. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2013, 46, 95-100.	0.4	1
2620	Complementary Detection of Embryotoxic Properties of Substances in the Neural and Cardiac Embryonic Stem Cell Tests. <i>Toxicological Sciences</i> , 2013, 132, 118-130.	1.4	37
2621	3DScapeCS: application of three dimensional, parallel, dynamic network visualization in Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 322.	1.2	14
2622	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013, 14, 722.	1.2	73
2623	Computational approaches for discovery of common immunomodulators in fungal infections: towards broad-spectrum immunotherapeutic interventions. <i>BMC Microbiology</i> , 2013, 13, 224.	1.3	9
2624	<i>Saccharomyces cerevisiae</i> Genetics Predicts Candidate Therapeutic Genetic Interactions at the Mammalian Replication Fork. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 273-282.	0.8	34
2625	Pathway analysis of gene expression data from colonic biopsies distinguishes salmon from cod consumers. <i>Proceedings of the Nutrition Society</i> , 2013, 72, .	0.4	0
2626	Mapping the twin-arginine protein translocation network of <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2013, 13, 800-811.	1.3	15
2627	Pathways of Lipid Metabolism in Marine Algae, Co-Expression Network, Bottlenecks and Candidate Genes for Enhanced Production of EPA and DHA in Species of Chromista. <i>Marine Drugs</i> , 2013, 11, 4662-4697.	2.2	181
2628	Over-Expression of hNGF in Adult Human Olfactory Bulb Neural Stem Cells Promotes Cell Growth and Oligodendrocytic Differentiation. <i>PLoS ONE</i> , 2013, 8, e82206.	1.1	21
2629	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	2.8	379
2630	Network Characteristic Analysis of ADR-related Proteins and Identification of ADR-ADR Associations. <i>Scientific Reports</i> , 2013, 3, 1744.	1.6	15
2631	Identifying potential cancer driver genes by genomic data integration. <i>Scientific Reports</i> , 2013, 3, 3538.	1.6	60
2632	Screening for feature genes associated with hereditary hemochromatosis and functional analysis with DNA microarrays. <i>Genetics and Molecular Research</i> , 2013, 12, 6240-6248.	0.3	2

#	ARTICLE	IF	CITATIONS
2633	Transcriptome network analysis of potential candidate genes for heart failure. <i>Genetics and Molecular Research</i> , 2013, 12, 4687-4697.	0.3	7
2634	Comparison of Computational Tools for Protein-Protein Interaction (PPI) Mapping and Analysis. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013, 63, .	0.3	1
2635	Regulation network analysis of testicular seminoma at various stages of progression. <i>Genetics and Molecular Research</i> , 2013, 12, 4297-4307.	0.3	1
2636	Reanalysis of microarray data reveals insights into altered transcriptional activity of T helper 17 and regulatory T cell signaling in psoriasis. <i>Psoriasis: Targets and Therapy</i> , 0, , 31.	1.2	0
2637	BREEDING AND GENETICS SYMPOSIUM: Building single nucleotide polymorphism-derived gene regulatory networks: Towards functional genomewide association studies <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2013, 91, 530-536.	0.2	34
2638	Choline Protects Against Cardiac Hypertrophy Induced by Increased After-load. <i>International Journal of Biological Sciences</i> , 2013, 9, 295-302.	2.6	22
2639	Towards RVL , 2013, , .		4
2640	Comparison of Modules of Wild Type and Mutant Huntingtin and TP53 Protein Interaction Networks: Implications in Biological Processes and Functions. <i>PLoS ONE</i> , 2013, 8, e64838.	1.1	8
2641	Wrangling Phosphoproteomic Data to Elucidate Cancer Signaling Pathways. <i>PLoS ONE</i> , 2013, 8, e52884.	1.1	22
2642	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. <i>PLoS ONE</i> , 2013, 8, e53846.	1.1	13
2643	Host Responses to Melioidosis and Tuberculosis Are Both Dominated by Interferon-Mediated Signaling. <i>PLoS ONE</i> , 2013, 8, e54961.	1.1	55
2644	Alterations in the Colonic Microbiota in Response to Osmotic Diarrhea. <i>PLoS ONE</i> , 2013, 8, e55817.	1.1	102
2645	Dietary Sphingomyelin Lowers Hepatic Lipid Levels and Inhibits Intestinal Cholesterol Absorption in High-Fat-Fed Mice. <i>PLoS ONE</i> , 2013, 8, e55949.	1.1	44
2646	Next Generation Sequencing Reveals the Expression of a Unique miRNA Profile in Response to a Gram-Positive Bacterial Infection. <i>PLoS ONE</i> , 2013, 8, e57543.	1.1	93
2647	Gene Expression Profile of the Hippocampus of Rats Subjected to Chronic Immobilization Stress. <i>PLoS ONE</i> , 2013, 8, e57621.	1.1	35
2648	A Core Filamentation Response Network in <i>Candida albicans</i> Is Restricted to Eight Genes. <i>PLoS ONE</i> , 2013, 8, e58613.	1.1	90
2649	Systems Biology Elucidates Common Pathogenic Mechanisms between Nonalcoholic and Alcoholic-Fatty Liver Disease. <i>PLoS ONE</i> , 2013, 8, e58895.	1.1	47
2650	Network Class Superposition Analyses. <i>PLoS ONE</i> , 2013, 8, e59046.	1.1	3

#	ARTICLE	IF	CITATIONS
2651	Modular Biological Function Is Most Effectively Captured by Combining Molecular Interaction Data Types. PLoS ONE, 2013, 8, e62670.	1.1	16
2652	Relaxation Response Induces Temporal Transcriptome Changes in Energy Metabolism, Insulin Secretion and Inflammatory Pathways. PLoS ONE, 2013, 8, e62817.	1.1	223
2653	Genome-Wide Analysis Reveals Diversity of Rice Intronic miRNAs in Sequence Structure, Biogenesis and Function. PLoS ONE, 2013, 8, e63938.	1.1	11
2654	Transcriptional Dissection of Human Limbal Niche Compartments by Massive Parallel Sequencing. PLoS ONE, 2013, 8, e64244.	1.1	25
2655	Genome-Wide Methylated DNA Immunoprecipitation Analysis of Patients with Polycystic Ovary Syndrome. PLoS ONE, 2013, 8, e64801.	1.1	43
2656	Genomic Analysis of Stress Response against Arsenic in <i>Caenorhabditis elegans</i> . PLoS ONE, 2013, 8, e66431.	1.1	27
2657	Unravelling the Complexity of Human Olfactory Receptor Repertoire by Copy Number Analysis across Population Using High Resolution Arrays. PLoS ONE, 2013, 8, e66843.	1.1	13
2658	An Improved Method for TAL Effectors DNA-Binding Sites Prediction Reveals Functional Convergence in TAL Repertoires of <i>Xanthomonas oryzae</i> Strains. PLoS ONE, 2013, 8, e68464.	1.1	102
2659	Distinct Pools of Non-Glycolytic Substrates Differentiate Brain Regions and Prime Region-Specific Responses of Mitochondria. PLoS ONE, 2013, 8, e68831.	1.1	21
2660	Exploring the Sources of Bacterial Spoilers in Beefsteaks by Culture-Independent High-Throughput Sequencing. PLoS ONE, 2013, 8, e70222.	1.1	176
2661	Voting-Based Cancer Module Identification by Combining Topological and Data-Driven Properties. PLoS ONE, 2013, 8, e70498.	1.1	9
2662	Genomic Phenotyping by Barcode Sequencing Broadly Distinguishes between Alkylating Agents, Oxidizing Agents, and Non-Genotoxic Agents, and Reveals a Role for Aromatic Amino Acids in Cellular Recovery after Quinone Exposure. PLoS ONE, 2013, 8, e73736.	1.1	2
2663	A Purine Analog Synergizes with Chloroquine (CQ) by Targeting <i>Plasmodium falciparum</i> Hsp90 (PfHsp90). PLoS ONE, 2013, 8, e75446.	1.1	29
2664	SIDD: A Semantically Integrated Database towards a Global View of Human Disease. PLoS ONE, 2013, 8, e75504.	1.1	46
2665	Soil-Borne Bacterial Structure and Diversity Does Not Reflect Community Activity in Pampa Biome. PLoS ONE, 2013, 8, e76465.	1.1	52
2666	Breast Tumors with Elevated Expression of 1q Candidate Genes Confer Poor Clinical Outcome and Sensitivity to Ras/PI3K Inhibition. PLoS ONE, 2013, 8, e77553.	1.1	48
2667	Inferring Polymorphism-Induced Regulatory Gene Networks Active in Human Lymphocyte Cell Lines by Weighted Linear Mixed Model Analysis of Multiple RNA-Seq Datasets. PLoS ONE, 2013, 8, e78868.	1.1	4
2668	Genome-Wide Computational Prediction and Analysis of Core Promoter Elements across Plant Monocots and Dicots. PLoS ONE, 2013, 8, e79011.	1.1	45

#	ARTICLE	IF	CITATIONS
2669	Role of Tumor Necrosis Factor- $\alpha$ in the Human Systemic Endotoxin-Induced Transcriptome. PLoS ONE, 2013, 8, e79051.	1.1	14
2670	Vitamin D Receptor, an Important Transcription Factor Associated with Aldosterone-Producing Adenoma. PLoS ONE, 2013, 8, e82309.	1.1	12
2671	Systematic Identification of Core Transcription Factors Mediating Dysregulated Links Bridging Inflammatory Bowel Diseases and Colorectal Cancer. PLoS ONE, 2013, 8, e83495.	1.1	3
2672	Microarray and Degradome Sequencing Reveal MicroRNA Differential Expression Profiles and Their Targets in <i>Pinellia pedatisecta</i> . PLoS ONE, 2013, 8, e75978.	1.1	8
2673	Toxicological Effects of the Different Substances in Tobacco Smoke on Human Embryonic Development by a Systems Chemo-Biology Approach. PLoS ONE, 2013, 8, e61743.	1.1	31
2674	Genes associated with disc degeneration identified using microarray gene expression profiling and bioinformatics analysis. Genetics and Molecular Research, 2013, 12, 1431-1439.	0.3	7
2675	Network statistics of genetically-driven gene co-expression modules in mouse crosses. Frontiers in Genetics, 2013, 4, 291.	1.1	4
2676	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. Frontiers in Microbiology, 2013, 4, 106.	1.5	112
2677	Exploiting a Reference Genome in Terms of Duplications: The Network of Paralogs and Single Copy Genes in <i>Arabidopsis thaliana</i> . Biology, 2013, 2, 1465-1487.	1.3	6
2678	Synthetic Genetic Targeting of Genome Instability in Cancer. Cancers, 2013, 5, 739-761.	1.7	31
2679	Construction and Analysis of the Cell Surface $\alpha$ 's Protein Network for Human Sperm-Egg Interaction. , 2013, 2013, 1-8.		8
2680	Pivotal regulatory network and genes in osteosarcoma. Archives of Medical Science, 2013, 3, 569-575.	0.4	14
2681	Proteomics and Metabolomics in Aortic Stenosis: Studying Healthy Valves for a Better Understanding of the Disease. , 2013, , .		0
2682	Suborganizations of Institutions in Library and Information Science Journals. Information (Switzerland), 2013, 4, 351-366.	1.7	10
2683	Inferring Transcriptional Regulatory Relationships Among Genes in Breast Cancer: An Application of Bayes' Theorem. International Journal of Statistics and Probability, 2014, 3, .	0.1	2
2684	High-Throughput Screening for the Identification of New Therapeutic Options for Metastatic Pheochromocytoma and Paraganglioma. PLoS ONE, 2014, 9, e90458.	1.1	9
2685	Multi-Tissue Omics Analyses Reveal Molecular Regulatory Networks for Puberty in Composite Beef Cattle. PLoS ONE, 2014, 9, e102551.	1.1	125
2686	BiNA: A Visual Analytics Tool for Biological Network Data. PLoS ONE, 2014, 9, e87397.	1.1	31

#	ARTICLE	IF	CITATIONS
2687	Network Analysis Reveals Ecological Links between N-Fixing Bacteria and Wood-Decaying Fungi. PLoS ONE, 2014, 9, e88141.	1.1	129
2688	Footprints of Directional Selection in Wild Atlantic Salmon Populations: Evidence for Parasite-Driven Evolution?. PLoS ONE, 2014, 9, e91672.	1.1	37
2689	Dynamics of Regulatory Networks in Gastrin-Treated Adenocarcinoma Cells. PLoS ONE, 2014, 9, e78349.	1.1	3
2690	DACH1: Its Role as a Classifier of Long Term Good Prognosis in Luminal Breast Cancer. PLoS ONE, 2014, 9, e84428.	1.1	24
2691	Integrative Gene Network Construction to Analyze Cancer Recurrence Using Semi-Supervised Learning. PLoS ONE, 2014, 9, e86309.	1.1	44
2692	Mucosa-Associated Bacterial Microbiome of the Gastrointestinal Tract of Weaned Pigs and Dynamics Linked to Dietary Calcium-Phosphorus. PLoS ONE, 2014, 9, e86950.	1.1	106
2693	The Role of Viral and Host MicroRNAs in the Aujeszky's Disease Virus during the Infection Process. PLoS ONE, 2014, 9, e86965.	1.1	21
2694	Computational Study on the Inhibitor Binding Mode and Allosteric Regulation Mechanism in Hepatitis C Virus NS3/4A Protein. PLoS ONE, 2014, 9, e87077.	1.1	19
2695	Proteomic Analysis of Detergent Resistant Membrane Domains during Early Interaction of Macrophages with Rough and Smooth Brucella melitensis. PLoS ONE, 2014, 9, e91706.	1.1	10
2696	A microRNA Signature Associated with Early Recurrence in Breast Cancer. PLoS ONE, 2014, 9, e91884.	1.1	72
2697	Studying the System-Level Involvement of MicroRNAs in Parkinson's Disease. PLoS ONE, 2014, 9, e93751.	1.1	21
2698	Investigating the Relation between Stochastic Differentiation, Homeostasis and Clonal Expansion in Intestinal Crypts via Multiscale Modeling. PLoS ONE, 2014, 9, e97272.	1.1	18
2699	GWAS in a Box: Statistical and Visual Analytics of Structured Associations via GenAMap. PLoS ONE, 2014, 9, e97524.	1.1	7
2700	Glucocorticoid-Induced Reversal of Interleukin-1 $\beta$ -Stimulated Inflammatory Gene Expression in Human Oviductal Cells. PLoS ONE, 2014, 9, e97997.	1.1	9
2701	Interactome Profile of the Host Cellular Proteins and the Nonstructural Protein 2 of Porcine Reproductive and Respiratory Syndrome Virus. PLoS ONE, 2014, 9, e99176.	1.1	16
2702	Discovering Functional Modules across Diverse Maize Transcriptomes Using COB, the Co-Expression Browser. PLoS ONE, 2014, 9, e99193.	1.1	25
2703	Early-Life Environmental Variation Affects Intestinal Microbiota and Immune Development in New-Born Piglets. PLoS ONE, 2014, 9, e100040.	1.1	181
2704	The Genetic Structure of Staphylococcus aureus Populations from the Southwest Pacific. PLoS ONE, 2014, 9, e100300.	1.1	21



#	ARTICLE	IF	CITATIONS
2705	Community Shifts in the Surface Microbiomes of the Coral <i>Porites astreoides</i> with Unusual Lesions. PLoS ONE, 2014, 9, e100316.	1.1	113
2706	IIS – Integrated Interactome System: A Web-Based Platform for the Annotation, Analysis and Visualization of Protein-Metabolite-Gene-Drug Interactions by Integrating a Variety of Data Sources and Tools. PLoS ONE, 2014, 9, e100385.	1.1	58
2707	Novel Insights into the Regulatory Architecture of CD4+ T Cells in Rheumatoid Arthritis. PLoS ONE, 2014, 9, e100690.	1.1	22
2708	Identification of Novel Elements of the <i>Drosophila</i> Blisterome Sheds Light on Potential Pathological Mechanisms of Several Human Diseases. PLoS ONE, 2014, 9, e101133.	1.1	8
2709	Visualizing Molecular Profiles of Glioblastoma with GBM-BioDP. PLoS ONE, 2014, 9, e101239.	1.1	52
2710	Expansion of Human Mesenchymal Stromal Cells from Fresh Bone Marrow in a 3D Scaffold-Based System under Direct Perfusion. PLoS ONE, 2014, 9, e102359.	1.1	81
2711	Artificial Neural Network Inference (ANNI): A Study on Gene-Gene Interaction for Biomarkers in Childhood Sarcomas. PLoS ONE, 2014, 9, e102483.	1.1	48
2712	Systems Pharmacology Dissection of Multi-Scale Mechanisms of Action for Herbal Medicines in Stroke Treatment and Prevention. PLoS ONE, 2014, 9, e102506.	1.1	35
2713	Construction and Analysis of the Protein-Protein Interaction Networks Based on Gene Expression Profiles of Parkinson's Disease. PLoS ONE, 2014, 9, e103047.	1.1	59
2714	Response of <i>Saccharomyces cerevisiae</i> to the Stimulation of Lipopolysaccharide. PLoS ONE, 2014, 9, e104428.	1.1	10
2715	Dynamic Modularity of Host Protein Interaction Networks in <i>Salmonella Typhi</i> Infection. PLoS ONE, 2014, 9, e104911.	1.1	6
2716	De-Novo Learning of Genome-Scale Regulatory Networks in <i>S. cerevisiae</i> . PLoS ONE, 2014, 9, e106479.	1.1	18
2717	Meta-Analysis of Gene Expression Signatures Reveals Hidden Links among Diverse Biological Processes in <i>Arabidopsis</i> . PLoS ONE, 2014, 9, e108567.	1.1	2
2718	Network Analysis Identifies SOD2 mRNA as a Potential Biomarker for Parkinson's Disease. PLoS ONE, 2014, 9, e109042.	1.1	30
2719	CSF Proteomics of Secondary Phase Spinal Cord Injury in Human Subjects: Perturbed Molecular Pathways Post Injury. PLoS ONE, 2014, 9, e110885.	1.1	31
2720	Taxonomic and Functional Diversity Provides Insight into Microbial Pathways and Stress Responses in the Saline Qinghai Lake, China. PLoS ONE, 2014, 9, e111681.	1.1	12
2721	CollaborationViz: Interactive Visual Exploration of Biomedical Research Collaboration Networks. PLoS ONE, 2014, 9, e111928.	1.1	11
2722	Protein Interaction Networks Reveal Novel Autism Risk Genes within GWAS Statistical Noise. PLoS ONE, 2014, 9, e112399.	1.1	14

#	ARTICLE	IF	CITATIONS
2723	Community Structure Detection for Overlapping Modules through Mathematical Programming in Protein Interaction Networks. PLoS ONE, 2014, 9, e112821.	1.1	18
2724	A Chemical Proteomics Approach for the Search of Pharmacological Targets of the Antimalarial Clinical Candidate Albitiazolium in Plasmodium falciparum Using Photocrosslinking and Click Chemistry. PLoS ONE, 2014, 9, e113918.	1.1	22
2725	The Human Pancreas Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e115421.	1.1	35
2726	ReNE: A Cytoscape Plugin for Regulatory Network Enhancement. PLoS ONE, 2014, 9, e115585.	1.1	15
2727	Identifying Glioblastoma Gene Networks Based on Hypergeometric Test Analysis. PLoS ONE, 2014, 9, e115842.	1.1	15
2728	The Kidney Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e116125.	1.1	49
2729	RRHGE: A Novel Approach to Classify the Estrogen Receptor Based Breast Cancer Subtypes. Scientific World Journal, The, 2014, 2014, 1-13.	0.8	3
2730	Gene Expression Profile Analysis in Epilepsy by Using the Partial Least Squares Method. Scientific World Journal, The, 2014, 2014, 1-5.	0.8	5
2731	Elementary Flux Mode Analysis of Acetyl-CoA Pathway in <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. Advances in Bioinformatics, 2014, 2014, 1-10.	5.7	15
2732	Exploring the miRNA-mRNA Regulatory Network in Clear Cell Renal Cell Carcinomas by Next-Generation Sequencing Expression Profiles. BioMed Research International, 2014, 2014, 1-11.	0.9	36
2733	Identification of therapeutic target genes with DNA microarray in multiple myeloma cell line treated by IKK1 <sup>2</sup> /NF- $\kappa$ B inhibitor. Acta Cirurgica Brasileira, 2014, 29, 696-702.	0.3	2
2734	Improving Collaboration by Standardization Efforts in Systems Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 61.	2.0	52
2735	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. Frontiers in Bioengineering and Biotechnology, 2014, 2, 69.	2.0	25
2736	R-Based Software for the Integration of Pathway Data into Bioinformatic Algorithms. Biology, 2014, 3, 85-100.	1.3	18
2737	Hope for GWAS: Relevant Risk Genes Uncovered from GWAS Statistical Noise. International Journal of Molecular Sciences, 2014, 15, 17601-17621.	1.8	2
2738	Dual Linkage of a Locus to Left Ventricular Mass and a Cardiac Gene Co-Expression Network Driven by a Chromosome Domain. Frontiers in Cardiovascular Medicine, 2014, 1, 11.	1.1	2
2739	categoryCompare, an analytical tool based on feature annotations. Frontiers in Genetics, 2014, 5, 98.	1.1	29
2740	Toward a systems-level understanding of gene regulatory, protein interaction, and metabolic networks in cyanobacteria. Frontiers in Genetics, 2014, 5, 191.	1.1	19

#	ARTICLE	IF	CITATIONS
2741	Spatial gradients in trace metal concentrations in the surface microlayer of the Mediterranean Sea. <i>Frontiers in Marine Science</i> , 2014, 1, .	1.2	27
2742	The impact of the pathogen <i>Rhizoctonia solani</i> and its beneficial counterpart <i>Bacillus amyloliquefaciens</i> on the indigenous lettuce microbiome. <i>Frontiers in Microbiology</i> , 2014, 5, 175.	1.5	141
2743	Gene regulatory network analysis reveals differences in site-specific cell fate determination in mammalian brain. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 437.	1.8	28
2744	Investigating the structure of semantic networks in low and high creative persons. <i>Frontiers in Human Neuroscience</i> , 2014, 8, 407.	1.0	214
2745	Computational Strategies for a System-Level Understanding of Metabolism. <i>Metabolites</i> , 2014, 4, 1034-1087.	1.3	54
2746	Water Relationships in the U.S. Southwest: Characterizing Water Management Networks Using Natural Language Processing. <i>Water (Switzerland)</i> , 2014, 6, 1601-1641.	1.2	9
2747	How Do Bioinformatics Approaches Apply to the Analysis and Understanding of Disease Pathology?. , 2014, , 4140-4157.		2
2748	KEGGscape: a Cytoscape app for pathway data integration. <i>F1000Research</i> , 2014, 3, 144.	0.8	65
2749	Oxido-reductive regulation of vascular remodeling by receptor tyrosine kinase ROS1. <i>Journal of Clinical Investigation</i> , 2014, 124, 5159-5174.	3.9	38
2750	Systems Biology Analyses of the Placenta. , 2014, , 259-274.		4
2751	Adenylate kinase 2 deficiency limits survival and regulates various genes during larval stages of <i>Drosophila melanogaster</i> . <i>Journal of Medical Investigation</i> , 2014, 61, 137-150.	0.2	11
2752	Integrative Bioinformatics Approaches to Analyze Molecular Events in Pluripotency. <i>Biology and Medicine (Aligarh)</i> , 2014, 06, .	0.3	1
2753	Interactive Visualization for Patient-to-Patient Comparison. <i>Genomics and Informatics</i> , 2014, 12, 21.	0.4	15
2754	Stratified Pathway Analysis to Identify Gene Sets Associated with Oral Contraceptive Use and Breast Cancer. <i>Cancer Informatics</i> , 2014, 13s4, CIN.S13973.	0.9	3
2755	Biomarkers for combat-related PTSD: focus on molecular networks from high-dimensional data. <i>HÅrgre Utbildning</i> , 2014, 5, .	1.4	22
2756	Proteome-wide analysis reveals an age-associated cellular phenotype of in situ aged human fibroblasts. <i>Aging</i> , 2014, 6, 856-872.	1.4	65
2757	Evaluation and Identification of Protein Blood Biomarkers for Alzheimer's Disease: A Systematic Review and Integrative Analysis. <i>Journal of Molecular Biomarkers &amp; Diagnosis</i> , 2014, 05, .	0.4	0
2758	Poly (ADP-ribose) in the pathogenesis of Parkinson's disease. <i>BMB Reports</i> , 2014, 47, 424-432.	1.1	40

#	ARTICLE	IF	CITATIONS
2759	Defining the human gallbladder proteome by transcriptomics and affinity proteomics. <i>Proteomics</i> , 2014, 14, 2498-2507.	1.3	19
2760	Databases, Standards, and Modeling Platforms for Systems Biology. , 2014, , 169-182.		0
2761	ToppMiR: ranking microRNAs and their mRNA targets based on biological functions and context. <i>Nucleic Acids Research</i> , 2014, 42, W107-W113.	6.5	21
2762	JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. <i>Bioinformatics</i> , 2014, 30, 1029-1030.	1.8	52
2763	Interactome analyses of Salmonella pathogenicity islands reveal SicA indispensable for virulence. <i>Journal of Theoretical Biology</i> , 2014, 363, 188-197.	0.8	46
2764	Gene-environment interaction research in psychiatric epidemiology: a framework and implications for study design. <i>Social Psychiatry and Psychiatric Epidemiology</i> , 2014, 49, 1525-1529.	1.6	8
2765	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1828-1843.	2.5	45
2766	Influenza A Immunomics and Public Health Omics: The Dynamic Pathway Interplay in Host Response to H1N1 Infection. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 167-183.	1.0	12
2767	New Insights into Schizophrenia Disease Genes Interactome in the Human Brain: Emerging Targets and Therapeutic Implications in the Postgenomics Era. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 754-766.	1.0	8
2768	Zinc proteome interaction network as a model to identify nutrient-affected pathways in human pathologies. <i>Genes and Nutrition</i> , 2014, 9, 436.	1.2	28
2769	Transcriptomic analysis of the late stages of grapevine ( <i>Vitis vinifera</i> cv. Cabernet Sauvignon) berry ripening reveals significant induction of ethylene signaling and flavor pathways in the skin. <i>BMC Plant Biology</i> , 2014, 14, 370.	1.6	105
2770	Network analysis of ChIP-Seq data reveals key genes in prostate cancer. <i>European Journal of Medical Research</i> , 2014, 19, 47.	0.9	6
2771	Transcriptional response of <i>Saccharomyces cerevisiae</i> to potassium starvation. <i>BMC Genomics</i> , 2014, 15, 1040.	1.2	6
2772	The effects of hemorrhagic parenchymal infarction on the establishment of sensori-motor structural and functional connectivity in early infancy. <i>Neuroradiology</i> , 2014, 56, 985-994.	1.1	40
2773	Genome wide screening of RNAi factors of Sf21 cells reveal several novel pathway associated proteins. <i>BMC Genomics</i> , 2014, 15, 775.	1.2	18
2774	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	6.5	27
2775	Topology analysis and visualization of Potyvirus protein-protein interaction network. <i>BMC Systems Biology</i> , 2014, 8, 129.	3.0	31
2776	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. <i>Genome Biology</i> , 2014, 15, 512.	3.8	475

#	ARTICLE	IF	CITATIONS
2777	No3CoGP: non-conserved and conserved coexpressed gene pairs. BMC Research Notes, 2014, 7, 886.	0.6	2
2778	Transcriptomics of the late gestation ovine fetal brain: modeling the co-expression of immune marker genes. BMC Genomics, 2014, 15, 1001.	1.2	11
2779	Phosphite-induced changes of the transcriptome and secretome in <i>Solanum tuberosum</i> leading to resistance against <i>Phytophthora infestans</i> . BMC Plant Biology, 2014, 14, 254.	1.6	77
2780	Invariance and plasticity in the <i>Drosophila melanogaster</i> metabolomic network in response to temperature. BMC Systems Biology, 2014, 8, 139.	3.0	19
2781	Large differences in global transcriptional regulatory programs of normal and tumor colon cells. BMC Cancer, 2014, 14, 708.	1.1	31
2782	Databases for Bioenergy-Related Enzymes. , 2014, , 95-107.		2
2783	Clone Mapper: An Online Suite of Tools for RNAi Experiments in <i>Caenorhabditis elegans</i> . G3: Genes, Genomes, Genetics, 2014, 4, 2137-2145.	0.8	17
2784	Global gene expression profiling identifies ALDH2, CCNE1 and SMAD3 as potential prognostic markers in upper tract urothelial carcinoma. BMC Cancer, 2014, 14, 836.	1.1	25
2785	A HIF-1 network reveals characteristics of epithelial-mesenchymal transition in acute promyelocytic leukemia. Genome Medicine, 2014, 6, 84.	3.6	18
2786	Metabolic reprogramming induced by ketone bodies diminishes pancreatic cancer cachexia. Cancer & Metabolism, 2014, 2, 18.	2.4	182
2787	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. BMC Genomics, 2014, 15, 852.	1.2	10
2788	Short-term airborne particulate matter exposure alters the epigenetic landscape of human genes associated with the mitogen-activated protein kinase network: a cross-sectional study. Environmental Health, 2014, 13, 94.	1.7	55
2789	New insight into HCV E1/E2 region of genotype 4a. Virology Journal, 2014, 11, 231.	1.4	3
2790	Inhibition of Protein Geranylgeranylation Specifically Interferes with CD40-Dependent B Cell Activation, Resulting in a Reduced Capacity To Induce T Cell Immunity. Journal of Immunology, 2014, 193, 5294-5305.	0.4	29
2791	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. Science Translational Medicine, 2014, 6, 234ra57.	5.8	58
2792	New Tricks for "Old" Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. Genome Biology and Evolution, 2014, 6, 2897-2917.	1.1	14
2793	A Systems Biology Approach Identifies Effective Tumor "Stroma Common Targets for Oral Squamous Cell Carcinoma. Cancer Research, 2014, 74, 2306-2315.	0.4	32
2794	Computational Approaches for Visualization and Integration of Omics Data. Comprehensive Analytical Chemistry, 2014, , 443-454.	0.7	0

#	ARTICLE	IF	CITATIONS
2795	Long non-coding RNAs. <i>RNA Biology</i> , 2014, 11, 373-390.	1.5	59
2796	Proposed metrics on ecosystem health. , 2014, , .		7
2797	TraceRNA: A Web Application for Competing Endogenous RNA Exploration. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 548-557.	5.1	2
2798	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. <i>Bioinformatics</i> , 2014, 30, 621-628.	1.8	37
2799	A conserved extraordinarily long serine homopolymer in Dictyostelid amoebae. <i>Heredity</i> , 2014, 112, 215-218.	1.2	3
2800	PATHOME: an algorithm for accurately detecting differentially expressed subpathways. <i>Oncogene</i> , 2014, 33, 4941-4951.	2.6	70
2801	Clinical interpretation of CNVs with cross-species phenotype data. <i>Journal of Medical Genetics</i> , 2014, 51, 766-772.	1.5	23
2802	Machine Learning Approaches Distinguish Multiple Stress Conditions using Stress-Responsive Genes and Identify Candidate Genes for Broad Resistance in Rice. <i>Plant Physiology</i> , 2014, 164, 481-495.	2.3	129
2803	Functional features and protein network of human sperm-egg interaction. <i>Systems Biology in Reproductive Medicine</i> , 2014, 60, 329-337.	1.0	18
2804	9 Transcriptomics of Industrial Filamentous Fungi: A New View on Regulation, Physiology, and Application. , 2014, , 209-232.		2
2805	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014, 5, 5719.	5.8	100
2806	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843.	2.6	79
2807	Specific gene-regulation networks during the pre-implantation development of the pig embryo as revealed by deep sequencing. <i>BMC Genomics</i> , 2014, 15, 4.	1.2	130
2808	ECOD: An Evolutionary Classification of Protein Domains. <i>PLoS Computational Biology</i> , 2014, 10, e1003926.	1.5	321
2809	Noma Affected Children from Niger Have Distinct Oral Microbial Communities Based on High-Throughput Sequencing of 16S rRNA Gene Fragments. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3240.	1.3	14
2810	Digitally Researching the Network Drawings of Mark Lombardi. <i>Leonardo</i> , 2014, 47, 278-278.	0.2	1
2811	Locus heterogeneity disease genes encode proteins with high interconnectivity in the human protein interaction network. <i>Frontiers in Genetics</i> , 2014, 5, 434.	1.1	8
2812	Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , 2014, 5, 422.	2.2	29

#	ARTICLE	IF	CITATIONS
2813	A comprehensive analysis of the Omp85/TpsB protein superfamily structural diversity, taxonomic occurrence, and evolution. <i>Frontiers in Microbiology</i> , 2014, 5, 370.	1.5	78
2814	Hantavirus Immunology of Rodent Reservoirs: Current Status and Future Directions. <i>Viruses</i> , 2014, 6, 1317-1335.	1.5	50
2815	Lsd1 Restricts the Number of Germline Stem Cells by Regulating Multiple Targets in Escort Cells. <i>PLoS Genetics</i> , 2014, 10, e1004200.	1.5	58
2816	MicroRNA Regulation of Bovine Monocyte Inflammatory and Metabolic Networks in an <i>In Vivo</i> Infection Model. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 957-971.	0.8	62
2817	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A. thaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	2.9	249
2818	Proteomics of bronchial biopsies: Galectin-3 as a predictive biomarker of airway remodelling modulation in omalizumab-treated severe asthma patients. <i>Immunology Letters</i> , 2014, 162, 2-10.	1.1	95
2819	Incremental network querying in biological networks. , 2014, , .		4
2820	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	1.5	70
2821	Transcriptional Correlates of Disease Outcome in Anticoagulant-Treated Non-Human Primates Infected with Ebolavirus. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3061.	1.3	22
2822	Regression Analysis of Combined Gene Expression Regulation in Acute Myeloid Leukemia. <i>PLoS Computational Biology</i> , 2014, 10, e1003908.	1.5	62
2823	Essential Functional Modules for Pathogenic and Defensive Mechanisms in <i>Candida albicans</i> Infections. <i>BioMed Research International</i> , 2014, 2014, 1-15.	0.9	7
2824	Differential Protein Network Analysis of the Immune Cell Lineage. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	5
2825	MicroRNA Expression Profiling Altered by Variant Dosage of Radiation Exposure. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	20
2826	Systematic Expression Profiling Analysis Identifies Specific MicroRNA-Gene Interactions that May Differentiate between Active and Latent Tuberculosis Infection. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	26
2827	Plasma Cholesterol-Induced Lesion Networks Activated before Regression of Early, Mature, and Advanced Atherosclerosis. <i>PLoS Genetics</i> , 2014, 10, e1004201.	1.5	64
2828	HoPaCI-DB: host- <i>Pseudomonas</i> and <i>Coxiella</i> interaction database. <i>Nucleic Acids Research</i> , 2014, 42, D671-D676.	6.5	21
2829	Illuminating Microbial Dark Matter in Meromictic Sakinaw Lake. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6807-6818.	1.4	109
2830	A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	9



#	ARTICLE	IF	CITATIONS
2831	CGBayesNets: Conditional Gaussian Bayesian Network Learning and Inference with Mixed Discrete and Continuous Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003676.	1.5	57
2832	Biomarker Analysis Revealed Distinct Profiles of Innate and Adaptive Immunity in Infants with Ocular Lesions of Congenital Toxoplasmosis. <i>Mediators of Inflammation</i> , 2014, 2014, 1-13.	1.4	47
2833	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003517.	1.5	167
2834	Impact of interspecific interactions on antimicrobial activity among soil bacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 567.	1.5	109
2835	Community detection for networks with unipartite and bipartite structure. <i>New Journal of Physics</i> , 2014, 16, 093001.	1.2	9
2836	Survey of Network-Based Approaches to Research of Cardiovascular Diseases. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	8
2837	Telling metabolic stories to explore metabolomics data: a case study on the yeast response to cadmium exposure. <i>Bioinformatics</i> , 2014, 30, 61-70.	1.8	13
2838	Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. <i>Nucleic Acids Research</i> , 2014, 42, e76-e76.	6.5	55
2839	A Web-Based Tool for Visualization of Biomolecular Network Comparison. <i>Applied Mechanics and Materials</i> , 2014, 556-562, 5482-5487.	0.2	0
2840	Functional toxicology: tools to advance the future of toxicity testing. <i>Frontiers in Genetics</i> , 2014, 5, 110.	1.1	32
2841	Protein-protein interaction and gene co-expression maps of ARFs and Aux/IAAs in Arabidopsis. <i>Frontiers in Plant Science</i> , 2014, 5, 744.	1.7	175
2842	Integration Strategy Is a Key Step in Network-Based Analysis and Dramatically Affects Network Topological Properties and Inferring Outcomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	5
2843	Leveraging additional knowledge to support coherent bicluster discovery in gene expression data. <i>Intelligent Data Analysis</i> , 2014, 18, 837-855.	0.4	8
2844	Epigenome-Guided Analysis of the Transcriptome of Plaque Macrophages during Atherosclerosis Regression Reveals Activation of the Wnt Signaling Pathway. <i>PLoS Genetics</i> , 2014, 10, e1004828.	1.5	31
2845	Omics-Based Testing for Direct Immunotoxicity. , 2014, , 89-124.		1
2846	Differentially expressed genes and interacting pathways in bladder cancer revealed by bioinformatic analysis. <i>Molecular Medicine Reports</i> , 2014, 10, 1746-1752.	1.1	8
2847	Studying network morphology in common developmental genomes. , 2014, , .		0
2848	Integration, navigation and exploration of plant topology networks using the property-graph model. , 2014, , .		1

#	ARTICLE	IF	CITATIONS
2849	An information theoretic approach to assessing gene-ontology-driven similarity and its application. International Journal of Data Mining and Bioinformatics, 2014, 9, 121.	0.1	0
2850	Inferring gene regulatory networks from perturbed gene expression data using a dynamic Bayesian network with a Markov Chain Monte Carlo algorithm. , 2014, , .		1
2851	Radiobiology worker risk assessment using stress indicators and proteomics. International Journal of Low Radiation, 2014, 9, 199.	0.1	1
2852	Transcriptome profiling of gene expression in fall dormant and nondormant alfalfa. Genomics Data, 2014, 2, 282-284.	1.3	2
2853	Global biotic interactions: An open infrastructure to share and analyze species-interaction datasets. Ecological Informatics, 2014, 24, 148-159.	2.3	161
2854	Pharmacological class data representation in the Web Ontology Language (OWL). , 2014, , .		1
2855	Personalized microbial network inference via co-regularized spectral clustering. , 2014, , .		0
2856	Understanding mass cooperation through visualization. , 2014, , .		2
2857	Community Code Engagements. , 2014, , .		21
2858	Towards a Unified and Modular Approach for Visual Analysis of Enterprise Models. , 2014, , .		11
2859	Nucleotide excision repair/transcription gene defects in the fetus and impaired TFIIH-mediated function in transcription in placenta leading to preeclampsia. BMC Genomics, 2014, 15, 373.	1.2	10
2860	$\beta$ 21-integrin-dependent migration of microglia in response to neuron-released $\beta$ 1-synuclein. Experimental and Molecular Medicine, 2014, 46, e91-e91.	3.2	48
2861	Genomic convergence and network analysis approach to identify candidate genes in Alzheimer's disease. BMC Genomics, 2014, 15, 199.	1.2	91
2862	A novel systems pharmacology model for herbal medicine injection: a case using reduning injection. BMC Complementary and Alternative Medicine, 2014, 14, 430.	3.7	52
2863	Characterization of bacteriophage communities and CRISPR profiles from dental plaque. BMC Microbiology, 2014, 14, 175.	1.3	83
2864	The genetics of vascular incidents associated with second-generation antipsychotic administration. Expert Review of Clinical Pharmacology, 2014, 7, 75-90.	1.3	1
2865	Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks. IEEE Transactions on Visualization and Computer Graphics, 2014, 20, 1903-1912.	2.9	11
2866	Human Tra2 proteins jointly control a CHEK1 splicing switch among alternative and constitutive target exons. Nature Communications, 2014, 5, 4760.	5.8	47

#	ARTICLE	IF	CITATIONS
2867	Evolution of Bacterial Protein-Tyrosine Kinases and Their Relaxed Specificity Toward Substrates. <i>Genome Biology and Evolution</i> , 2014, 6, 800-817.	1.1	35
2868	Evaluation of database-derived pathway development for enabling biomarker discovery for hepatotoxicity. <i>Biomarkers in Medicine</i> , 2014, 8, 185-200.	0.6	21
2869	Photoperiodic Control of Carbon Distribution during the Floral Transition in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 565-584.	3.1	73
2870	Indicators and functionalities of exploitation of academic staff CV using semantic web technologies. , 2014, , .		0
2871	Pheno2GRN. , 2014, , .		0
2872	Multiple Omics Uncovers Host-Gut Microbial Mutualism During Prebiotic Fructooligosaccharide Supplementation. <i>DNA Research</i> , 2014, 21, 469-480.	1.5	101
2873	Linking signaling pathways to transcriptional programs in breast cancer. <i>Genome Research</i> , 2014, 24, 1869-1880.	2.4	57
2874	A Comprehensive Proteomic View of Responses of A549 Type II Alveolar Epithelial Cells to Human Respiratory Syncytial Virus Infection. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3250-3269.	2.5	28
2875	DINIES: drug-target interaction network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2014, 42, W39-W45.	6.5	97
2876	The pain interactome: Connecting pain-specific protein interactions. <i>Pain</i> , 2014, 155, 2243-2252.	2.0	65
2877	Organized Modularity in the Interactome: Evidence from the Analysis of Dynamic Organization in the Cell Cycle. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1264-1270.	1.9	4
2878	Sensory interaction between 3-mercaptohexan-1-ol and 2-isobutyl-3-methoxypyrazine in de-aromatized Sauvignon Blanc wine. <i>Australian Journal of Grape and Wine Research</i> , 2014, 20, 178-185.	1.0	26
2879	Identification of common gene networks responsive to radiotherapy in human cancer cells. <i>Cancer Gene Therapy</i> , 2014, 21, 542-548.	2.2	11
2880	Shared Molecular Pathways and Gene Networks for Cardiovascular Disease and Type 2 Diabetes Mellitus in Women Across Diverse Ethnicities. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 911-919.	5.1	48
2881	Semantic Breakthrough in Drug Discovery. <i>Synthesis Lectures on the Semantic Web: Theory and Technology</i> , 2014, 4, 1-142.	5.0	4
2882	Semi-Automatic Editing of Graphs with Customized Layouts. <i>Computer Graphics Forum</i> , 2014, 33, 381-390.	1.8	10
2883	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. <i>Cell</i> , 2014, 159, 1511-1523.	13.5	546
2884	High-Dose Simvastatin Exhibits Enhanced Lipid-Lowering Effects Relative to Simvastatin/Ezetimibe Combination Therapy. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 955-964.	5.1	13

#	ARTICLE	IF	CITATIONS
2885	Proteome and Phosphoproteome Characterization Reveals New Response and Defense Mechanisms of <i>Brachypodium distachyon</i> Leaves under Salt Stress. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 632-652.	2.5	121
2886	An R-based tool for miRNA data analysis and correlation with clinical ontologies. , 2014, , .		0
2887	Systems biology analysis of omeprazole therapy in cirrhosis demonstrates significant shifts in gut microbiota composition and function. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 307, G951-G957.	1.6	125
2888	Network Analysis in the Investigation of Chronic Respiratory Diseases. From Basics to Application. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 190, 981-988.	2.5	42
2889	Associating co-authorship patterns with publications in high-impact journals. <i>Journal of Biomedical Informatics</i> , 2014, 52, 311-318.	2.5	26
2890	Correlates of gut community composition across an ant species ( <i>Cephalotes</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 1284-1300.	2.0	82
2891	Comparative analysis of sequence covariation methods to mine evolutionary hubs: Examples from selected GPCR families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2141-2156.	1.5	11
2892	Network Pharmacology: A Rosetta Stone for Traditional Chinese Medicine. <i>Drug Development Research</i> , 2014, 75, 299-312.	1.4	224
2893	Integration of prior biological knowledge and epigenetic information enhances the prediction accuracy of the Bayesian Wnt pathway. <i>Integrative Biology (United Kingdom)</i> , 2014, 6, 1034-1048.	0.6	11
2894	Acetylome Analysis Reveals Diverse Functions of Lysine Acetylation in <i>Mycobacterium tuberculosis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3352-3366.	2.5	170
2895	Adjustable properties of visual representations: Improving the quality of human-information interaction. <i>Journal of the Association for Information Science and Technology</i> , 2014, 65, 455-482.	1.5	28
2896	Large-scale profiling of metabolic dysregulation in ovarian cancer. <i>International Journal of Cancer</i> , 2015, 136, 516-526.	2.3	100
2897	Helping Hands for Budding Prospects: ENTH/ANTH/VHS Accessory Proteins in Endocytosis, Vacuolar Transport, and Secretion. <i>Plant Cell</i> , 2014, 26, 4232-4244.	3.1	44
2898	Dramatic Changes in 67 miRNAs During Initiation of First Wave of Spermatogenesis in <i>Mus musculus</i> Testis: Global Regulatory Insights Generated by miRNA-mRNA Network Analysis. <i>Biology of Reproduction</i> , 2014, 91, 69.	1.2	15
2899	Surfaceome Profiling Reveals Regulators of Neural Stem Cell Function. <i>Stem Cells</i> , 2014, 32, 258-268.	1.4	22
2900	Drug-Like Protein-Protein Interaction Modulators: Challenges and Opportunities for Drug Discovery and Chemical Biology. <i>Molecular Informatics</i> , 2014, 33, 414-437.	1.4	93
2901	Pathway Analysis Approaches for Rare and Common Variants: Insights From Genetic Analysis Workshop 18. <i>Genetic Epidemiology</i> , 2014, 38, S86-91.	0.6	19
2902	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	6.5	210

#	ARTICLE	IF	CITATIONS
2903	Neurolysin Knockout Mice Generation and Initial Phenotype Characterization. <i>Journal of Biological Chemistry</i> , 2014, 289, 15426-15440.	1.6	41
2904	Comparative analysis of bacterial community-metagenomics in coastal Gulf of Mexico sediment microcosms following exposure to Macondo oil (MC252). <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 993-1009.	0.7	21
2905	Comparison of Transcriptional Profiles Between CD4+ and CD8+ T Cells in HIV Type 1-Infected Patients. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 134-141.	0.5	11
2906	Biological Network Module-Based Model for the Analysis of Differential Expression in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 5743-5750.	1.8	5
2907	The Equine PeptideAtlas: A resource for developing proteomics-based veterinary research. <i>Proteomics</i> , 2014, 14, 763-773.	1.3	17
2908	Construction and Application of a Protein Interaction Map for White Spot Syndrome Virus (WSSV). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 269-282.	2.5	26
2909	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. <i>Stem Cell Reports</i> , 2014, 3, 858-875.	2.3	32
2910	DIVE: a data intensive visualization engine. <i>Bioinformatics</i> , 2014, 30, 593-595.	1.8	12
2911	Microbiomes of Unreactive and Pathologically Altered Ileocecal Lymph Nodes of Slaughter Pigs. <i>Applied and Environmental Microbiology</i> , 2014, 80, 193-203.	1.4	27
2912	Genome-wide copy number scan identifies <i>IRF6</i> involvement in Van der Woude syndrome in an Indian family. <i>Genetical Research</i> , 2014, 96, e12.	0.3	2
2913	Enscosin/Map7 promotes microtubule growth and centrosome separation in <i>Drosophila</i> neural stem cells. <i>Journal of Cell Biology</i> , 2014, 204, 1111-1121.	2.3	60
2914	Evaluating Outcome-Related Recruitment and Geographic Recruitment Bias in a Respondent-Driven Sample of People Who Inject Drugs in Tijuana, Mexico. <i>AIDS and Behavior</i> , 2014, 18, 2325-2337.	1.4	17
2915	Architecture for interoperable software in biology. <i>Briefings in Bioinformatics</i> , 2014, 15, 626-636.	3.2	4
2916	Mechanism of action of Salvianolic Acid B by module-based network analysis. <i>Bio-Medical Materials and Engineering</i> , 2014, 24, 1333-1340.	0.4	11
2917	Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. <i>BMC Bioinformatics</i> , 2014, 15, 333.	1.2	93
2918	CIG-P: Circular Interaction Graph for Proteomics. <i>BMC Bioinformatics</i> , 2014, 15, 344.	1.2	0
2919	Label-free proteomic analysis to confirm the predicted proteome of <i>Corynebacterium pseudotuberculosis</i> under nitrosative stress mediated by nitric oxide. <i>BMC Genomics</i> , 2014, 15, 1065.	1.2	29
2920	Integrative analysis of high-throughput RNAi screen data identifies the FER and CRKL tyrosine kinases as new regulators of the mitogenic ERK-dependent pathways in transformed cells. <i>BMC Genomics</i> , 2014, 15, 1169.	1.2	5

#	ARTICLE	IF	CITATIONS
2921	The temporal foliar transcriptome of the perennial C3 desert plant <i>Rhazya stricta</i> in its natural environment. <i>BMC Plant Biology</i> , 2014, 14, 2.	1.6	27
2922	Meta-analysis of differentially expressed genes in osteosarcoma based on gene expression data. <i>BMC Medical Genetics</i> , 2014, 15, 80.	2.1	61
2923	Mathematical and computational modeling in biology at multiple scales. <i>Theoretical Biology and Medical Modelling</i> , 2014, 11, 52.	2.1	12
2924	Partial least squares based gene expression analysis in renal failure. <i>Diagnostic Pathology</i> , 2014, 9, 137.	0.9	3
2925	NetworkViewer: visualizing biochemical reaction networks with embedded rendering of molecular interaction rules. <i>BMC Systems Biology</i> , 2014, 8, 70.	3.0	12
2926	Metabolomics of <i>ApcMin/+</i> mice genetically susceptible to intestinal cancer. <i>BMC Systems Biology</i> , 2014, 8, 72.	3.0	16
2927	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2014, 7, 109.	6.2	69
2928	Nitrogen-driven stem elongation in poplar is linked with wood modification and gene clusters for stress, photosynthesis and cell wall formation. <i>BMC Plant Biology</i> , 2014, 14, 391.	1.6	41
2929	A common gene expression signature in Huntington's disease patient brain regions. <i>BMC Medical Genomics</i> , 2014, 7, 60.	0.7	49
2930	Linking hypothetical knowledge patterns to disease molecular signatures for biomarker discovery in Alzheimer's disease. <i>Genome Medicine</i> , 2014, 6, 97.	3.6	6
2932	A systems biology approach to identify proliferative biomarkers and pathways in breast cancer. , 2014, , .		1
2933	Glycoproteomic Analysis of Prostate Cancer Tissues by SWATH Mass Spectrometry Discovers N-acylethanolamine Acid Amidase and Protein Tyrosine Kinase 7 as Signatures for Tumor Aggressiveness. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1753-1768.	2.5	165
2934	CEBPA exerts a specific and biologically important proapoptotic role in pancreatic $\beta^2$ cells through its downstream network targets. <i>Molecular Biology of the Cell</i> , 2014, 25, 2333-2341.	0.9	14
2935	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. <i>Molecular and Cellular Oncology</i> , 2014, 1, e957981.	0.3	1
2936	BloodChIP: a database of comparative genome-wide transcription factor binding profiles in human blood cells. <i>Nucleic Acids Research</i> , 2014, 42, D172-D177.	6.5	43
2937	Investigation of the therapeutic effectiveness of active components in Sini decoction by a comprehensive GC/LC-MS based metabolomics and network pharmacology approaches. <i>Molecular BioSystems</i> , 2014, 10, 3310-3321.	2.9	35
2938	Anti-inflammatory mechanism research of tanshinone II A by module-based network analysis. <i>Bio-Medical Materials and Engineering</i> , 2014, 24, 3815-3824.	0.4	16
2939	Disruption of murine <i>Tcte3-3</i> induces tissue specific apoptosis via co-expression of <i>Anxa5</i> and <i>Pebp1</i> . <i>Computational Biology and Chemistry</i> , 2014, 53, 214-225.	1.1	5

#	ARTICLE	IF	CITATIONS
2940	GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. <i>Nucleic Acids Research</i> , 2014, 42, e32-e32.	6.5	9
2941	Evolutionary History of Trihelix Family and Their Functional Diversification. <i>DNA Research</i> , 2014, 21, 499-510.	1.5	47
2942	<i>De Novo</i> Assembly and Annotation of the Transcriptome of the Agricultural Weed <i>Ipomoea purpurea</i> Uncovers Gene Expression Changes Associated with Herbicide Resistance. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2035-2047.	0.8	48
2943	Methylcrotonyl-CoA Carboxylase Regulates Triacylglycerol Accumulation in the Model Diatom <i>Phaeodactylum tricornutum</i>. <i>Plant Cell</i> , 2014, 26, 1681-1697.	3.1	136
2944	Construction and analysis of microRNAâ€¢transcription factor regulation network in arabidopsis. <i>IET Systems Biology</i> , 2014, 8, 76-86.	0.8	2
2945	Selective Activity of the Histone Deacetylase Inhibitor AR-42 against Leukemia Stem Cells: A Novel Potential Strategy in Acute Myelogenous Leukemia. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 1979-1990.	1.9	49
2946	Extensive Gene Remodeling in the Viral World: New Evidence for Nongradual Evolution in the Mobilome Network. <i>Genome Biology and Evolution</i> , 2014, 6, 2195-2205.	1.1	26
2947	TSLP signaling pathway map: a platform for analysis of TSLP-mediated signaling. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau007-bau007.	1.4	71
2948	Combination of microRNA expression profiling with genome-wide SNP genotyping to construct a coronary artery disease-related miRNA-miRNA synergistic network. <i>BioScience Trends</i> , 2014, 8, 297-307.	1.1	23
2949	Bioprospecting in the Genomic Age. <i>Advances in Applied Microbiology</i> , 2014, 87, 111-146.	1.3	10
2950	Inhibition of Cyclooxygenase-2 Prevents Chronic and Recurrent Cystitis. <i>EBioMedicine</i> , 2014, 1, 46-57.	2.7	92
2952	Biological Network Modeling and Analysis. , 2014, , 203-244.		0
2953	Visualizing time-related data in biology, a review. <i>Briefings in Bioinformatics</i> , 2014, 15, 771-782.	3.2	35
2954	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	3.5	328
2955	E-cadherin interactome complexity and robustness resolved by quantitative proteomics. <i>Science Signaling</i> , 2014, 7, rs7.	1.6	160
2956	Phosphoproteomic Analysis of Protein Phosphorylation Networks in <i>Tetrahymena thermophila</i> , a Model Single-celled Organism. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 503-519.	2.5	21
2957	Biomarker development for pancreatic ductal adenocarcinoma using integrated analysis of mRNA and miRNA expression. , 2014, , .		2
2958	HyperModules: identifying clinically and phenotypically significant network modules with disease mutations for biomarker discovery. <i>Bioinformatics</i> , 2014, 30, 2230-2232.	1.8	28



#	ARTICLE	IF	CITATIONS
2959	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau006-bau006.	1.4	64
2960	Multi-level Modeling of Light-Induced Stomatal Opening Offers New Insights into Its Regulation by Drought. PLoS Computational Biology, 2014, 10, e1003930.	1.5	77
2961	Nutrigenomics. , 2014, , 501-515.		0
2962	Expanding the catalog of <i>cas</i> genes with metagenomes. Nucleic Acids Research, 2014, 42, 2448-2459.	6.5	25
2963	Data Mining for Identifying Novel Associations and Temporal Relationships with Charcot Foot. Journal of Diabetes Research, 2014, 2014, 1-13.	1.0	30
2964	A Network Map of FGF-1/FGFR Signaling System. Journal of Signal Transduction, 2014, 2014, 1-16.	2.0	80
2965	Application and comparative performance of network modularity algorithms to ecological communities classification. Acta Societatis Botanicorum Poloniae, 2014, 83, 93-102.	0.8	2
2966	Copy Number Loss of the Interferon Gene Cluster in Melanomas Is Linked to Reduced T Cell Infiltrate and Poor Patient Prognosis. PLoS ONE, 2014, 9, e109760.	1.1	192
2967	INsPeCT: INtegrative Platform for Cancer Transcriptomics. Cancer Informatics, 2014, 13, CIN.S13630.	0.9	9
2968	Integration of partial least squares and Monte Carlo gene expression analysis in coronary artery disease. Experimental and Therapeutic Medicine, 2014, 7, 1151-1154.	0.8	2
2969	A Pluralistic Account of Homology: Adapting the Models to the Data. Molecular Biology and Evolution, 2014, 31, 501-516.	3.5	37
2970	NetworkAnalyst - integrative approaches for protein-protein interaction network analysis and visual exploration. Nucleic Acids Research, 2014, 42, W167-W174.	6.5	398
2971	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- $\beta$ 2. Science Signaling, 2014, 7, rs5.	1.6	39
2972	Aberrant gene expression in mucosa adjacent to tumor reveals a molecular crosstalk in colon cancer. Molecular Cancer, 2014, 13, 46.	7.9	108
2973	Evolutionary patterns of <i>Escherichia coli</i> small RNAs and their regulatory interactions. Rna, 2014, 20, 994-1003.	1.6	53
2974	Network Analysis of Plasmidomes: The <i>Azospirillum brasilense</i> Sp245 Case. International Journal of Evolutionary Biology, 2014, 2014, 1-14.	1.0	17
2975	Gene Expression Analysis in Tubule Interstitial Compartments Reveals Candidate Agents for IgA Nephropathy. Kidney and Blood Pressure Research, 2014, 39, 361-368.	0.9	9
2976	Integrating <i>Omics</i> Technologies to Study Pulmonary Physiology and Pathology at the Systems Level. Cellular Physiology and Biochemistry, 2014, 33, 1239-1260.	1.1	12

#	ARTICLE	IF	CITATIONS
2977	Identification of Hipk2 as an essential regulator of white fat development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7373-7378.	3.3	38
2978	NetVenn: an integrated network analysis web platform for gene lists. <i>Nucleic Acids Research</i> , 2014, 42, W161-W166.	6.5	29
2979	Fetal Alcohol Syndrome, Chemo-Biology and OMICS: Ethanol Effects on Vitamin Metabolism During Neurodevelopment as Measured by Systems Biology Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 344-363.	1.0	10
2980	Associative Transcriptomics Study Dissects the Genetic Architecture of Seed Glucosinolate Content in <i>Brassica napus</i> . <i>DNA Research</i> , 2014, 21, 613-625.	1.5	94
2981	Fine-scale population structure analysis of seven local Swiss sheep breeds using genome-wide SNP data. <i>Animal Genetic Resources = Ressources Genetiques Animales = Recursos Geneticos Animales</i> , 2014, 55, 67-76.	0.2	16
2982	Minimum dominating sets in cell cycle specific protein interaction networks. , 2014, , .		8
2983	Critical Components of the Pluripotency Network Are Targets for the p300/CBP Interacting Protein (p/CIP) in Embryonic Stem Cells. <i>Stem Cells</i> , 2014, 32, 204-215.	1.4	16
2984	The urine microRNA profile may help monitor post-transplant renal graft function. <i>Kidney International</i> , 2014, 85, 439-449.	2.6	76
2985	Traditional plant-based remedies to control gastrointestinal disorders in livestock in the regions of Kamina and Kaniama (Katanga province, Democratic Republic of Congo). <i>Journal of Ethnopharmacology</i> , 2014, 153, 686-693.	2.0	15
2986	Proteomic and meta-transcriptomic study on lymph node metastasis in gastric cancer. <i>EuPA Open Proteomics</i> , 2014, 3, 183-194.	2.5	0
2987	Exploration of the mechanism of pattern-specific treatments in coronary heart disease with network pharmacology approach. <i>Computers in Biology and Medicine</i> , 2014, 51, 198-204.	3.9	11
2988	Protein-protein interaction network analysis and gene set enrichment analysis in epilepsy patients with brain cancer. <i>Journal of Clinical Neuroscience</i> , 2014, 21, 316-319.	0.8	14
2989	A Pou5f1/Oct4 dependent Klf2a, Klf2b, and Klf17 regulatory sub-network contributes to EVL and ectoderm development during zebrafish embryogenesis. <i>Developmental Biology</i> , 2014, 385, 433-447.	0.9	41
2990	Landscape of the relationship between type 2 diabetes and coronary heart disease through an integrated gene network analysis. <i>Gene</i> , 2014, 539, 30-36.	1.0	14
2991	Residue interaction network analysis of Dronpa and a DNA clamp. <i>Journal of Theoretical Biology</i> , 2014, 348, 55-64.	0.8	63
2992	Identification of rice genes associated with cosmic-ray response via co-expression gene network analysis. <i>Gene</i> , 2014, 541, 82-91.	1.0	9
2993	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. <i>Cell</i> , 2014, 156, 691-704.	13.5	238
2994	The Human Interactome Knowledge Base (HINT-KB): an integrative human protein interaction database enriched with predicted protein-protein interaction scores using a novel hybrid technique. <i>Artificial Intelligence Review</i> , 2014, 42, 427-443.	9.7	5

#	ARTICLE	IF	CITATIONS
2995	Activating Transcription Factor 4 Links Metabolic Stress to Interleukin-6 Expression in Macrophages. <i>Diabetes</i> , 2014, 63, 152-161.	0.3	95
2996	Network-assisted analysis to prioritize GWAS results: principles, methods and perspectives. <i>Human Genetics</i> , 2014, 133, 125-138.	1.8	86
2997	Study of differential effects of TGF-beta3/BMP2 on chondrogenesis in MSC cells by gene microarray data analysis. <i>Molecular and Cellular Biochemistry</i> , 2014, 385, 191-198.	1.4	15
2998	Graph database benchmarking on cloud environments with XGDBench. <i>Automated Software Engineering</i> , 2014, 21, 509-533.	2.2	17
2999	Patterns of Rare and Abundant Marine Microbial Eukaryotes. <i>Current Biology</i> , 2014, 24, 813-821.	1.8	450
3000	Discovery of Consensus Gene Signature and Intermodular Connectivity Defining Self-Renewal of Human Embryonic Stem Cells. <i>Stem Cells</i> , 2014, 32, 1468-1479.	1.4	22
3001	Top-down controls on bacterial community structure: microbial network analysis of bacteria, T4-like viruses and protists. <i>ISME Journal</i> , 2014, 8, 816-829.	4.4	300
3002	Mantra 2.0: an online collaborative resource for drug mode of action and repurposing by network analysis. <i>Bioinformatics</i> , 2014, 30, 1787-1788.	1.8	74
3003	An analysis of the structure and evolution of the scientific collaboration network of computer intelligence in games. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014, 395, 523-536.	1.2	16
3004	Development of a consumer product ingredient database for chemical exposure screening and prioritization. <i>Food and Chemical Toxicology</i> , 2014, 65, 269-279.	1.8	79
3005	Identifying functions of protein complexes based on topology similarity with random forest. <i>Molecular BioSystems</i> , 2014, 10, 514.	2.9	5
3006	Leucine-Rich Repeat Kinase 2 Binds to Neuronal Vesicles through Protein Interactions Mediated by Its C-Terminal WD40 Domain. <i>Molecular and Cellular Biology</i> , 2014, 34, 2147-2161.	1.1	91
3007	Experimental and Computational Tools for Analysis of Signaling Networks in Primary Cells. <i>Current Protocols in Immunology</i> , 2014, 104, 11.11.1-11.11.23.	3.6	2
3008	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. <i>Protein and Cell</i> , 2014, 5, 59-68.	4.8	26
3009	Dormancy within <i>Staphylococcus epidermidis</i> biofilms: a transcriptomic analysis by RNA-seq. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2585-2596.	1.7	25
3010	Weighting schemes in metabolic graphs for identifying biochemical routes. <i>Systems and Synthetic Biology</i> , 2014, 8, 47-57.	1.0	2
3011	Identification of Late Blight Resistance-Related Metabolites and Genes in Potato through Nontargeted Metabolomics. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 584-595.	1.0	65
3012	Computational developments in microRNA-regulated protein-protein interactions. <i>BMC Systems Biology</i> , 2014, 8, 14.	3.0	10

#	ARTICLE	IF	CITATIONS
3013	Genome-wide analysis of the bHLH transcription factor family in Chinese cabbage ( <i>Brassica rapa</i> ssp.) Tj ETQq0 0 0 1gBT /Overlock 10 Tf	1.8	104
3014	Risk miRNA screening of ovarian cancer based on miRNA functional synergistic network. <i>Journal of Ovarian Research</i> , 2014, 7, 9.	1.3	15
3015	ISAAC - InterSpecies Analysing Application using Containers. <i>BMC Bioinformatics</i> , 2014, 15, 18.	1.2	5
3016	Functional Modules Analysis Based on Coexpression Network in Pancreatic Ductal Adenocarcinoma. <i>Pathology and Oncology Research</i> , 2014, 20, 293-299.	0.9	5
3017	Molecular characterization of a heat inducible rice gene, OsHSP1, and implications for rice thermotolerance. <i>Genes and Genomics</i> , 2014, 36, 151-161.	0.5	10
3018	Software platforms to facilitate reconstructing genome-scale metabolic networks. <i>Environmental Microbiology</i> , 2014, 16, 49-59.	1.8	69
3019	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
3020	Gene expression profiling and bioinformatics analysis of gastric carcinoma. <i>Experimental and Molecular Pathology</i> , 2014, 96, 361-366.	0.9	20
3021	Transcriptome profiling in response to different types of ionizing radiation and identification of multiple radio marker genes in rice. <i>Physiologia Plantarum</i> , 2014, 150, 604-619.	2.6	33
3022	Computational gene network study on antibiotic resistance genes of <i>Acinetobacter baumannii</i> . <i>Computers in Biology and Medicine</i> , 2014, 48, 17-27.	3.9	27
3023	Mass spectrometry in plant metabolomics strategies: from analytical platforms to data acquisition and processing. <i>Natural Product Reports</i> , 2014, 31, 784.	5.2	149
3024	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <i>ISME Journal</i> , 2014, 8, 493-503.	4.4	40
3025	Group VII Ethylene Response Factor diversification and regulation in four species from flood-prone environments. <i>Plant, Cell and Environment</i> , 2014, 37, 2421-2432.	2.8	58
3026	A Large Scale Huntingtin Protein Interaction Network Implicates Rho GTPase Signaling Pathways in Huntington Disease. <i>Journal of Biological Chemistry</i> , 2014, 289, 6709-6726.	1.6	83
3027	Phylogeny and phylogeography of the <i>Tuber brumale</i> aggr.. <i>Mycorrhiza</i> , 2014, 24, 101-113.	1.3	22
3028	System-based approaches to decode the molecular links in Parkinson's disease and diabetes. <i>Neurobiology of Disease</i> , 2014, 72, 84-91.	2.1	87
3029	Comparative interactomes of SIRT6 and SIRT7: Implication of functional links to aging. <i>Proteomics</i> , 2014, 14, 1610-1622.	1.3	69
3030	C12 gep oncogene inhibits FOXO1 in hepatocellular carcinoma as a consequence of miR-135b and miR-194 dysregulation. <i>Cellular Signalling</i> , 2014, 26, 1456-1465.	1.7	28

#	ARTICLE	IF	CITATIONS
3031	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014, 8, 1101-1114.	4.4	174
3032	Integrative Literature and Data Mining to Rank Disease Candidate Genes. <i>Methods in Molecular Biology</i> , 2014, 1159, 207-226.	0.4	1
3033	The construction of an amino acid network for understanding protein structure and function. <i>Amino Acids</i> , 2014, 46, 1419-1439.	1.2	92
3034	Machine learning-based prediction of drug-drug interactions by integrating drug phenotypic, therapeutic, chemical, and genomic properties. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, e278-e286.	2.2	264
3035	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <i>Molecular Ecology</i> , 2014, 23, 1268-1283.	2.0	276
3036	Understanding Protein-Nanoparticle Interaction: A New Gateway to Disease Therapeutics. <i>Bioconjugate Chemistry</i> , 2014, 25, 1078-1090.	1.8	76
3037	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 486-497.	1.9	77
3038	River organic matter shapes microbial communities in the sediment of the Rhône prodelta. <i>ISME Journal</i> , 2014, 8, 2327-2338.	4.4	64
3039	Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in <i>Arabidopsis</i> and <i>Nicotiana benthamiana</i> . <i>Plant Cell</i> , 2014, 26, 1698-1711.	3.1	180
3040	Chemical Text Mining for Lead Discovery. , 2014, , 415-449.		1
3041	Uncovering the molecular networks in periodontitis. <i>Proteomics - Clinical Applications</i> , 2014, 8, 748-761.	0.8	69
3042	Potential biomarkers and latent pathways for vasculitis based on latent pathway identification analysis. <i>International Journal of Rheumatic Diseases</i> , 2014, 17, 671-678.	0.9	2
3043	Quantitative phosphoproteomic analysis of host responses in human lung epithelial (A549) cells during influenza virus infection. <i>Virus Research</i> , 2014, 179, 53-63.	1.1	21
3044	Tamoxifen Integromics and Personalized Medicine: Dynamic Modular Transformations Underpinning Response to Tamoxifen in Breast Cancer Treatment. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 15-33.	1.0	18
3045	Filling-in Void and Sparse Regions in Protein Sequence Space by Protein-Like Artificial Sequences Enables Remarkable Enhancement in Remote Homology Detection Capability. <i>Journal of Molecular Biology</i> , 2014, 426, 962-979.	2.0	15
3046	Genomic and transcriptomic plasticity in treatment-naïve ovarian cancer. <i>Genome Research</i> , 2014, 24, 200-211.	2.4	72
3047	Biological networks 101: Computational modeling for molecular biologists. <i>Gene</i> , 2014, 533, 379-384.	1.0	21
3048	Coexpression network analysis associated with call of rice seedlings for encountering heat stress. <i>Plant Molecular Biology</i> , 2014, 84, 125-143.	2.0	90

#	ARTICLE	IF	CITATIONS
3049	Identification of Enriched PTM Crosstalk Motifs from Large-Scale Experimental Data Sets. <i>Journal of Proteome Research</i> , 2014, 13, 249-259.	1.8	40
3050	Analytical metabolomics-based approaches to pancreatic cancer. <i>TrAC - Trends in Analytical Chemistry</i> , 2014, 55, 94-116.	5.8	13
3051	Algorithms and tools for protein-protein interaction networks clustering, with a special focus on population-based stochastic methods. <i>Bioinformatics</i> , 2014, 30, 1343-1352.	1.8	91
3052	Using semantic predications to uncover drug-drug interactions in clinical data. <i>Journal of Biomedical Informatics</i> , 2014, 49, 134-147.	2.5	50
3054	Unifying immunology with informatics and multiscale biology. <i>Nature Immunology</i> , 2014, 15, 118-127.	7.0	140
3055	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014, 506, 58-62.	13.7	530
3056	A proteomic survey of widespread protein aggregation in yeast. <i>Molecular BioSystems</i> , 2014, 10, 851.	2.9	53
3057	<i>Enterococcus faecalis</i> reconfigures its transcriptional regulatory network activation at different copper levels. <i>Metallomics</i> , 2014, 6, 572.	1.0	31
3058	Software applications for flux balance analysis. <i>Briefings in Bioinformatics</i> , 2014, 15, 108-122.	3.2	94
3059	MetDraw: automated visualization of genome-scale metabolic network reconstructions and high-throughput data. <i>Bioinformatics</i> , 2014, 30, 1327-1328.	1.8	26
3060	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. <i>Nature Methods</i> , 2014, 11, 94-99.	9.0	130
3061	From proteomes to complexomes in the era of systems biology. <i>Proteomics</i> , 2014, 14, 24-41.	1.3	35
3062	Integrating In Silico Resources to Map a Signaling Network. <i>Methods in Molecular Biology</i> , 2014, 1101, 197-245.	0.4	18
3063	The cell-cycle interactome: a source of growth regulators?. <i>Journal of Experimental Botany</i> , 2014, 65, 2715-2730.	2.4	43
3064	Resources for Functional Genomics Studies in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2014, 197, 1-18.	1.2	61
3065	Data management strategies for multinational large-scale systems biology projects. <i>Briefings in Bioinformatics</i> , 2014, 15, 65-78.	3.2	28
3066	Renal Agenesis in Kallmann Syndrome: A Network Approach. <i>Annals of Human Genetics</i> , 2014, 78, 424-433.	0.3	5
3067	Phenolic metabolites and substantial microbiome changes in pig feces by ingesting grape seed proanthocyanidins. <i>Food and Function</i> , 2014, 5, 2298-2308.	2.1	109

#	ARTICLE	IF	CITATIONS
3068	13C metabolic flux analysis of recombinant expression hosts. <i>Current Opinion in Biotechnology</i> , 2014, 30, 238-245.	3.3	28
3069	A network approach to clinical intervention in neurodegenerative diseases. <i>Trends in Molecular Medicine</i> , 2014, 20, 694-703.	3.5	76
3070	Insight into Protein S-nitrosylation in <i>Chlamydomonas reinhardtii</i> . <i>Antioxidants and Redox Signaling</i> , 2014, 21, 1271-1284.	2.5	81
3071	Spatial Variation in Transcript and Protein Abundance of Atlantic Salmon during Feeding Migration in the Baltic Sea. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13969-13977.	4.6	22
3072	Stimulus-evoked potentials contribute to map the epileptogenic zone during stereo-EEG presurgical monitoring. <i>Human Brain Mapping</i> , 2014, 35, 4267-4281.	1.9	44
3073	CHOPPI: A web tool for the analysis of immunogenicity risk from host cell proteins in CHO-based protein production. <i>Biotechnology and Bioengineering</i> , 2014, 111, 2170-2182.	1.7	47
3074	Beyond modules and hubs: the potential of gene coexpression networks for investigating molecular mechanisms of complex brain disorders. <i>Genes, Brain and Behavior</i> , 2014, 13, 13-24.	1.1	229
3075	Dynamic transcription factor activity profiles reveal key regulatory interactions during megakaryocytic and erythroid differentiation. <i>Biotechnology and Bioengineering</i> , 2014, 111, 2082-2094.	1.7	9
3076	Graph Exploration by Multiple Linked Metric Views. , 2014, , .		6
3077	Investigating the functional implications of reinforcing feedback loops in transcriptional regulatory networks. <i>Molecular BioSystems</i> , 2014, 10, 3238-3248.	2.9	5
3078	Annotation and retrieval in protein interaction databases. <i>European Physical Journal Plus</i> , 2014, 129, 1.	1.2	0
3079	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 397-406.	2.5	2,819
3080	Using PeptideAtlas, SRMATlas, and PASSEL: Comprehensive Resources for Discovery and Targeted Proteomics. <i>Current Protocols in Bioinformatics</i> , 2014, 46, 13.25.1-28.	25.8	51
3081	The human liver-specific proteome defined by transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014, 28, 2901-2914.	0.2	73
3082	A distinct glucose metabolism signature of acute myeloid leukemia with prognostic value. <i>Blood</i> , 2014, 124, 1645-1654.	0.6	232
3083	Drug repositioning by applying gene expression profiles generated by integrating chemical structure similarity and gene semantic similarity. <i>Molecular BioSystems</i> , 2014, 10, 1126.	2.9	34
3084	Defining the genome-wide role of CRE1 during carbon catabolite repression in <i>Trichoderma reesei</i> using RNA-Seq analysis. <i>Fungal Genetics and Biology</i> , 2014, 73, 93-103.	0.9	71
3085	Coordinated regulation of photosynthesis in rice increases yield and tolerance to environmental stress. <i>Nature Communications</i> , 2014, 5, 5302.	5.8	254



#	ARTICLE	IF	CITATIONS
3086	New Insights about Enzyme Evolution from Large Scale Studies of Sequence and Structure Relationships. <i>Journal of Biological Chemistry</i> , 2014, 289, 30221-30228.	1.6	57
3087	Identification of Kinase Inhibitor Targets in the Lung Cancer Microenvironment by Chemical and Phosphoproteomics. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 2751-2762.	1.9	21
3088	An integrated molecular dynamics, principal component analysis and residue interaction network approach reveals the impact of M184V mutation on HIV reverse transcriptase resistance to lamivudine. <i>Molecular BioSystems</i> , 2014, 10, 2215-2228.	2.9	52
3089	Modular community structure suggests metabolic plasticity during the transition to polar night in ice-covered Antarctic lakes. <i>ISME Journal</i> , 2014, 8, 778-789.	4.4	181
3090	Extraction of SAR information from activity cliff clusters via matching molecular series. <i>European Journal of Medicinal Chemistry</i> , 2014, 87, 454-460.	2.6	12
3091	Gene Expression Variability as a Unifying Element of the Pluripotency Network. <i>Stem Cell Reports</i> , 2014, 3, 365-377.	2.3	24
3092	SeaBase: A Multispecies Transcriptomic Resource and Platform for Gene Network Inference. <i>Integrative and Comparative Biology</i> , 2014, 54, 250-263.	0.9	17
3093	Affinity purification mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , 2014, 9, 2539-2554.	5.5	169
3094	An in silico toxicogenomics approach for inferring potential diseases associated with maleic acid. <i>Chemico-Biological Interactions</i> , 2014, 223, 38-44.	1.7	12
3095	Systematic pipeline for the analysis of microRNA-gene interactions in active and latent TB infection. , 2014, , .		0
3096	New Approaches to Comparative and Animal Stress Biology Research in the Post-genomic Era: A Contextual Overview. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 138-146.	1.9	8
3097	Metalprint: an information repository of mammalian imprinted genes. <i>Development (Cambridge)</i> , 2014, 141, 2516-2523.	1.2	68
3098	iMAD, a genetic screening strategy for dissecting complex interactions between a pathogen and its host. <i>Nature Protocols</i> , 2014, 9, 1916-1930.	5.5	5
3099	Screening genes crucial for pediatric pilocytic astrocytoma using weighted gene coexpression network analysis combined with methylation data analysis. <i>Cancer Gene Therapy</i> , 2014, 21, 448-455.	2.2	26
3100	An evidence-based knowledgebase of pulmonary arterial hypertension to identify genes and pathways relevant to pathogenesis. <i>Molecular BioSystems</i> , 2014, 10, 732-740.	2.9	16
3101	Dissecting active ingredients of Chinese medicine by content-weighted ingredient target network. <i>Molecular BioSystems</i> , 2014, 10, 1905-1911.	2.9	31
3102	A novel network pharmacology approach to analyse traditional herbal formulae: the Liu-Wei-Di-Huang pill as a case study. <i>Molecular BioSystems</i> , 2014, 10, 1014-1022.	2.9	215
3103	Boolean modeling: a logic based dynamic approach for understanding signaling and regulatory networks and for making useful predictions. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 353-369.	6.6	122

#	ARTICLE	IF	CITATIONS
3104	A Web of Possibilities: Network-Based Discovery of Protein Interaction Codes. <i>Journal of Proteome Research</i> , 2014, 13, 5333-5338.	1.8	16
3105	Yeast cells with impaired drug resistance accumulate glycerol and glucose. <i>Molecular BioSystems</i> , 2014, 10, 93-102.	2.9	12
3106	Proteomic analysis of human substantia nigra identifies novel candidates involved in Parkinson's disease pathogenesis. <i>Proteomics</i> , 2014, 14, 784-794.	1.3	85
3107	Molecular networks and the evolution of human cognitive specializations. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 52-59.	1.5	7
3108	Platelet-specific collagen receptor glycoprotein VI gene variants affect recurrent pregnancy loss. <i>Fertility and Sterility</i> , 2014, 102, 1078-1084.e3.	0.5	10
3109	DIVE: A Graph-Based Visual-Analytics Framework for Big Data. <i>IEEE Computer Graphics and Applications</i> , 2014, 34, 26-37.	1.0	34
3111	The Wall-associated Kinase gene family in rice genomes. <i>Plant Science</i> , 2014, 229, 181-192.	1.7	59
3112	Compensatory Role of Double Mutation N348I/M184V on Nevirapine Binding Landscape: Insight from Molecular Dynamics Simulation. <i>Protein Journal</i> , 2014, 33, 432-446.	0.7	15
3113	Method for the Evaluation of Structure-Activity Relationship Information Associated with Coordinated Activity Cliffs. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 6553-6563.	2.9	17
3114	Nitrate Shaped the Selenate-Reducing Microbial Community in a Hydrogen-Based Biofilm Reactor. <i>Environmental Science &amp; Technology</i> , 2014, 48, 3395-3402.	4.6	106
3115	Early Targets of miR-34a in Neuroblastoma. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2114-2131.	2.5	29
3116	CNBP modulates the transcription of Wnt signaling pathway components. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1151-1160.	0.9	22
3117	CCNB1 is a prognostic biomarker for ER+ breast cancer. <i>Medical Hypotheses</i> , 2014, 83, 359-364.	0.8	117
3119	Systems approach identifies TGA1 and TGA4 transcription factors as important regulatory components of the nitrate response of <i>Arabidopsis thaliana</i> roots. <i>Plant Journal</i> , 2014, 80, 1-13.	2.8	247
3120	PREDAC-H5: A user-friendly tool for the automated surveillance of antigenic variants for the HPAI H5N1 virus. <i>Infection, Genetics and Evolution</i> , 2014, 28, 62-63.	1.0	7
3121	Identification of <i>Mytilus edulis</i> genetic regulators during early development. <i>Gene</i> , 2014, 551, 65-78.	1.0	26
3122	Characterization of the Human NEK7 Interactome Suggests Catalytic and Regulatory Properties Distinct from Those of NEK6. <i>Journal of Proteome Research</i> , 2014, 13, 4074-4090.	1.8	32
3123	Integrated transcriptome analysis reveals miRNA-mRNA crosstalk in laryngeal squamous cell carcinoma. <i>Genomics</i> , 2014, 104, 249-256.	1.3	20

#	ARTICLE	IF	CITATIONS
3124	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. <i>Molecular Biology and Evolution</i> , 2014, 31, 2156-2169.	3.5	79
3125	CombiMotif: A new algorithm for network motifs discovery in protein-protein interaction networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014, 416, 309-320.	1.2	0
3126	Duodenal CCK Cells from Male Mice Express Multiple Hormones Including Ghrelin. <i>Endocrinology</i> , 2014, 155, 3339-3351.	1.4	58
3127	Cellulolytic <i>Streptomyces</i> Strains Associated with Herbivorous Insects Share a Phylogenetically Linked Capacity To Degrade Lignocellulose. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4692-4701.	1.4	70
3128	Randomised clinical trial: <i>Lactobacillus GG</i> modulates gut microbiome, metabolome and endotoxemia in patients with cirrhosis. <i>Alimentary Pharmacology and Therapeutics</i> , 2014, 39, 1113-1125.	1.9	234
3129	Human Proteins with Target Sites of Multiple Post-Translational Modification Types Are More Prone to Be Involved in Disease. <i>Journal of Proteome Research</i> , 2014, 13, 2735-2748.	1.8	31
3130	Practical aspects of genome-wide association interaction analysis. <i>Human Genetics</i> , 2014, 133, 1343-1358.	1.8	32
3131	Genetic Dissection of Leaf Development in <i>Brassica rapa</i> Using a Genetical Genomics Approach. <i>Plant Physiology</i> , 2014, 164, 1309-1325.	2.3	40
3132	Overexpression of the <i>OsChl1</i> gene, encoding a putative laccase precursor, increases tolerance to drought and salinity stress in transgenic <i>Arabidopsis</i> . <i>Gene</i> , 2014, 552, 98-105.	1.0	48
3133	Conformational propensities and dynamics of a $\beta^3$ -crystallin, an intrinsically disordered protein. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 12703.	1.3	8
3134	Global Protein-Protein Interaction Network of Rice Sheath Blight Pathogen. <i>Journal of Proteome Research</i> , 2014, 13, 3277-3293.	1.8	25
3135	Complex Chemical Reaction Networks from Heuristics-Aided Quantum Chemistry. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 897-907.	2.3	100
3136	Activity Cliff Networks for Medicinal Chemistry. <i>Drug Development Research</i> , 2014, 75, 291-298.	1.4	6
3137	Drug-Disease Association and Drug-Repositioning Predictions in Complex Diseases Using Causal Inference-Probabilistic Matrix Factorization. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 2562-2569.	2.5	95
3138	Identification of a human neonatal immune-metabolic network associated with bacterial infection. <i>Nature Communications</i> , 2014, 5, 4649.	5.8	112
3139	Functional Module Search in Protein Networks based on Semantic Similarity Improves the Analysis of Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1877-1889.	2.5	4
3140	Discovery of Function in the Enolase Superfamily: $\alpha$ -Mannuronate and $\beta$ -Gluconate Dehydratases in the $\alpha$ -Mannuronate Dehydratase Subgroup. <i>Biochemistry</i> , 2014, 53, 2722-2731.	1.2	28
3141	Investigation of key miRNAs and target genes in bladder cancer using miRNA profiling and bioinformatic tools. <i>Molecular Biology Reports</i> , 2014, 41, 8127-8135.	1.0	50

#	ARTICLE	IF	CITATIONS
3142	Immunoinformatics: A Brief Review. <i>Methods in Molecular Biology</i> , 2014, 1184, 23-55.	0.4	74
3143	Target-Independent Prediction of Drug Synergies Using Only Drug Lipophilicity. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 2286-2293.	2.5	30
3144	<i>In Silico</i> Prediction and Automatic LC-MS/MS Annotation of Green Tea Metabolites in Urine. <i>Analytical Chemistry</i> , 2014, 86, 4767-4774.	3.2	39
3145	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1690-1704.	2.5	323
3146	The RNA expression signature of the HepG2 cell line as determined by the integrated analysis of miRNA and mRNA expression profiles. <i>Gene</i> , 2014, 548, 91-100.	1.0	17
3147	Insights into the lysine acetylproteome of human sperm. <i>Journal of Proteomics</i> , 2014, 109, 199-211.	1.2	52
3148	Transcriptomic profiling revealed an important role of cell wall remodeling and ethylene signaling pathway during salt acclimation in Arabidopsis. <i>Plant Molecular Biology</i> , 2014, 86, 303-317.	2.0	126
3149	Delineation of a FOXA1/ER $\alpha$ /AGR2 Regulatory Loop That Is Dysregulated in Endocrine Therapy-Resistant Breast Cancer. <i>Molecular Cancer Research</i> , 2014, 12, 1829-1839.	1.5	35
3150	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
3151	Combinatorial therapy discovery using mixed integer linear programming. <i>Bioinformatics</i> , 2014, 30, 1456-1463.	1.8	73
3152	Early Diagnosis of Complex Diseases by Molecular Biomarkers, Network Biomarkers, and Dynamical Network Biomarkers. <i>Medicinal Research Reviews</i> , 2014, 34, 455-478.	5.0	252
3153	Nascent histamine induces $\alpha$ -synuclein and caspase-3 on human cells. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 580-586.	1.0	7
3154	Epigenetic Targeting of Ovarian Cancer Stem Cells. <i>Cancer Research</i> , 2014, 74, 4922-4936.	0.4	136
3155	Network-based approach reveals Y chromosome influences prostate cancer susceptibility. <i>Computers in Biology and Medicine</i> , 2014, 54, 24-31.	3.9	21
3156	Synchronous dynamics and correlations between bacteria and phytoplankton in a subtropical drinking water reservoir. <i>FEMS Microbiology Ecology</i> , 2014, 90, 126-138.	1.3	72
3157	Discovery of a new ATP-binding motif involved in peptidic azoline biosynthesis. <i>Nature Chemical Biology</i> , 2014, 10, 823-829.	3.9	77
3158	CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4468-77.	3.3	297
3159	Systematic Prioritization and Integrative Analysis of Copy Number Variations in Schizophrenia Reveal Key Schizophrenia Susceptibility Genes. <i>Schizophrenia Bulletin</i> , 2014, 40, 1285-1299.	2.3	41

#	ARTICLE	IF	CITATIONS
3160	Bioinformatic approaches to augment study of epithelial-to-mesenchymal transition in lung cancer. <i>Physiological Genomics</i> , 2014, 46, 699-724.	1.0	26
3161	Comparison of the physiological effects and transcriptome responses of <i>Populus simonii</i> under different abiotic stresses. <i>Plant Molecular Biology</i> , 2014, 86, 139-156.	2.0	41
3162	De novo assembly of red clover transcriptome based on RNA-Seq data provides insight into drought response, gene discovery and marker identification. <i>BMC Genomics</i> , 2014, 15, 453.	1.2	117
3163	The <i>Arabidopsis</i> Kinome: phylogeny and evolutionary insights into functional diversification. <i>BMC Genomics</i> , 2014, 15, 548.	1.2	116
3164	Coral-zooxanthellae meta-transcriptomics reveals integrated response to pollutant stress. <i>BMC Genomics</i> , 2014, 15, 591.	1.2	27
3165	Identification and characterization of three chemosensory receptor families in the cotton bollworm <i>Helicoverpa armigera</i> . <i>BMC Genomics</i> , 2014, 15, 597.	1.2	86
3166	A network-based approach to dissect the cilia/centrosome complex interactome. <i>BMC Genomics</i> , 2014, 15, 658.	1.2	19
3167	A systems biology approach identified different regulatory networks targeted by KSHV miR-K12-11 in B cells and endothelial cells. <i>BMC Genomics</i> , 2014, 15, 668.	1.2	12
3168	The peach volatilome modularity is reflected at the genetic and environmental response levels in a QTL mapping population. <i>BMC Plant Biology</i> , 2014, 14, 137.	1.6	29
3169	PhosFox: a bioinformatics tool for peptide-level processing of LC-MS/MS-based phosphoproteomic data. <i>Proteome Science</i> , 2014, 12, 36.	0.7	12
3170	Pathway analysis for genetic association studies: to do, or not to do? That is the question. <i>BMC Proceedings</i> , 2014, 8, S103.	1.8	2
3171	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014, 8, S2.	1.8	13
3172	Global transcriptome-wide analysis of CIK cells identify distinct roles of IL-2 and IL-15 in acquisition of cytotoxic capacity against tumor. <i>BMC Medical Genomics</i> , 2014, 7, 49.	0.7	29
3173	A system based network approach to ethanol tolerance in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2014, 8, 90.	3.0	19
3174	KeyPathwayMiner 4.0: condition-specific pathway analysis by combining multiple omics studies and networks with Cytoscape. <i>BMC Systems Biology</i> , 2014, 8, 99.	3.0	59
3175	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. <i>Genome Medicine</i> , 2014, 6, 59.	3.6	20
3176	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260
3177	Rule-based modeling: a computational approach for studying biomolecular site dynamics in cell signaling systems. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 13-36.	6.6	97

#	ARTICLE	IF	CITATIONS
3178	Integrated miRNA and mRNA transcriptomes of porcine alveolar macrophages (PAM cells) identifies strain-specific miRNA molecular signatures associated with H-PRRSV and N-PRRSV infection. <i>Molecular Biology Reports</i> , 2014, 41, 5863-5875.	1.0	31
3179	Identification of Related Peptides through the Analysis of Fragment Ion Mass Shifts. <i>Journal of Proteome Research</i> , 2014, 13, 4002-4011.	1.8	7
3180	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <i>Nature Chemical Biology</i> , 2014, 10, 963-968.	3.9	416
3181	Composition and Topology of Activity Cliff Clusters Formed by Bioactive Compounds. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 451-461.	2.5	40
3182	Biological Network Exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , 2014, 47, 8.13.1-24.	25.8	780
3183	Proteomic Profiling of the Acid Stress Response in <i>Lactobacillus plantarum</i> 423. <i>Journal of Proteome Research</i> , 2014, 13, 4028-4039.	1.8	79
3184	Comprehensive analysis of VQ motif-containing gene expression in rice defense responses to three pathogens. <i>Plant Cell Reports</i> , 2014, 33, 1493-1505.	2.8	46
3186	Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54.	1.6	66
3187	Identifying gene expression profile of spinal cord injury in rat by bioinformatics strategy. <i>Molecular Biology Reports</i> , 2014, 41, 3169-3177.	1.0	25
3188	Interaction network analysis revealed biomarkers in myocardial infarction. <i>Molecular Biology Reports</i> , 2014, 41, 4997-5003.	1.0	12
3189	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318
3190	KIFCI, a novel putative prognostic biomarker for ovarian adenocarcinomas: delineating protein interaction networks and signaling circuitries. <i>Journal of Ovarian Research</i> , 2014, 7, 53.	1.3	37
3191	TCMSP: a database of systems pharmacology for drug discovery from herbal medicines. <i>Journal of Cheminformatics</i> , 2014, 6, 13.	2.8	2,919
3192	Replica Exchange Molecular Dynamics Simulations Provide Insight into Substrate Recognition by Small Heat Shock Proteins. <i>Biophysical Journal</i> , 2014, 106, 2644-2655.	0.2	32
3193	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. <i>Bioinformatics</i> , 2014, 30, 2627-2635.	1.8	79
3194	inSARA: Intuitive and Interactive SAR Interpretation by Reduced Graphs and Hierarchical MCS-Based Network Navigation. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1578-1595.	2.5	10
3195	Targeted protein quantification using sparse reference labeling. <i>Nature Methods</i> , 2014, 11, 301-304.	9.0	9
3196	Influence of DNA Extraction Method, 16S rRNA Targeted Hypervariable Regions, and Sample Origin on Microbial Diversity Detected by 454 Pyrosequencing in Marine Chemosynthetic Ecosystems. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4626-4639.	1.4	87



#	ARTICLE	IF	CITATIONS
3197	Correlation network analysis reveals relationships between diet-induced changes in human gut microbiota and metabolic health. <i>Nutrition and Diabetes</i> , 2014, 4, e122-e122.	1.5	84
3198	Expression of Transthyretin during bovine myogenic satellite cell differentiation. <i>In Vitro Cellular and Developmental Biology - Animal</i> , 2014, 50, 756-765.	0.7	7
3199	Screening of Critical Genes in Lung Adenocarcinoma via Network Analysis of Gene Expression Profile. <i>Pathology and Oncology Research</i> , 2014, 20, 853-858.	0.9	12
3200	Identifying pathogenic processes by integrating microarray data with prior knowledge. <i>BMC Bioinformatics</i> , 2014, 15, 115.	1.2	2
3201	A web-based protein interaction network visualizer. <i>BMC Bioinformatics</i> , 2014, 15, 129.	1.2	21
3202	Identification of mycoparasitism-related genes against the phytopathogen <i>Sclerotinia sclerotiorum</i> through transcriptome and expression profile analysis in <i>Trichoderma harzianum</i> . <i>BMC Genomics</i> , 2014, 15, 204.	1.2	99
3203	From SNP co-association to RNA co-expression: Novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , 2014, 15, 232.	1.2	44
3204	Genome-wide identification of heat shock proteins (Hsps) and Hsp interactors in rice: Hsp70s as a case study. <i>BMC Genomics</i> , 2014, 15, 344.	1.2	59
3205	Longissimus dorsi transcriptome analysis of purebred and crossbred Iberian pigs differing in muscle characteristics. <i>BMC Genomics</i> , 2014, 15, 413.	1.2	77
3206	Gene co-expression network analysis identifies porcine genes associated with variation in <i>Salmonella</i> shedding. <i>BMC Genomics</i> , 2014, 15, 452.	1.2	65
3207	Tracking of time-varying genomic regulatory networks with a LASSO-Kalman smoother. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2014, 2014, 3.	1.4	9
3208	Comparative metabolism of cellulose, sophorose and glucose in <i>Trichoderma reesei</i> using high-throughput genomic and proteomic analyses. <i>Biotechnology for Biofuels</i> , 2014, 7, 41.	6.2	131
3209	Integrative analysis reveals disease-associated genes and biomarkers for prostate cancer progression. <i>BMC Medical Genomics</i> , 2014, 7, S3.	0.7	23
3210	The human testis-specific proteome defined by transcriptomics and antibody-based profiling. <i>Molecular Human Reproduction</i> , 2014, 20, 476-488.	1.3	189
3211	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. <i>Journal of Animal Science</i> , 2014, 92, 2832-2845.	0.2	77
3212	Concordance of white matter and gray matter abnormalities in autism spectrum disorders: A voxel-based meta-analysis study. <i>Human Brain Mapping</i> , 2014, 35, 2073-2098.	1.9	47
3213	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	1.6	6
3214	Identifying and prioritizing disease-related genes based on the network topological features. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2214-2221.	1.1	6



#	ARTICLE	IF	CITATIONS
3215	The lung-specific proteome defined by integration of transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014, 28, 5184-5196.	0.2	54
3216	Combination of a discovery LC-MS/MS analysis and a label-free quantification for the characterization of an epithelial-mesenchymal transition signature. <i>Journal of Proteomics</i> , 2014, 110, 183-194.	1.2	10
3217	A Review on Applications of Graph Theory in Network Analysis of Biological Processes. <i>International Journal of Intelligent Computing in Medical Sciences and Image Processing</i> , 2014, 6, 27-43.	0.5	2
3218	Mechanistic and Bioinformatic Investigation of a Conserved Active Site Helix in $\beta$ -Isopropylmalate Synthase from <i>Mycobacterium tuberculosis</i> , a Member of the DRE-TIM Metallolyase Superfamily. <i>Biochemistry</i> , 2014, 53, 2915-2925.	1.2	14
3219	MS/MS-based networking and peptidogenomics guided genome mining revealed the stenothricin gene cluster in <i>Streptomyces roseosporus</i> . <i>Journal of Antibiotics</i> , 2014, 67, 99-104.	1.0	64
3220	Presence and utility of intrinsically disordered regions in kinases. <i>Molecular BioSystems</i> , 2014, 10, 2876-2888.	2.9	26
3221	Viral proteins that bridge unconnected proteins and components in the human PPI network. <i>Molecular BioSystems</i> , 2014, 10, 2448-2458.	2.9	11
3222	Nuclear Cytoplasmic Trafficking of Proteins is a Major Response of Human Fibroblasts to Oxidative Stress. <i>Journal of Proteome Research</i> , 2014, 13, 4398-4423.	1.8	14
3223	Large-Scale Identification of Gibberellin-Related Transcription Factors Defines Group VII ETHYLENE RESPONSE FACTORS as Functional DELLA Partners. <i>Plant Physiology</i> , 2014, 166, 1022-1032.	2.3	124
3224	EDAG Positively Regulates Erythroid Differentiation and Modifies GATA1 Acetylation Through Recruiting p300. <i>Stem Cells</i> , 2014, 32, 2278-2289.	1.4	27
3225	Land-use and management practices affect soil ammonia oxidiser community structure, activity and connectedness. <i>Soil Biology and Biochemistry</i> , 2014, 78, 138-148.	4.2	24
3226	The antidepressant drug Carbamazepine induces differential transcriptome expression in the brain of Atlantic salmon, <i>Salmo salar</i> . <i>Aquatic Toxicology</i> , 2014, 151, 114-123.	1.9	35
3227	Prioritization of Candidate Genes for Periodontitis Using Multiple Computational Tools. <i>Journal of Periodontology</i> , 2014, 85, 1059-1069.	1.7	37
3228	Ontology Integration for Linked Data. <i>Journal on Data Semantics</i> , 2014, 3, 237-254.	2.0	48
3229	Recent advances in modeling languages for pathway maps and computable biological networks. <i>Drug Discovery Today</i> , 2014, 19, 193-198.	3.2	45
3230	ReVealD: A user-driven domain-specific interactive search platform for biomedical research. <i>Journal of Biomedical Informatics</i> , 2014, 47, 112-130.	2.5	30
3231	Analysis of the heterochromatin protein 1 (HP1) interactome in <i>Drosophila</i> . <i>Journal of Proteomics</i> , 2014, 102, 137-147.	1.2	28
3232	<i>Callithrix penicillata</i> : A feasible experimental model for dengue virus infection. <i>Immunology Letters</i> , 2014, 158, 126-133.	1.1	17

#	ARTICLE	IF	CITATIONS
3233	Autoimmune profiling with protein microarrays in clinical applications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 977-987.	1.1	19
3234	A Mitochondrial RNAi Screen Defines Cellular Bioenergetic Determinants and Identifies an Adenylate Kinase as a Key Regulator of ATP Levels. <i>Cell Reports</i> , 2014, 7, 907-917.	2.9	73
3235	Genome-wide analysis of the GRAS gene family in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Genomics</i> , 2014, 103, 135-146.	1.3	114
3236	Network pharmacology analyses of the antithrombotic pharmacological mechanism of Fufang Xueshuantong Capsule with experimental support using disseminated intravascular coagulation rats. <i>Journal of Ethnopharmacology</i> , 2014, 154, 735-744.	2.0	74
3237	VRK1 interacts with p53 forming a basal complex that is activated by UV-induced DNA damage. <i>FEBS Letters</i> , 2014, 588, 692-700.	1.3	35
3238	Exploring the Biological and Chemical Complexity of the Ligases. <i>Journal of Molecular Biology</i> , 2014, 426, 2098-2111.	2.0	11
3239	Insights into miRNA regulation of the human glycome. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 774-779.	1.0	33
3240	Identifying functional modules for coronary artery disease by a prior knowledge-based approach. <i>Gene</i> , 2014, 537, 260-268.	1.0	11
3241	High-throughput identification of off-targets for the mechanistic study of severe adverse drug reactions induced by analgesics. <i>Toxicology and Applied Pharmacology</i> , 2014, 274, 24-34.	1.3	14
3242	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. <i>Livestock Science</i> , 2014, 161, 201-209.	0.6	35
3243	The Vac14-interaction Network Is Linked to Regulators of the Endolysosomal and Autophagic Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1397-1411.	2.5	51
3244	Phosphoproteomic Analysis Provides Novel Insights into Stress Responses in <i>Phaeodactylum tricornutum</i> , a Model Diatom. <i>Journal of Proteome Research</i> , 2014, 13, 2511-2523.	1.8	39
3245	Integrated microRNA-mRNA analysis of coronary artery disease. <i>Molecular Biology Reports</i> , 2014, 41, 5505-5511.	1.0	19
3246	Gene coexpression patterns during early development of the native <i>Arabidopsis</i> reproductive meristem: novel candidate developmental regulators and patterns of functional redundancy. <i>Plant Journal</i> , 2014, 79, 861-877.	2.8	29
3247	Gene Expression Profiles of Entorhinal Cortex in Alzheimer's Disease and Other Dementias. <i>American Journal of Alzheimer's Disease and Other Dementias</i> , 2014, 29, 526-532.	0.9	28
3248	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during <i>Arabidopsis</i> Leaf Development. <i>Plant Cell</i> , 2014, 26, 210-229.	3.1	219
3249	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. <i>American Journal of Human Genetics</i> , 2014, 94, 870-883.	2.6	116
3250	Informatics in Radiology: Radiology Gamuts Ontology: Differential Diagnosis for the Semantic Web. <i>Radiographics</i> , 2014, 34, 254-264.	1.4	24

#	ARTICLE	IF	CITATIONS
3251	Human Dopamine Receptors Interaction Network (DRIN): A systems biology perspective on topology, stability and functionality of the network. <i>Journal of Theoretical Biology</i> , 2014, 357, 169-183.	0.8	7
3252	rRNA-based monitoring of the microbiota involved in Fontina PDO cheese production in relation to different stages of cow lactation. <i>International Journal of Food Microbiology</i> , 2014, 185, 127-135.	2.1	46
3253	Preeclampsia: Integrated network model of platelet biomarkers interaction as a tool to evaluate the hemostatic/immunological interface. <i>Clinica Chimica Acta</i> , 2014, 436, 193-201.	0.5	9
3254	NetBioV: an R package for visualizing large network data in biology and medicine. <i>Bioinformatics</i> , 2014, 30, 2834-2836.	1.8	44
3255	Dynamic Estrogen Receptor Interactomes Control Estrogen-Responsive Trefoil Factor (TFF) Locus Cell-Specific Activities. <i>Molecular and Cellular Biology</i> , 2014, 34, 2418-2436.	1.1	20
3256	Traditional Chinese herbs as chemical resource library for drug discovery of anti-infective and anti-inflammatory. <i>Journal of Ethnopharmacology</i> , 2014, 155, 589-598.	2.0	29
3257	Interactions between Distant ceRNAs in Regulatory Networks. <i>Biophysical Journal</i> , 2014, 106, 2254-2266.	0.2	41
3258	Pathway and network analysis in proteomics. <i>Journal of Theoretical Biology</i> , 2014, 362, 44-52.	0.8	98
3259	Proteome analysis of the HIV-1 Gag interactome. <i>Virology</i> , 2014, 460-461, 194-206.	1.1	46
3260	Phylogenetic and syntenic analyses of the 12-spanner drug:H + antiporter family 1 (DHA1) in pathogenic <i>Candida</i> species: evolution of MDR1 and FLU1 genes. <i>Genomics</i> , 2014, 104, 45-57.	1.3	11
3261	Molecular modeling and residue interaction network studies on the mechanism of binding and resistance of the HCV NS5B polymerase mutants to VX-222 and ANA598. <i>Antiviral Research</i> , 2014, 104, 40-51.	1.9	35
3262	Phosphoproteome analysis reveals differences in phosphosite profiles between tumorigenic and non-tumorigenic epithelial cells. <i>Journal of Proteomics</i> , 2014, 96, 67-81.	1.2	11
3263	EpiMiner: A three-stage co-information based method for detecting and visualizing epistatic interactions. , 2014, 24, 1-13.		31
3264	Computational Study on the Drug Resistance Mechanism against HCV NS3/4A Protease Inhibitors Vaniprevir and MK-5172 by the Combination Use of Molecular Dynamics Simulation, Residue Interaction Network, and Substrate Envelope Analysis. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 621-633.	2.5	59
3265	A practical data processing workflow for multi-OMICS projects. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 52-62.	1.1	48
3266	Involvement of the Nrf2 Pathway in the Regulation of Pterostilbene-Induced Apoptosis in HeLa Cells via ER Stress. <i>Journal of Pharmacological Sciences</i> , 2014, 126, 216-229.	1.1	24
3267	Module function and two-way clustering analysis of Epstein-Barr virus-related nasopharyngeal cancer. <i>Genetics and Molecular Research</i> , 2014, 13, 1823-1831.	0.3	1
3268	Recovery of brain biomarkers following peroxisome proliferator-activated receptor agonist neuroprotective treatment before ischemic stroke. <i>Proteome Science</i> , 2014, 12, 24.	0.7	17

#	ARTICLE	IF	CITATIONS
3269	Tissue-Specific Expression and Regulatory Networks of Pig MicroRNAome. PLoS ONE, 2014, 9, e89755.	1.1	22
3270	Analysis of protein-protein interaction network and functional modules on primary osteoporosis. European Journal of Medical Research, 2014, 19, 15.	0.9	4
3272	Transcriptome profile of OVCAR3 cisplatin-resistant ovarian cancer cell line. BMC Bioinformatics, 2014, 15, .	1.2	7
3273	Module-based functional pathway enrichment analysis of a protein-protein interaction network to study the effects of intestinal microbiota depletion in mice. Molecular Medicine Reports, 2014, 9, 2205-2212.	1.1	6
3274	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. Plant Genome, 2014, 7, plantgenome2013.08.0027.	1.6	15
3275	Mapping genomic features to functional traits through microbial whole genome sequences. International Journal of Bioinformatics Research and Applications, 2014, 10, 461.	0.1	6
3276	Construction and validation of a gene co-expression network in grapevine ( <i>Vitis vinifera</i> . L.). Horticulture Research, 2014, 1, 14040.	2.9	32
3277	Network Analysis of Free Energy Landscape of Metastable States of Hexatic Smectic B Liquid Crystal. Journal of the Physical Society of Japan, 2014, 83, 104603.	0.7	7
3278	Methods for analyzing next-generation sequencing data I. Introduction. Japanese Journal of Lactic Acid Bacteria, 2014, 25, 87-94.	0.1	2
3279	Normalized ImQCM: An Algorithm for Detecting Weak Quasi-Cliques in Weighted Graph with Applications in Gene Co-Expression Module Discovery in Cancers. Cancer Informatics, 2014, 13s3, CIN.S14021.	0.9	47
3280	Bioinformatics analysis identifies miR-221 as a core regulator in hepatocellular carcinoma and its silencing suppresses tumor properties. Oncology Reports, 2014, 32, 1200-1210.	1.2	44
3281	Analysis of differentially expressed genes between rheumatoid arthritis and osteoarthritis based on the gene co-expression network. Molecular Medicine Reports, 2014, 10, 119-124.	1.1	19
3282	RASSF1A promotes apoptosis and suppresses the proliferation of ovarian cancer cells. International Journal of Molecular Medicine, 2014, 33, 1153-1160.	1.8	15
3283	cytoHubba: identifying hub objects and sub-networks from complex interactome. BMC Systems Biology, 2014, 8, S11.	3.0	3,371
3284	Transcriptome and miRNA network analysis of familial hypercholesterolemia. International Journal of Molecular Medicine, 2014, 33, 670-676.	1.8	6
3285	Antitumor mechanism research of cryptotanshinone by module-based network analysis. , 2014, , .		0
3286	Building blocks for graph based network analysis. , 2014, , .		1
3287	Identification of key genes and crucial modules associated with coronary artery disease by bioinformatics analysis. International Journal of Molecular Medicine, 2014, 34, 863-869.	1.8	24

#	ARTICLE	IF	CITATIONS
3288	Vertical Semantic Discovery: The SICH Approach on NPS. , 2014, , .		0
3289	cDNA microarray and bioinformatic analysis for the identification of key genes in Alzheimer's disease. International Journal of Molecular Medicine, 2014, 33, 457-461.	1.8	6
3290	Integrated analysis of differential gene expression profiles in hippocampi to identify candidate genes involved in Alzheimer's disease. Molecular Medicine Reports, 2015, 12, 6679-6687.	1.1	16
3291	PUFA diets alter the microRNA expression profiles in an inflammation rat model. Molecular Medicine Reports, 2015, 11, 4149-4157.	1.1	36
3292	A computational strategy for predicting lineage specifiers in stem cell subpopulations. Stem Cell Research, 2015, 15, 427-434.	0.3	10
3293	An interactomic approach for identification of putative drug targets in <i>Listeria monocytogenes</i> . International Journal of Bioinformatics Research and Applications, 2015, 11, 315.	0.1	2
3294	DARPA's Big Mechanism program. Physical Biology, 2015, 12, 045008.	0.8	48
3295	Differential variability and correlation of gene expression identifies key genes involved in neuronal differentiation. BMC Systems Biology, 2015, 9, 82.	3.0	9
3296	Readability metric feedback for aiding node-link visualization designers. IBM Journal of Research and Development, 2015, 59, 14:1-14:16.	3.2	22
3297	The structural importance of less abundant species in Prince William Sound food web. Israel Journal of Ecology and Evolution, 2015, 61, 77-89.	0.2	6
3298	A visual spreadsheet using HTML5 for whole genome display. , 2015, , .		1
3299	Regionalization and risk. Multinational Business Review, 2015, 23, 355-373.	1.4	2
3300	The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells. BMC Systems Biology, 2015, 9, S3.	3.0	5
3301	Extensive differential protein phosphorylation as intraerythrocytic <i>Plasmodium falciparum</i> schizonts develop into extracellular invasive merozoites. Proteomics, 2015, 15, 2716-2729.	1.3	61
3302	Quantitative proteomics and network analysis of SSA1 and SSB1 deletion mutants reveals robustness of chaperone HSP70 network in <i>Saccharomyces cerevisiae</i> . Proteomics, 2015, 15, 3126-3139.	1.3	12
3303	Clustering-based gene-subnetwork biomarker identification using gene expression data. , 2015, , .		0
3304	Constructing, conducting and interpreting animal social network analysis. Journal of Animal Ecology, 2015, 84, 1144-1163.	1.3	653
3305	Integration of omics data in aging research: from biomarkers to systems biology. Aging Cell, 2015, 14, 933-944.	3.0	103

#	ARTICLE	IF	CITATIONS
3306	Circulating microRNA signature of genotype-by-age interactions in the long-lived Ames dwarf mouse. <i>Aging Cell</i> , 2015, 14, 1055-1066.	3.0	54
3307	Identification of key genes associated with the human abdominal aortic aneurysm based on the gene expression profile. <i>Molecular Medicine Reports</i> , 2015, 12, 7891-7898.	1.1	4
3308	Gut bacterial diversity of the tribes of India and comparison with the worldwide data. <i>Scientific Reports</i> , 2015, 5, 18563.	1.6	133
3309	Integrative analysis of human protein, function and disease networks. <i>Scientific Reports</i> , 2015, 5, 14344.	1.6	32
3310	A Systems Biology-Based Investigation into the Pharmacological Mechanisms of Sheng-ma-bie-jia-tang Acting on Systemic Lupus Erythematosus by Multi-Level Data Integration. <i>Scientific Reports</i> , 2015, 5, 16401.	1.6	29
3311	Similar morphological and molecular signatures shared by female and male germline stem cells. <i>Scientific Reports</i> , 2014, 4, 5580.	1.6	42
3312	Identification of the differentially expressed genes associated with familial combined hyperlipidemia using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2015, 11, 4032-4038.	1.1	6
3313	MicroRNA and gene expression profiling of response to lithium treatment for bipolar I disorder. , 2015, , .		1
3314	Functional scale-free networks in the two-dimensional Abelian sandpile model. <i>Physical Review E</i> , 2015, 92, 012822.	0.8	3
3315	Gene sequence analysis and screening of feature genes in spinal cord injury. <i>Molecular Medicine Reports</i> , 2015, 11, 3615-3620.	1.1	0
3316	RNA regulatory networks diversified through curvature of the PUF protein scaffold. <i>Nature Communications</i> , 2015, 6, 8213.	5.8	56
3317	Vitroprocines, new antibiotics against <i>Acinetobacter baumannii</i> , discovered from marine <i>Vibrio</i> sp. QWI-06 using mass-spectrometry-based metabolomics approach. <i>Scientific Reports</i> , 2015, 5, 12856.	1.6	33
3318	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , 2015, 5, 11566.	1.6	36
3319	Regulation of transcription factors on sexual dimorphism of fig wasps. <i>Scientific Reports</i> , 2015, 5, 10696.	1.6	2
3320	A comprehensive analysis of differentially expressed genes and pathways in abdominal aortic aneurysm. <i>Molecular Medicine Reports</i> , 2015, 12, 2707-2714.	1.1	13
3322	Research Resource: Androgen Receptor Activity Is Regulated Through the Mobilization of Cell Surface Receptor Networks. <i>Molecular Endocrinology</i> , 2015, 29, 1195-1218.	3.7	8
3323	Visualization of network data for effective semantic analysis. , 2015, , .		1
3324	An Alien in the Group: Eusocial Male Bees Sharing Nonspecific Reproductive Aggregations. <i>Journal of Insect Science</i> , 2015, 15, 157.	0.6	10

#	ARTICLE	IF	CITATIONS
3325	DNA methylation profiling identifies two splenic marginal zone lymphoma subgroups with different clinical and genetic features. <i>Blood</i> , 2015, 125, 1922-1931.	0.6	53
3326	Colony stimulating factor-1 receptor signaling networks inhibit mouse macrophage inflammatory responses by induction of microRNA-21. <i>Blood</i> , 2015, 125, e1-e13.	0.6	120
3328	Integrative analysis of multi-omics data for identifying multi-markers for diagnosing pancreatic cancer. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	35
3329	Quantitative assessment of gene expression network module-validation methods. <i>Scientific Reports</i> , 2015, 5, 15258.	1.6	20
3330	Chemogenomic profiling of <i>Plasmodium falciparum</i> as a tool to aid antimalarial drug discovery. <i>Scientific Reports</i> , 2015, 5, 15930.	1.6	34
3331	Pathogenic mechanisms of lung adenocarcinoma in smokers and non-smokers determined by gene expression interrogation. <i>Oncology Letters</i> , 2015, 10, 1350-1370.	0.8	16
3332	TRRUST: a reference database of human transcriptional regulatory interactions. <i>Scientific Reports</i> , 2015, 5, 11432.	1.6	339
3333	Integrated analysis of miRNA/mRNA network in placenta identifies key factors associated with labor onset of Large White and Qingping sows. <i>Scientific Reports</i> , 2015, 5, 13074.	1.6	12
3334	Direct production of XYDMY sex reversal female medaka ( <i>Oryzias latipes</i> ) by embryo microinjection of TALENs. <i>Scientific Reports</i> , 2015, 5, 14057.	1.6	18
3335	Ant trophallactic networks: simultaneous measurement of interaction patterns and food dissemination. <i>Scientific Reports</i> , 2015, 5, 12496.	1.6	58
3336	Loss-of-function of $\beta$ -catenin bar-1 slows development and activates the Wnt pathway in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2014, 4, 4926.	1.6	22
3337	Bioinformatics analysis of the target gene of fibroblast growth factor receptor 3 in bladder cancer and associated molecular mechanisms. <i>Oncology Letters</i> , 2015, 10, 543-549.	0.8	7
3338	Antigenic Patterns and Evolution of the Human Influenza A (H1N1) Virus. <i>Scientific Reports</i> , 2015, 5, 14171.	1.6	47
3339	Identification of candidate target genes for human peripheral arterial disease using weighted gene co-expression network analysis. <i>Molecular Medicine Reports</i> , 2015, 12, 8107-8112.	1.1	9
3340	Construction of biological networks from unstructured information based on a semi-automated curation workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav057.	1.4	33
3341	Exploring the association between interleukin-1 $\beta$ and its interacting proteins in Alzheimer's disease. <i>Molecular Medicine Reports</i> , 2015, 11, 3219-3228.	1.1	16
3342	Comparative transcriptome analysis between metastatic and non-metastatic gastric cancer reveals potential biomarkers. <i>Molecular Medicine Reports</i> , 2015, 11, 386-392.	1.1	13
3344	Integrated genomic approaches identify major pathways and upstream regulators in late onset Alzheimer's disease. <i>Scientific Reports</i> , 2015, 5, 12393.	1.6	114



#	ARTICLE	IF	CITATIONS
3345	Differential expression of microRNAs and their target genes in non-small-cell lung cancer. <i>Molecular Medicine Reports</i> , 2015, 11, 2034-2040.	1.1	23
3346	Drug target prioritization by perturbed gene expression and network information. <i>Scientific Reports</i> , 2015, 5, 17417.	1.6	107
3347	Identification of hub subnetwork based on topological features of genes in breast cancer. <i>International Journal of Molecular Medicine</i> , 2015, 35, 664-674.	1.8	30
3348	A novel analysis strategy for integrating methylation and expression data reveals core pathways for thyroid cancer aetiology. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	3
3349	A chemicalâ€“genetic interaction map of small molecules using highâ€“throughput imaging in cancer cells. <i>Molecular Systems Biology</i> , 2015, 11, 846.	3.2	79
3350	Phylogenomic Networks of Microbial Genome Evolution. , 2015, , 4.1.1-1-4.1.1-18.		0
3351	Role of innate immunity-triggered pathways in the pathogenesis of Sickle Cell Disease: a meta-analysis of gene expression studies. <i>Scientific Reports</i> , 2015, 5, 17822.	1.6	48
3352	Exploring novel mechanistic insights in Alzheimerâ€™s disease by assessing reliability of protein interactions. <i>Scientific Reports</i> , 2015, 5, 13634.	1.6	9
3353	Metabolomic analysis with GC-MS to reveal potential metabolites and biological pathways involved in Pb & Cd stress response of radish roots. <i>Scientific Reports</i> , 2015, 5, 18296.	1.6	103
3354	Phosphoproteome dynamics of <i>Saccharomyces cerevisiae</i> under heat shock and cold stress. <i>Molecular Systems Biology</i> , 2015, 11, 813.	3.2	54
3355	A systems biology approach to identify intelligence quotient score-related genomic regions and pathways relevant to potential therapeutic treatments. <i>Scientific Reports</i> , 2014, 4, 4176.	1.6	15
3356	Identification of genes associated with laryngeal squamous cell carcinoma samples based on bioinformatic analysis. <i>Molecular Medicine Reports</i> , 2015, 12, 3386-3392.	1.1	6
3357	GRAPHIE: graph based histology image explorer. <i>BMC Bioinformatics</i> , 2015, 16, S10.	1.2	5
3358	A genomeâ€“scale screen reveals contextâ€“dependent ovarian cancer sensitivity to miRNA overexpression. <i>Molecular Systems Biology</i> , 2015, 11, 842.	3.2	10
3359	Efficient Test and Visualization of Multi-Set Intersections. <i>Scientific Reports</i> , 2015, 5, 16923.	1.6	306
3360	Gene Coexpression Networks in Human Brain Developmental Transcriptomes Implicate the Association of Long Noncoding RNAs with Intellectual Disability. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S29435.	1.0	19
3361	Genomic, Proteomic, and Metabolomic Data Integration Strategies. <i>Biomarker Insights</i> , 2015, 10s4, BMI.S29511.	1.0	74
3362	Transcriptome Analysis in Domesticated Species: Challenges and Strategies. <i>Bioinformatics and Biology Insights</i> , 2015, 9S4, BBI.S29334.	1.0	17

#	ARTICLE	IF	CITATIONS
3363	Visualization of Genome Diversity in German Shepherd Dogs. <i>Bioinformatics and Biology Insights</i> , 2015, 9s2, BBI.S30524.	1.0	6
3364	Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12467.	1.0	38
3365	The L1TD1 Protein Interactome Reveals the Importance of Post-transcriptional Regulation in Human Pluripotency. <i>Stem Cell Reports</i> , 2015, 4, 519-528.	2.3	25
3366	Expression analysis of the estrogen receptor target genes in renal cell carcinoma. <i>Molecular Medicine Reports</i> , 2015, 11, 75-82.	1.1	6
3368	A Comprehensive Inter-Tissue Crosstalk Analysis Underlying Progression and Control of Obesity and Diabetes. <i>Scientific Reports</i> , 2015, 5, 12340.	1.6	21
3369	Protein-protein interaction network and mechanism analysis in ischemic stroke. <i>Molecular Medicine Reports</i> , 2015, 11, 29-36.	1.1	16
3370	Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	8
3371	Transcriptome analysis of breast cancer in African American women. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	0
3372	PathwayMatrix: visualizing binary relationships between proteins in biological pathways. <i>BMC Proceedings</i> , 2015, 9, S3.	1.8	16
3373	Extended LineSets: a visualization technique for the interactive inspection of biological pathways. <i>BMC Proceedings</i> , 2015, 9, S4.	1.8	16
3374	ReactionFlow: an interactive visualization tool for causality analysis in biological pathways. <i>BMC Proceedings</i> , 2015, 9, S6.	1.8	28
3375	A differential network analysis approach for lineage specifier prediction in stem cell subpopulations. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15012.	1.4	20
3376	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. <i>Scientific Reports</i> , 2015, 5, 12063.	1.6	19
3377	Network reconstruction and validation of the Snf1/AMPK pathway in baker's yeast based on a comprehensive literature review. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15007.	1.4	20
3378	A complex network analysis of the Brazilian Power Test System. , 2015, , .		3
3379	Epistatic analysis of NSAIDs hypersensitivity using high performance computing. , 2015, , .		1
3380	Diffusion kernel to identify missing PPIs in protein network biomarker. , 2015, , .		5
3381	Highly proliferative primitive fetal liver hematopoietic stem cells are fueled by oxidative metabolic pathways. <i>Stem Cell Research</i> , 2015, 15, 715-721.	0.3	59

#	ARTICLE	IF	CITATIONS
3382	NDEx, the Network Data Exchange. <i>Cell Systems</i> , 2015, 1, 302-305.	2.9	247
3383	Gene expression analysis at the onset of sex differentiation in turbot ( <i>Scophthalmus maximus</i> ). <i>BMC Genomics</i> , 2015, 16, 973.	1.2	54
3384	CRISPR/Cas9-mediated heterozygous knockout of the autism gene CHD8 and characterization of its transcriptional networks in neurodevelopment. <i>Molecular Autism</i> , 2015, 6, 55.	2.6	135
3385	Prospecting major genes in dairy buffaloes. <i>BMC Genomics</i> , 2015, 16, 872.	1.2	97
3386	Development and Application of Network Toxicology in Safety Research of Chinese Materia Medica. <i>Chinese Herbal Medicines</i> , 2015, 7, 27-38.	1.2	5
3387	Psychoactive pharmaceuticals as environmental contaminants may disrupt highly inter-connected nodes in an Autism-associated protein-protein interaction network. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	11
3388	Bioinformatics analysis of thousands of TCGA tumors to determine the involvement of epigenetic regulators in human cancer. <i>BMC Genomics</i> , 2015, 16, S5.	1.2	29
3389	Co-occurrence of resistance genes to antibiotics, biocides and metals reveals novel insights into their co-selection potential. <i>BMC Genomics</i> , 2015, 16, 964.	1.2	587
3390	Gene expression profiling of the human natural killer cell response to Fc receptor activation: unique enhancement in the presence of interleukin-12. <i>BMC Medical Genomics</i> , 2015, 8, 66.	0.7	15
3391	Metabolome of human gut microbiome is predictive of host dysbiosis. <i>GigaScience</i> , 2015, 4, 42.	3.3	95
3392	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	1.4	16
3393	Following the Footsteps of Chlamydial Gene Regulation. <i>Molecular Biology and Evolution</i> , 2015, 32, msv193.	3.5	30
3394	Pathways with PathWhiz. <i>Nucleic Acids Research</i> , 2015, 43, W552-W559.	6.5	27
3395	The role of CRKL in breast cancer metastasis: insights from systems biology. <i>Systems and Synthetic Biology</i> , 2015, 9, 141-146.	1.0	3
3396	A translational bioinformatic approach in identifying and validating an interaction between Vitamin A and CYP19A1. <i>BMC Genomics</i> , 2015, 16, S17.	1.2	2
3397	Cross-tissue and cross-species analysis of gene expression in skeletal muscle and electric organ of African weakly-electric fish ( <i>Teleostei</i> ; <i>Mormyridae</i> ). <i>BMC Genomics</i> , 2015, 16, 668.	1.2	38
3398	Comprehensive data resources and analytical tools for pathological association of aminoacyl tRNA synthetases with cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav022-bav022.	1.4	4
3399	Differential ligand-signaling network of CCL19/CCL21-CCR7 system. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav106.	1.4	32

#	ARTICLE	IF	CITATIONS
3400	A quantitative proteomic analysis of cellular responses to high glucose media in Chinese hamster ovary cells. <i>Biotechnology Progress</i> , 2015, 31, 1026-1038.	1.3	30
3401	Genome-wide expression and methylation profiles reveal candidate genes and biological processes underlying synovial inflammatory tissue of patients with osteoarthritis. <i>International Journal of Rheumatic Diseases</i> , 2015, 18, 783-790.	0.9	15
3402	The yeast $\beta$ -crystallin/NADPH:quinone oxidoreductase (Zta1p) is under nutritional control by the target of rapamycin pathway and is involved in the regulation of argininosuccinate lyase mRNA half-life. <i>FEBS Journal</i> , 2015, 282, 1953-1964.	2.2	6
3403	Structural insights into N-terminal to C-terminal interactions and implications for thermostability of a $\beta$ -triophosphate isomerase barrel enzyme. <i>FEBS Journal</i> , 2015, 282, 3543-3555.	2.2	16
3404	An integrated network of microRNA and gene expression in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, S5.	1.2	24
3405	Integrated analyses to reconstruct microRNA-mediated regulatory networks in mouse liver using high-throughput profiling. <i>BMC Genomics</i> , 2015, 16, S12.	1.2	12
3406	Context-based resolution of semantic conflicts in biological pathways. <i>BMC Medical Informatics and Decision Making</i> , 2015, 15, S3.	1.5	5
3407	Comparative proteomic analysis of hypertrophic chondrocytes in osteoarthritis. <i>Clinical Proteomics</i> , 2015, 12, 12.	1.1	49
3408	mAPKL: R/ Bioconductor package for detecting gene exemplars and revealing their characteristics. <i>BMC Bioinformatics</i> , 2015, 16, 291.	1.2	3
3409	htsint: a Python library for sequencing pipelines that combines data through gene set generation. <i>BMC Bioinformatics</i> , 2015, 16, 307.	1.2	1
3410	Low reproductive skew despite high male-biased operational sex ratio in a glass frog with paternal care. <i>BMC Evolutionary Biology</i> , 2015, 15, 181.	3.2	18
3411	Analysis of 5â€™ gene regions reveals extraordinary conservation of novel non-coding sequences in a wide range of animals. <i>BMC Evolutionary Biology</i> , 2015, 15, 227.	3.2	7
3412	Identification of four functionally important microRNA families with contrasting differential expression profiles between drought-tolerant and susceptible rice leaf at vegetative stage. <i>BMC Genomics</i> , 2015, 16, 692.	1.2	85
3413	Integrative analysis of the microRNA-mRNA response to radiochemotherapy in primary head and neck squamous cell carcinoma cells. <i>BMC Genomics</i> , 2015, 16, 654.	1.2	10
3414	Genome-wide identification and functional analysis of lincRNAs acting as miRNA targets or decoys in maize. <i>BMC Genomics</i> , 2015, 16, 793.	1.2	94
3415	Deciphering the association between gene function and spatial gene-gene interactions in 3D human genome conformation. <i>BMC Genomics</i> , 2015, 16, 880.	1.2	17
3416	Transcriptome-wide functional characterization reveals novel relationships among differentially expressed transcripts in developing soybean embryos. <i>BMC Genomics</i> , 2015, 16, 928.	1.2	21
3417	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine ( <i>Vitis vinifera</i> L.) cultivars. <i>BMC Genomics</i> , 2015, 16, 946.	1.2	41

#	ARTICLE	IF	CITATIONS
3418	Transcriptomic characterization of the dorsal lobes after hepatectomy of the ventral lobe in zebrafish. <i>BMC Genomics</i> , 2015, 16, 979.	1.2	7
3419	An integrative analysis of small molecule transcriptional responses in the human malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2015, 16, 1030.	1.2	12
3420	Similar striatal gene expression profiles in the striatum of the YAC128 and HdhQ150 mouse models of Huntington's disease are not reflected in mutant Huntingtin inclusion prevalence. <i>BMC Genomics</i> , 2015, 16, 1079.	1.2	7
3421	Reconstruction of temporal activity of microRNAs from gene expression data in breast cancer cell line. <i>BMC Genomics</i> , 2015, 16, 1077.	1.2	5
3422	Deep sequencing transcriptional fingerprinting of rice kernels for dissecting grain quality traits. <i>BMC Genomics</i> , 2015, 16, 1091.	1.2	18
3423	Using host-pathogen protein interactions to identify and characterize <i>Francisella tularensis</i> virulence factors. <i>BMC Genomics</i> , 2015, 16, 1106.	1.2	33
3424	Impact of microRNA-130a on the neutrophil proteome. <i>BMC Immunology</i> , 2015, 16, 70.	0.9	10
3425	Using the combined analysis of transcripts and metabolites to propose key genes for differential terpene accumulation across two regions. <i>BMC Plant Biology</i> , 2015, 15, 240.	1.6	72
3426	Bayesian modeling suggests that IL-12 (p40), IL-13 and MCP-1 drive murine cytokine networks in vivo. <i>BMC Systems Biology</i> , 2015, 9, 76.	3.0	9
3427	Reconstruction of gene networks using prior knowledge. <i>BMC Systems Biology</i> , 2015, 9, 84.	3.0	18
3428	Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. <i>Cell Communication and Signaling</i> , 2015, 13, 42.	2.7	58
3429	Proteins interaction network and modeling of IGVH mutational status in chronic lymphocytic leukemia. <i>Theoretical Biology and Medical Modelling</i> , 2015, 12, 12.	2.1	11
3430	Meta-analysis of transcriptomic responses as a means to identify pulmonary disease outcomes for engineered nanomaterials. <i>Particle and Fibre Toxicology</i> , 2015, 13, 25.	2.8	48
3431	Inferring interaction type in gene regulatory networks using co-expression data. <i>Algorithms for Molecular Biology</i> , 2015, 10, 23.	0.3	22
3432	Molecular-docking study of malaria drug target enzyme transketolase in <i>Plasmodium falciparum</i> 3D7 portends the novel approach to its treatment. <i>Source Code for Biology and Medicine</i> , 2015, 10, 7.	1.7	33
3433	CyNetworkBMA: a Cytoscape app for inferring gene regulatory networks. <i>Source Code for Biology and Medicine</i> , 2015, 10, 11.	1.7	5
3434	Functional dyadicity and heterophilicity of gene-gene interactions in statistical epistasis networks. <i>BioData Mining</i> , 2015, 8, 43.	2.2	11
3435	Human induced pluripotent stem cell derived neurons as a model for Williams-Beuren syndrome. <i>Molecular Brain</i> , 2015, 8, 77.	1.3	33

#	ARTICLE	IF	CITATIONS
3436	Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome changes and differential capacity to inhibit tumor growth. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 62.	3.5	11
3437	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. <i>Genome Biology</i> , 2015, 16, 84.	3.8	36
3438	Design principles for cancer therapy guided by changes in complexity of protein-protein interaction networks. <i>Biology Direct</i> , 2015, 10, 32.	1.9	26
3439	MicroRNA-derived network analysis of differentially methylated genes in schizophrenia, implicating GABA receptor B1 [GABBR1] and protein kinase B [AKT1]. <i>Biology Direct</i> , 2015, 10, 59.	1.9	8
3440	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. <i>Genome Medicine</i> , 2015, 7, 105.	3.6	30
3441	PyMine: a PyMOL plugin to integrate and visualize data for drug discovery. <i>BMC Research Notes</i> , 2015, 8, 517.	0.6	33
3442	Proteomic analysis of extracellular vesicles from medullospheres reveals a role for iron in the cancer progression of medulloblastoma. <i>Molecular and Cellular Therapies</i> , 2015, 3, 8.	0.2	19
3443	Data integration in biological research: an overview. <i>Journal of Biological Research</i> , 2015, 22, 9.	2.2	59
3444	CerebralWeb: a Cytoscape.js plug-in to visualize networks stratified by subcellular localization. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav041.	1.4	7
3445	Characterization of the relative importance of human- and infrastructure-associated bacteria in grey water: a case study. <i>Journal of Applied Microbiology</i> , 2015, 119, 289-301.	1.4	18
3446	Proteomic screening and identification of microRNA targets in glioma cells. <i>Proteomics</i> , 2015, 15, 2602-2617.	1.3	6
3447	Quantitative proteomics using SILAC: Principles, applications, and developments. <i>Proteomics</i> , 2015, 15, 3175-3192.	1.3	158
3448	Sparse networks of directly coupled, polymorphic, and functional side chains in allosteric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 497-516.	1.5	5
3449	Cross-Disciplinary Detection and Analysis of Network Motifs. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S23619.	1.0	16
3450	Analysis of MicroRNA Expression Profile Identifies Novel Biomarkers for Non-small Cell Lung Cancer. <i>Tumori</i> , 2015, 101, 104-110.	0.6	33
3451	Integrative network analysis of rifampin-regulated miRNAs and their functions in human hepatocytes. <i>Bio-Medical Materials and Engineering</i> , 2015, 26, S1985-S1991.	0.4	4
3452	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic ocean bacterioplankton. <i>Environmental Microbiology</i> , 2015, 17, 3642-3661.	1.8	51
3453	Causal biological network database: a comprehensive platform of causal biological network models focused on the pulmonary and vascular systems. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav030.	1.4	89

#	ARTICLE	IF	CITATIONS
3454	Gut metabolites and bacterial community networks during a pilot intervention study with flaxseeds in healthy adult men. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1614-1628.	1.5	95
3455	Proteomic analysis of the herpes simplex virus 1 virion protein 16 transactivator protein in infected cells. <i>Proteomics</i> , 2015, 15, 1957-1967.	1.3	16
3456	Genome-wide screen of fission yeast mutants for sensitivity to 6-azauracil, an inhibitor of transcriptional elongation. <i>Yeast</i> , 2015, 32, 643-655.	0.8	13
3457	Atmospheric N deposition alters connectance, but not functional potential among saprotrophic bacterial communities. <i>Molecular Ecology</i> , 2015, 24, 3170-3180.	2.0	41
3458	The origin and genetic differentiation of the socially parasitic aphid <i>Tamalia inquilinus</i> . <i>Molecular Ecology</i> , 2015, 24, 5751-5766.	2.0	11
3459	Cross-Species Network Analysis Uncovers Conserved Nitrogen-Regulated Network Modules in Rice. <i>Plant Physiology</i> , 2015, 168, 1830-1843.	2.3	50
3460	The protein interactome of collapsin response mediator protein 2 (CRMP2/DPYSL2) reveals novel partner proteins in brain tissue. <i>Proteomics - Clinical Applications</i> , 2015, 9, 817-831.	0.8	37
3461	Protein-protein interaction network of gene expression in the hydrocortisone-treated keloid. <i>International Journal of Dermatology</i> , 2015, 54, 549-554.	0.5	6
3462	Gut dysbiosis in acute-on-chronic liver failure and its predictive value for mortality. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2015, 30, 1429-1437.	1.4	131
3463	Low dietary iron intake restrains the intestinal inflammatory response and pathology of enteric infection by foodborne bacterial pathogens. <i>European Journal of Immunology</i> , 2015, 45, 2553-2567.	1.6	56
3464	Dose-responsive gene expression in suberoylanilide hydroxamic acid-treated resting CD4+ T cells. <i>Aids</i> , 2015, 29, 2235-2244.	1.0	18
3465	Convergent Science Physical Oncology. <i>Convergent Science Physical Oncology</i> , 2015, 1, 010201.	2.6	0
3466	Uncovering low-dimensional, miR-based signatures of acute myeloid and lymphoblastic leukemias with a machine-learning-driven network approach. <i>Convergent Science Physical Oncology</i> , 2015, 1, 025002.	2.6	10
3467	kpath: integration of metabolic pathway linked data. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav053.	1.4	8
3468	Label-free quantification reveals major proteomic changes in <i>Pseudomonas putida</i> F1 during the exponential growth phase. <i>Proteomics</i> , 2015, 15, 3244-3252.	1.3	17
3469	Bisphenol A affects placental layers morphology and angiogenesis during early pregnancy phase in mice. <i>Journal of Applied Toxicology</i> , 2015, 35, 1278-1291.	1.4	74
3470	EBprot: Statistical analysis of labeling-based quantitative proteomics data. <i>Proteomics</i> , 2015, 15, 2580-2591.	1.3	14
3471	The effect of anthropogenic arsenic contamination on the earthworm microbiome. <i>Environmental Microbiology</i> , 2015, 17, 1884-1896.	1.8	118



#	ARTICLE	IF	CITATIONS
3472	Brief Exercises Affect Gene Expression in Circulating Monocytes. <i>Scandinavian Journal of Immunology</i> , 2015, 82, 429-435.	1.3	14
3474	Selecting key genes associated with osteosarcoma based on a differential expression network. <i>Genetics and Molecular Research</i> , 2015, 14, 17708-17717.	0.3	12
3475	Partial least squares-based gene expression analysis in preeclampsia. <i>Genetics and Molecular Research</i> , 2015, 14, 6598-6604.	0.3	5
3476	The Unfolding MD Simulations of Cyclophilin: Analyzed by Surface Contact Networks and Their Associated Metrics. <i>PLoS ONE</i> , 2015, 10, e0142173.	1.1	5
3477	Protein networks in induced sputum from smokers and COPD patients. <i>International Journal of COPD</i> , 2015, 10, 1957.	0.9	21
3478	Pathway and Network Approaches for Identification of Cancer Signature Markers from Omics Data. <i>Journal of Cancer</i> , 2015, 6, 54-65.	1.2	44
3479	Gene expression profiles and protein&ndash;protein interaction network analysis in AIDS patients with HIV-associated encephalitis and dementia. <i>HIV/AIDS - Research and Palliative Care</i> , 2015, 7, 265.	0.4	12
3480	Screening of crucial long non-coding RNAs in oral epithelial dysplasia by serial analysis of gene expression. <i>Genetics and Molecular Research</i> , 2015, 14, 11729-11738.	0.3	6
3481	Role of NSC319726 in ovarian cancer based on the bioinformatics analyses. <i>OncoTargets and Therapy</i> , 2015, 8, 3757.	1.0	5
3482	Integrated microRNA-mRNA analysis of pancreatic ductal adenocarcinoma. <i>Genetics and Molecular Research</i> , 2015, 14, 10288-10297.	0.3	19
3483	Modular Transcriptional Networks of the Host Pulmonary Response during Early and Late Pneumococcal Pneumonia. <i>Molecular Medicine</i> , 2015, 21, 430-441.	1.9	12
3484	A Regulatory Role for the Insulin- and BDNF-Linked RORA in the Hippocampus: Implications for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 44, 827-838.	1.2	32
3485	Nodes with high centrality in protein interaction networks are responsible for driving signaling pathways in diabetic nephropathy. <i>PeerJ</i> , 2015, 3, e1284.	0.9	38
3486	Analysis of the gene-protein interaction network in glioma. <i>Genetics and Molecular Research</i> , 2015, 14, 14196-14206.	0.3	8
3487	Archaeal Communities in a Heterogeneous Hypersaline-Alkaline Soil. <i>Archaea</i> , 2015, 2015, 1-11.	2.3	24
3488	Bioinformatics Resources for MicroRNA Discovery. <i>Biomarker Insights</i> , 2015, 10s4, BMI.S29513.	1.0	9
3489	Evidence and potential clinical significance of changes in gene network interactions in ovarian cancer. <i>Journal of Biomedical Engineering and Informatics</i> , 2015, 2, 1.	0.2	2
3490	DDA: A Novel Network-Based Scoring Method to Identify Disease-Disease Associations. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S35237.	1.0	27

#	ARTICLE	IF	CITATIONS
3491	Tools for visualization and analysis of molecular networks, pathways, and -omics data. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2015, 8, 11.	1.6	50
3492	Ethnoveterinary management of cattle helminthiasis among the Fulani and the Mossi (Central Burkina) Tj ETQq1 1 0.784314 rgBT /Over 8, 2207.	0.1	6
3493	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 58.	2.0	13
3494	MetabNet: An R Package for Metabolic Association Analysis of High-Resolution Metabolomics Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 87.	2.0	40
3495	Evolution by Pervasive Gene Fusion in Antibiotic Resistance and Antibiotic Synthesizing Genes. <i>Computation</i> , 2015, 3, 114-127.	1.0	3
3496	Proteomics Analysis of Cellular Proteins Co-Immunoprecipitated with Nucleoprotein of Influenza A Virus (H7N9). <i>International Journal of Molecular Sciences</i> , 2015, 16, 25982-25998.	1.8	42
3497	Bioinformatics Mining and Modeling Methods for the Identification of Disease Mechanisms in Neurodegenerative Disorders. <i>International Journal of Molecular Sciences</i> , 2015, 16, 29179-29206.	1.8	47
3498	Cancerâ€“Osteoblast Interaction Reduces Sost Expression in Osteoblasts and Up-Regulates lncRNA MALAT1 in Prostate Cancer. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 503-519.	1.4	32
3499	Gene Expression, Protein Function and Pathways of Arabidopsis thaliana Responding to Silver Nanoparticles in Comparison to Silver Ions, Cold, Salt, Drought, and Heat. <i>Nanomaterials</i> , 2015, 5, 436-467.	1.9	104
3500	Parametric linear hybrid automata for complex environmental systems modeling. <i>Frontiers in Environmental Science</i> , 2015, 3, .	1.5	2
3501	A predicted protein interactome identifies conserved global networks and disease resistance subnetworks in maize. <i>Frontiers in Genetics</i> , 2015, 6, 201.	1.1	35
3502	Genomic basis of evolutionary change: evolving immunity. <i>Frontiers in Genetics</i> , 2015, 6, 222.	1.1	8
3503	Functional characterization of drought-responsive modules and genes in <i>Oryza sativa</i> : a network-based approach. <i>Frontiers in Genetics</i> , 2015, 6, 256.	1.1	46
3504	Exome sequencing of a colorectal cancer family reveals shared mutation pattern and predisposition circuitry along tumor pathways. <i>Frontiers in Genetics</i> , 2015, 6, 288.	1.1	11
3505	Precision Subtypes of T Cell-Mediated Rejection Identified by Molecular Profiles. <i>Frontiers in Immunology</i> , 2015, 6, 536.	2.2	4
3506	Proteome profiling of heat, oxidative, and salt stress responses in <i>Thermococcus kodakarensis</i> KOD1. <i>Frontiers in Microbiology</i> , 2015, 6, 605.	1.5	40
3507	Integrated inference and evaluation of hostâ€“fungi interaction networks. <i>Frontiers in Microbiology</i> , 2015, 6, 764.	1.5	63
3508	Sequence-based Analysis of the <i>Vitis vinifera</i> L. cv Cabernet Sauvignon Grape Must Mycobiome in Three South African Vineyards Employing Distinct Agronomic Systems. <i>Frontiers in Microbiology</i> , 2015, 6, 1358.	1.5	64

#	ARTICLE	IF	CITATIONS
3509	A Zinc-Dependent Protease AMZ-tk from a Thermophilic Archaeon is a New Member of the Archaemetzincin Protein Family. <i>Frontiers in Microbiology</i> , 2015, 6, 1380.	1.5	13
3510	Groundwater Isolation Governs Chemistry and Microbial Community Structure along Hydrologic Flowpaths. <i>Frontiers in Microbiology</i> , 2015, 6, 1457.	1.5	93
3511	Systems biology analysis of the proteomic alterations induced by MPP+, a Parkinson's disease-related mitochondrial toxin. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 14.	1.8	24
3512	Gene Expression Associated with Early and Late Chronotypes in <i>Drosophila melanogaster</i> . <i>Frontiers in Neurology</i> , 2015, 6, 100.	1.1	13
3513	Epigenetic modulation of brain gene networks for cocaine and alcohol abuse. <i>Frontiers in Neuroscience</i> , 2015, 9, 176.	1.4	69
3514	Screening the Molecular Targets of Ovarian Cancer Based on Bioinformatics Analysis. <i>Tumori</i> , 2015, 101, 384-389.	0.6	12
3515	Gene Expression Profiling Analysis of Castration-Resistant Prostate Cancer. <i>Medical Science Monitor</i> , 2015, 21, 205-212.	0.5	9
3516	Construction of gene/protein interaction networks for primary myelofibrosis and KEGG pathway-enrichment analysis of molecular compounds. <i>Genetics and Molecular Research</i> , 2015, 14, 16126-16132.	0.3	2
3517	Further insight into molecular mechanism underlying thoracic spinal cord injury using bioinformatics methods. <i>Molecular Medicine Reports</i> , 2015, 12, 7851-7858.	1.1	7
3518	Integrated Annotation and Analysis of In Situ Hybridization Images Using the ImAnno System: Application to the Ear and Sensory Organs of the Fetal Mouse. <i>PLoS ONE</i> , 2015, 10, e0118024.	1.1	0
3519	Biotic Stress Shifted Structure and Abundance of Enterobacteriaceae in the Lettuce Microbiome. <i>PLoS ONE</i> , 2015, 10, e0118068.	1.1	51
3520	Differential Network Analysis with Multiply Imputed Lipidomic Data. <i>PLoS ONE</i> , 2015, 10, e0121449.	1.1	3
3521	Characterization of the Avian Trojan Gene Family Reveals Contrasting Evolutionary Constraints. <i>PLoS ONE</i> , 2015, 10, e0121672.	1.1	3
3522	Genome-Wide Identification, Characterization and Evolutionary Analysis of Long Intergenic Noncoding RNAs in Cucumber. <i>PLoS ONE</i> , 2015, 10, e0121800.	1.1	98
3523	H-Ferritin-Regulated MicroRNAs Modulate Gene Expression in K562 Cells. <i>PLoS ONE</i> , 2015, 10, e0122105.	1.1	30
3524	De Novo Characterization of Fall Dormant and Nondormant Alfalfa ( <i>Medicago sativa</i> L.) Leaf Transcriptome and Identification of Candidate Genes Related to Fall Dormancy. <i>PLoS ONE</i> , 2015, 10, e0122170.	1.1	36
3525	Identification of Common Regulators of Genes in Co-Expression Networks Affecting Muscle and Meat Properties. <i>PLoS ONE</i> , 2015, 10, e0123678.	1.1	39
3526	Genomic and Clinical Effects Associated with a Relaxation Response Mind-Body Intervention in Patients with Irritable Bowel Syndrome and Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2015, 10, e0123861.	1.1	62

#	ARTICLE	IF	CITATIONS
3527	Inter-Chromosomal Contact Networks Provide Insights into Mammalian Chromatin Organization. PLoS ONE, 2015, 10, e0126125.	1.1	33
3528	Analysis of MÃ©xico's Narco-War Network (2007-2011). PLoS ONE, 2015, 10, e0126503.	1.1	21
3529	RulNet: A Web-Oriented Platform for Regulatory Network Inference, Application to Wheat -Omics Data. PLoS ONE, 2015, 10, e0127127.	1.1	12
3530	Pathways and Networks-Based Analysis of Candidate Genes Associated with Nicotine Addiction. PLoS ONE, 2015, 10, e0127438.	1.1	18
3531	Long Noncoding RNA Expression during Human B-Cell Development. PLoS ONE, 2015, 10, e0138236.	1.1	80
3532	The Orphan Nuclear Receptor TLX Is an Enhancer of STAT1-Mediated Transcription and Immunity to Toxoplasma gondii. PLoS Biology, 2015, 13, e1002200.	2.6	25
3533	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. PLoS Computational Biology, 2015, 11, e1004393.	1.5	74
3534	Structural Bridges through Fold Space. PLoS Computational Biology, 2015, 11, e1004466.	1.5	16
3535	Time-Dependent Transcriptional Changes in Axenic Giardia duodenalis Trophozoites. PLoS Neglected Tropical Diseases, 2015, 9, e0004261.	1.3	16
3536	Genome-Wide Collation of the Plasmodium falciparum WDR Protein Superfamily Reveals Malarial Parasite-Specific Features. PLoS ONE, 2015, 10, e0128507.	1.1	9
3537	The Identification of Novel Protein-Protein Interactions in Liver that Affect Glucagon Receptor Activity. PLoS ONE, 2015, 10, e0129226.	1.1	19
3538	Molecular Features of Triple Negative Breast Cancer: Microarray Evidence and Further Integrated Analysis. PLoS ONE, 2015, 10, e0129842.	1.1	17
3539	Cardioprotective Signature of Short-Term Caloric Restriction. PLoS ONE, 2015, 10, e0130658.	1.1	47
3540	Chinese Herbal Preparation Xuebijing Potently Inhibits Inflammasome Activation in Hepatocytes and Ameliorates Mouse Liver Ischemia-Reperfusion Injury. PLoS ONE, 2015, 10, e0131436.	1.1	13
3541	Differential miRNA Expression in Cells and Matrix Vesicles in Vascular Smooth Muscle Cells from Rats with Kidney Disease. PLoS ONE, 2015, 10, e0131589.	1.1	37
3542	Comparative Anterior Pituitary miRNA and mRNA Expression Profiles of Bama Minipigs and Landrace Pigs Reveal Potential Molecular Network Involved in Animal Postnatal Growth. PLoS ONE, 2015, 10, e0131987.	1.1	21
3543	Analysis of the Human Prostate-Specific Proteome Defined by Transcriptomics and Antibody-Based Profiling Identifies TMEM79 and ACOXL as Two Putative, Diagnostic Markers in Prostate Cancer. PLoS ONE, 2015, 10, e0133449.	1.1	23
3544	Environmental Interactions and Epistasis Are Revealed in the Proteomic Responses to Complex Stimuli. PLoS ONE, 2015, 10, e0134099.	1.1	11

#	ARTICLE	IF	CITATIONS
3545	Interleukin 21 Controls mRNA and MicroRNA Expression in CD40-Activated Chronic Lymphocytic Leukemia Cells. PLoS ONE, 2015, 10, e0134706.	1.1	16
3546	Cleanroom Maintenance Significantly Reduces Abundance but Not Diversity of Indoor Microbiomes. PLoS ONE, 2015, 10, e0134848.	1.1	56
3547	MicroRNA Expression Profiling of Human Respiratory Epithelium Affected by Invasive Candida Infection. PLoS ONE, 2015, 10, e0136454.	1.1	23
3548	The Role of ARF6 in Biliary Atresia. PLoS ONE, 2015, 10, e0138381.	1.1	66
3549	Cancer Specific Long Noncoding RNAs Show Differential Expression Patterns and Competing Endogenous RNA Potential in Hepatocellular Carcinoma. PLoS ONE, 2015, 10, e0141042.	1.1	112
3550	RNA-Seq Based Identification of Candidate Parasitism Genes of Cereal Cyst Nematode (Heterodera) Tj ETQq1 1 0.784314 rgBT/Overlaid	1.1	20
3551	Complete Genomic and Lysis-Cassette Characterization of the Novel Phage, KBNP1315, which Infects Avian Pathogenic Escherichia coli (APEC). PLoS ONE, 2015, 10, e0142504.	1.1	16
3552	Bioinformatics Analysis of the Effects of Tobacco Smoke on Gene Expression. PLoS ONE, 2015, 10, e0143377.	1.1	17
3553	Identification of New Molecular Entities (NMEs) as Potential Leads against Tuberculosis from Open Source Compound Repository. PLoS ONE, 2015, 10, e0144018.	1.1	26
3554	Identification of Major Signaling Pathways in Prion Disease Progression Using Network Analysis. PLoS ONE, 2015, 10, e0144389.	1.1	7
3555	Transcriptome Analysis of Ullrich Congenital Muscular Dystrophy Fibroblasts Reveals a Disease Extracellular Matrix Signature and Key Molecular Regulators. PLoS ONE, 2015, 10, e0145107.	1.1	23
3556	The Urinary Bladder Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2015, 10, e0145301.	1.1	25
3557	Escherichia coli under Ionic Silver Stress: An Integrative Approach to Explore Transcriptional, Physiological and Biochemical Responses. PLoS ONE, 2015, 10, e0145748.	1.1	21
3558	Systems pharmacology of adiposity reveals inhibition of EP300 as a common therapeutic mechanism of caloric restriction and resveratrol for obesity. Frontiers in Pharmacology, 2015, 6, 199.	1.6	24
3559	A comprehensive survey of the grapevine VQ gene family and its transcriptional correlation with WRKY proteins. Frontiers in Plant Science, 2015, 6, 417.	1.7	55
3560	Global analysis of lysine acetylation in strawberry leaves. Frontiers in Plant Science, 2015, 6, 739.	1.7	73
3561	Molecular evolution, characterization, and expression analysis of SnRK2 gene family in Pak-choi (Brassica rapa ssp. chinensis). Frontiers in Plant Science, 2015, 6, 879.	1.7	29
3562	Global analysis of WRKY transcription factor superfamily in Setaria identifies potential candidates involved in abiotic stress signaling. Frontiers in Plant Science, 2015, 6, 910.	1.7	96

#	ARTICLE	IF	CITATIONS
3563	Transcriptome analysis reveals regulatory networks underlying differential susceptibility to <i>Botrytis cinerea</i> in response to nitrogen availability in <i>Solanum lycopersicum</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 911.	1.7	41
3564	Transcriptional Regulatory Network Analysis of MYB Transcription Factor Family Genes in Rice. <i>Frontiers in Plant Science</i> , 2015, 6, 1157.	1.7	76
3565	Integrated miRNA-mRNA analysis of Epstein-Barr virus-positive nasopharyngeal carcinoma. <i>Genetics and Molecular Research</i> , 2015, 14, 6028-6036.	0.3	7
3566	Identification of potential therapeutic targets for melanoma using gene expression analysis. <i>Neoplasma</i> , 2015, 62, 733-739.	0.7	10
3567	Circulating small non coding RNA signature in head and neck squamous cell carcinoma. <i>Oncotarget</i> , 2015, 6, 19246-19263.	0.8	89
3568	Identification of Biomarkers for the Prognosis of Pancreatic Ductal Adenocarcinoma with miRNA Microarray Data. <i>International Journal of Biological Markers</i> , 2015, 30, 226-233.	0.7	4
3569	freeQuant: A Mass Spectrometry Label-Free Quantification Software Tool for Complex Proteome Analysis. <i>Scientific World Journal, The</i> , 2015, 2015, 1-11.	0.8	8
3570	miRNA Regulation Network Analysis in Qianliening Capsule Treatment of Benign Prostatic Hyperplasia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2015, 2015, 1-9.	0.5	3
3571	Trends in IT Innovation to Build a Next Generation Bioinformatics Solution to Manage and Analyse Biological Big Data Produced by NGS Technologies. <i>BioMed Research International</i> , 2015, 2015, 1-15.	0.9	26
3572	A Network Flow Approach to Predict Protein Targets and Flavonoid Backbones to Treat Respiratory Syncytial Virus Infection. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	13
3573	Analysis of Gene Profiles in Glioma Cells Identifies Potential Genes, miRNAs, and Target Sites of Migratory Cells. <i>Tumori</i> , 2015, 101, 542-548.	0.6	6
3574	Proteomic Study to Survey the CIGB-552 Antitumor Effect. <i>BioMed Research International</i> , 2015, 2015, 1-18.	0.9	6
3575	Identification of Differentially Expressed Genes in Pituitary Adenomas by Integrating Analysis of Microarray Data. <i>International Journal of Endocrinology</i> , 2015, 2015, 1-7.	0.6	19
3576	Protein Complex Discovery by Interaction Filtering from Protein Interaction Networks Using Mutual Rank Coexpression and Sequence Similarity. <i>BioMed Research International</i> , 2015, 2015, 1-7.	0.9	1
3577	mmnet: An R Package for Metagenomics Systems Biology Analysis. <i>BioMed Research International</i> , 2015, 2015, 1-5.	0.9	12
3578	Network-Based Association Study of Obesity and Type 2 Diabetes with Gene Expression Profiles. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	6
3579	Coexpression Network Analysis of miRNA-142 Overexpression in Neuronal Cells. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	4
3580	MicroRNA Polymorphisms in Cancer: A Literature Analysis. <i>Cancers</i> , 2015, 7, 1806-1814.	1.7	29

#	ARTICLE	IF	CITATIONS
3581	Gene Expression Patterns Associated with Peroxisome Proliferator-activated Receptor (PPAR) Signaling in the &lt;i>Longissimus dorsi&/i> of Hanwoo (Korean Cattle). <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 1075-1083.	2.4	31
3582	CEMTDD: The database for elucidating the relationships among herbs, compounds, targets and related diseases for Chinese ethnic minority traditional drugs. <i>Oncotarget</i> , 2015, 6, 17675-17684.	0.8	15
3583	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. <i>ELife</i> , 2015, 4, e07966.	2.8	50
3584	Precise assembly of complex beta sheet topologies from de novo designed building blocks. <i>ELife</i> , 2015, 4, .	2.8	15
3585	Glioblastoma and calcium signaling - analysis of calcium toolbox expression. <i>International Journal of Developmental Biology</i> , 2015, 59, 407-415.	0.3	26
3586	Knowledge Networks and Knowledge Adjacencies. , 2015, , .		0
3587	Analysis of Gene Expression During the Development of Congestive Heart Failure After Myocardial Infarction in Rat Models. <i>International Heart Journal</i> , 2015, 56, 444-449.	0.5	5
3588	The landscape of metastatic progression patterns across major human cancers. <i>Oncotarget</i> , 2015, 6, 570-583.	0.8	208
3589	Suppression of ASK1 <sup>2</sup> (AtSK32), a Clade III Arabidopsis GSK3, Leads to the Pollen Defect during Late Pollen Development. <i>Molecules and Cells</i> , 2015, 38, 506-517.	1.0	11
3590	Inference of the Arabidopsis Lateral Root Gene Regulatory Network Suggests a Bifurcation Mechanism That Defines Primordia Flanking and Central Zones. <i>Plant Cell</i> , 2015, 27, 1368-1388.	3.1	105
3591	Araport: the Arabidopsis Information Portal. <i>Nucleic Acids Research</i> , 2015, 43, D1003-D1009.	6.5	193
3592	Identification of protein complexes that bind to histone H3 combinatorial modifications using super-SILAC and weighted correlation network analysis. <i>Nucleic Acids Research</i> , 2015, 43, 1418-1432.	6.5	35
3593	A statistically inferred microRNA network identifies breast cancer target miR-940 as an actin cytoskeleton regulator. <i>Scientific Reports</i> , 2015, 5, 8336.	1.6	28
3594	New Compound Sets Identified from High Throughput Phenotypic Screening Against Three Kinetoplastid Parasites: An Open Resource. <i>Scientific Reports</i> , 2015, 5, 8771.	1.6	204
3595	Selective neuronal targeting, protection and signaling network analysis via dopamine-mediated mesoporous silica nanoparticles. <i>MedChemComm</i> , 2015, 6, 1117-1129.	3.5	12
3596	Transcription Factor PAX6 (Paired Box 6) Controls Limbal Stem Cell Lineage in Development and Disease. <i>Journal of Biological Chemistry</i> , 2015, 290, 20448-20454.	1.6	54
3597	Systematic Metabolomic Analysis of Eicosanoids after Omega-3 Polyunsaturated Fatty Acid Supplementation by a Highly Specific Liquid Chromatographyâ€“Tandem Mass Spectrometry-Based Method. <i>Journal of Proteome Research</i> , 2015, 14, 1843-1853.	1.8	75
3598	Genomeâ€“guided investigation of plant natural product biosynthesis. <i>Plant Journal</i> , 2015, 82, 680-692.	2.8	186



#	ARTICLE	IF	CITATIONS
3599	Examination of Epigenetic and other Molecular Factors Associated with mda-9/Syntenin Dysregulation in Cancer Through Integrated Analyses of Public Genomic Datasets. <i>Advances in Cancer Research</i> , 2015, 127, 49-121.	1.9	25
3600	Concatabominations: Identifying Unstable Taxa in Morphological Phylogenetics using a Heuristic Extension to Safe Taxonomic Reduction. <i>Systematic Biology</i> , 2015, 64, 137-143.	2.7	37
3601	CDD: NCBI's conserved domain database. <i>Nucleic Acids Research</i> , 2015, 43, D222-D226.	6.5	3,022
3602	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. <i>FEBS Letters</i> , 2015, 589, 2590-2602.	1.3	66
3603	cMonkey <sup>2</sup> : Automated, systematic, integrated detection of co-regulated gene modules for any organism. <i>Nucleic Acids Research</i> , 2015, 43, e87-e87.	6.5	45
3604	Metabolomic Markers of Altered Nucleotide Metabolism in Early Stage Adenocarcinoma. <i>Cancer Prevention Research</i> , 2015, 8, 410-418.	0.7	79
3605	Pathogenic pathways are activated in each major cell type of the glomerulus in the Cd2ap mutant mouse model of focal segmental glomerulosclerosis. <i>BMC Nephrology</i> , 2015, 16, 71.	0.8	8
3606	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. <i>Biochemical Journal</i> , 2015, 469, 71-82.	1.7	20
3607	Bioinformatics Analysis of Potential Candidates for Therapy of TDRD7 Deficiency-Induced Congenital Cataract. <i>Ophthalmic Research</i> , 2015, 54, 10-17.	1.0	5
3608	pwOmics: an R package for pathway-based integration of time-series omics data using public database knowledge. <i>Bioinformatics</i> , 2015, 31, 3072-3074.	1.8	30
3609	Early fermentation volatile metabolite profile of non-Saccharomyces yeasts in red and white grape must: A targeted approach. <i>LWT - Food Science and Technology</i> , 2015, 64, 412-422.	2.5	62
3610	Alpha-linolenic acid protects against cardiac injury and remodelling induced by beta-adrenergic overstimulation. <i>Food and Function</i> , 2015, 6, 2231-2239.	2.1	21
3611	The expression profile analysis of NKX2-5 knock-out embryonic mice to explore the pathogenesis of congenital heart disease. <i>Journal of Cardiology</i> , 2015, 66, 527-531.	0.8	10
3612	Genome-wide survey and expression analysis of the PUB family in Chinese cabbage ( <i>Brassica rapa</i> ssp.) Tj ETQq1 1 0.784314 ggBT /Over	1.0	37
3613	xiNET: Cross-link Network Maps With Residue Resolution. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1137-1147.	2.5	242
3614	Scoring Large-scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
3615	Detecting disease genes of non-small lung cancer based on consistently differential interactions. <i>Cancer and Metastasis Reviews</i> , 2015, 34, 195-208.	2.7	1
3616	Screening of candidate genes in fibroblasts derived from patients with Dupuytren's contracture using bioinformatics analysis. <i>Rheumatology International</i> , 2015, 35, 1343-1350.	1.5	4

#	ARTICLE	IF	CITATIONS
3617	Truncated Ubiquitin 5â€™ Regulatory Region from <i>Erianthus arundinaceus</i> Drives Enhanced Transgene Expression in Heterologous Systems. <i>Molecular Biotechnology</i> , 2015, 57, 820-835.	1.3	12
3618	Construction of regulatory networks mediated by small RNAs responsive to abiotic stresses in rice ( <i>Oryza sativa</i> ). <i>Computational Biology and Chemistry</i> , 2015, 58, 69-80.	1.1	9
3619	Are ta-siRNAs only originated from the cleavage site of miRNA on its target RNAs and phased in 21-nt increments?. <i>Gene</i> , 2015, 569, 127-135.	1.0	7
3620	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. <i>BMC Genomics</i> , 2015, 16, 330.	1.2	85
3621	Bioinformatic analysis of the effect of type II diabetes on skin wound healing. <i>Genetics and Molecular Research</i> , 2015, 14, 4802-4811.	0.3	3
3622	The functional interactome of <scp>PYHIN</scp> immune regulators reveals <scp>IFIX</scp> is a sensor of viral <scp>DNA</scp>. <i>Molecular Systems Biology</i> , 2015, 11, 787.	3.2	74
3623	PathRings: a web-based tool for exploration of ortholog and expression data in biological pathways. <i>BMC Bioinformatics</i> , 2015, 16, 165.	1.2	7
3624	ACTN4 and the pathways associated with cell motility and adhesion contribute to the process of lung cancer metastasis to the brain. <i>BMC Cancer</i> , 2015, 15, 277.	1.1	32
3625	Dysregulated mechanisms underlying Duchenne muscular dystrophy from co-expression network preservation analysis. <i>BMC Research Notes</i> , 2015, 8, 182.	0.6	24
3626	Deriving accurate microbiota profiles from human samples with low bacterial content through post-sequencing processing of Illumina MiSeq data. <i>Microbiome</i> , 2015, 3, 19.	4.9	179
3627	Functional Proteomic Analysis of Repressive Histone Methyltransferase Complexes Reveals ZNF518B as a G9A Regulator*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1435-1446.	2.5	39
3628	Bioinformatics, Interaction Network Analysis, and Neural Networks to Characterize Gene Expression of Radicular Cyst and Periapical Granuloma. <i>Journal of Endodontics</i> , 2015, 41, 877-883.	1.4	33
3629	Computational analysis of miRNA-target community network reveals cross talk among different metabolisms. <i>Genomics Data</i> , 2015, 5, 292-296.	1.3	7
3630	A protein interaction map of the LSU processome. <i>Genes and Development</i> , 2015, 29, 862-875.	2.7	41
3631	A network analysis of miRNA mediated gene regulation of rice: crosstalk among biological processes. <i>Molecular BioSystems</i> , 2015, 11, 2273-2280.	2.9	16
3632	Distinct soil microbial diversity under long-term organic and conventional farming. <i>ISME Journal</i> , 2015, 9, 1177-1194.	4.4	1,076
3634	Small-world networks of residue interactions in the Abl kinase complexes with cancer drugs: topology of allosteric communication pathways can determine drug resistance effects. <i>Molecular BioSystems</i> , 2015, 11, 2082-2095.	2.9	6
3635	Whole-exome sequencing of pancreatic cancer defines genetic diversity and therapeutic targets. <i>Nature Communications</i> , 2015, 6, 6744.	5.8	879

#	ARTICLE	IF	CITATIONS
3636	Expression of Human Skin-Specific Genes Defined by Transcriptomics and Antibody-Based Profiling. <i>Journal of Histochemistry and Cytochemistry</i> , 2015, 63, 129-141.	1.3	63
3637	Tctex1d2 associates with short-rib polydactyly syndrome proteins and is required for ciliogenesis. <i>Cell Cycle</i> , 2015, 14, 1116-1125.	1.3	25
3638	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	5.8	178
3639	Early transcriptional events linked to induction of diapause revealed by RNAseq in larvae of drosophilid fly, <i>Chymomyza costata</i> . <i>BMC Genomics</i> , 2015, 16, 720.	1.2	87
3640	LaNCoA: A Python toolkit for Language Networks Construction and Analysis. , 2015, , .		11
3641	OSNAP! Introducing the open semantic network analysis platform. <i>Proceedings of SPIE</i> , 2015, , .	0.8	2
3642	Proteomic signatures of antiplatelet drugs: new approaches to exploring drug effects. <i>Journal of Thrombosis and Haemostasis</i> , 2015, 13, S323-S331.	1.9	21
3643	Comparison of topological clustering within protein networks using edge metrics that evaluate full sequence, full structure, and active site microenvironment similarity. <i>Protein Science</i> , 2015, 24, 1423-1439.	3.1	14
3644	MUNA. , 2015, , .		5
3645	VISIONET: intuitive visualisation of overlapping transcription factor networks, with applications in cardiogenic gene discovery. <i>BMC Bioinformatics</i> , 2015, 16, 141.	1.2	6
3646	Genome-wide identification of the <i>Phaseolus vulgaris</i> sRNAome using small RNA and degradome sequencing. <i>BMC Genomics</i> , 2015, 16, 423.	1.2	49
3647	Transcriptional response of Atlantic salmon families to <i>Piscirickettsia salmonis</i> infection highlights the relevance of the iron-deprivation defence system. <i>BMC Genomics</i> , 2015, 16, 495.	1.2	94
3648	CytoASP: a Cytoscape app for qualitative consistency reasoning, prediction and repair in biological networks. <i>BMC Systems Biology</i> , 2015, 9, 34.	3.0	3
3649	Co-expression network of neural-differentiation genes shows specific pattern in schizophrenia. <i>BMC Medical Genomics</i> , 2015, 8, 23.	0.7	45
3650	Single-Cell Based Quantitative Assay of Chromosome Transmission Fidelity. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1043-1056.	0.8	24
3651	petal: A novel co-expression network modeling system. , 2015, , .		1
3652	Sphingosine kinase 2 is a chikungunya virus host factor co-localized with the viral replication complex. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-9.	3.0	44
3653	Whole-proteome genetic analysis of dependencies in assembly of a vertebrate kinetochore. <i>Journal of Cell Biology</i> , 2015, 211, 1141-1156.	2.3	42

#	ARTICLE	IF	CITATIONS
3654	Evolution of cis-regulatory elements and regulatory networks in duplicated genes of <i>Arabidopsis thaliana</i> . <i>Plant Physiology</i> , 2015, 169, pp.00717.2015.	2.3	52
3655	Comparative sequence analyses of genome and transcriptome reveal novel transcripts and variants in the Asian elephant <i>Elephas maximus</i> . <i>Journal of Biosciences</i> , 2015, 40, 891-907.	0.5	18
3656	Linking Phenotypes and Modes of Action Through High-Content Screen Fingerprints. <i>Assay and Drug Development Technologies</i> , 2015, 13, 415-427.	0.6	67
3657	CytoCom: a Cytoscape app to visualize, query and analyse disease comorbidity networks. <i>Bioinformatics</i> , 2015, 31, 969-971.	1.8	42
3658	Using kernelized partial canonical correlation analysis to study directly coupled side chains and allostery in small G proteins. <i>Bioinformatics</i> , 2015, 31, i124-i132.	1.8	2
3659	cyNeo4j: connecting Neo4j and Cytoscape. <i>Bioinformatics</i> , 2015, 31, 3868-3869.	1.8	22
3660	Evolution of the Translocation and Assembly Module (TAM). <i>Genome Biology and Evolution</i> , 2015, 7, 1628-1643.	1.1	62
3661	Integrating motif, DNA accessibility and gene expression data to build regulatory maps in an organism. <i>Nucleic Acids Research</i> , 2015, 43, 3998-4012.	6.5	36
3662	PheNetic: network-based interpretation of molecular profiling data. <i>Nucleic Acids Research</i> , 2015, 43, W244-W250.	6.5	24
3663	SCUDO: a tool for signature-based clustering of expression profiles. <i>Nucleic Acids Research</i> , 2015, 43, W188-W192.	6.5	15
3664	MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. <i>Nucleic Acids Research</i> , 2015, 43, W258-W263.	6.5	49
3665	A systems-level approach to parental genomic imprinting: the imprinted gene network includes extracellular matrix genes and regulates cell cycle exit and differentiation. <i>Genome Research</i> , 2015, 25, 353-367.	2.4	78
3666	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131.	5.8	93
3667	Long-term neural and physiological phenotyping of a single human. <i>Nature Communications</i> , 2015, 6, 8885.	5.8	353
3668	Evaluating the use of HILIC in large-scale, multi dimensional proteomics: Horses for courses?. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 105-114.	0.7	10
3669	Metabolomics to Explore Imidacloprid-Induced Toxicity in the Central Nervous System of the Freshwater Snail <i>Lymnaea stagnalis</i> . <i>Environmental Science &amp; Technology</i> , 2015, 49, 14529-14536.	4.6	37
3670	Big Data in <i>Caenorhabditis elegans</i> : quo vadis?. <i>Molecular Biology of the Cell</i> , 2015, 26, 3909-3914.	0.9	8
3671	COUPLED NETWORK APPROACH TO PREDICTABILITY OF FINANCIAL MARKET RETURNS AND NEWS SENTIMENTS. <i>International Journal of Theoretical and Applied Finance</i> , 2015, 18, 1550043.	0.2	19

#	ARTICLE	IF	CITATIONS
3672	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme. , 2015, , .		1
3673	Linking Genes to Cardiovascular Diseases: Gene Action and Gene-Environment Interactions. Journal of Cardiovascular Translational Research, 2015, 8, 506-527.	1.1	27
3674	Acute Cellular Rejection Elicits Distinct MicroRNA Signatures in Airway Epithelium of Lung Transplant Patients. Transplantation Direct, 2015, 1, e44.	0.8	8
3675	Acquisition of diabetes-related biological associations using a motif based network: Preliminary results. , 2015, , .		0
3676	The oncogenic FIP1L1-PDGFR<math>\beta</math>-fusion protein displays skewed signaling properties compared to its wild-type PDGFR<math>\beta</math>-counterpart. Jak-stat, 2015, 4, e1062596.	2.2	5
3677	ATria: A novel centrality algorithm applied to biological networks. , 2015, , .		1
3678	IspH-ROSP1 and IspH-UbiA: -Rosetta stone-proteins. Chemical Science, 2015, 6, 6813-6822.	3.7	6
3679	A cloud-based approach for Gene Regulatory Networks dynamics simulations. , 2015, , .		2
3680	A computational framework for integrative analysis of large microbial genomics data. , 2015, , .		1
3681	An approach for optimally extending mathematical models of signaling networks using omics data. , 2015, 2015, 6501-4.		1
3682	Guilt-by association approach to identify novel human aging-related genes using protein domains. , 2015, , .		0
3683	A Molecular-Level Landscape of Diet-Gut Microbiome Interactions: Toward Dietary Interventions Targeting Bacterial Genes. MBio, 2015, 6, e01263-15.	1.8	33
3684	Actions of Huangqi decoction against rat liver fibrosis: a gene expression profiling analysis. Chinese Medicine, 2015, 10, 39.	1.6	26
3685	Bipartite graphs for metagenomic data analysis and visualization. , 2015, , .		1
3686	Polyunsaturated Fatty Acids from Algae. Cellular Origin and Life in Extreme Habitats, 2015, , 467-481.	0.3	3
3687	Efficient exploration of pan-cancer networks by generalized covariance selection and interactive web content. Nucleic Acids Research, 2015, 43, e98-e98.	6.5	16
3688	Layer-Centered Approach for Multigraphs Visualization. , 2015, , .		4
3689	Data driven predictive analytics for a spindle's health. , 2015, , .		3

#	ARTICLE	IF	CITATIONS
3690	BmQGen: Biomedical query generator for knowledge discovery. , 2015, , .		7
3691	Bioinformatics Analysis of Proteome Changes in Calu-3 Cell Infected by Influenza A Virus (H5N1). Journal of Molecular Microbiology and Biotechnology, 2015, 25, 311-319.	1.0	1
3692	Genome-wide Analysis of Host-Plasmodium yoelii Interactions Reveals Regulators of the Type I Interferon Response. Cell Reports, 2015, 12, 661-672.	2.9	21
3693	Discovery of neighborhood relationships and regulatory patterns between breast cancer and inflammatory genes based on human co-expressed regulatory network. , 2015, , .		0
3694	Neuronal calcium signaling pathways are associated with the development of epilepsy. Molecular Medicine Reports, 2015, 11, 196-202.	1.1	14
3695	Expression profile analysis of microRNAs and downregulated miR-486-5p and miR-30a-5p in non-small cell lung cancer. Oncology Reports, 2015, 34, 1779-1786.	1.2	54
3696	Rapamycin reduces fibroblast proliferation without causing quiescence and induces STAT5A/B-mediated cytokine production. Nucleus, 2015, 6, 490-506.	0.6	16
3697	Multilevel systems biology modeling characterized the atheroprotective efficiencies of modified dairy fats in a hamster model. American Journal of Physiology - Heart and Circulatory Physiology, 2015, 309, H935-H945.	1.5	12
3698	Identification of genes associated with methotrexate resistance in methotrexate-resistant osteosarcoma cell lines. Journal of Orthopaedic Surgery and Research, 2015, 10, 136.	0.9	21
3699	Epistatic Analysis of Clarkson Disease. Procedia Computer Science, 2015, 51, 725-734.	1.2	6
3700	Functional Network Analysis Reveals Versatile MicroRNAs in Human Heart. Cellular Physiology and Biochemistry, 2015, 36, 1628-1643.	1.1	17
3701	<i>In silico</i> analysis and experimental validation of active compounds from fructus <i>Schisandrae chinensis</i> in protection from hepatic injury. Cell Proliferation, 2015, 48, 86-94.	2.4	5
3702	Skeletal muscle proteomic signature and metabolic impairment in pulmonary hypertension. Journal of Molecular Medicine, 2015, 93, 573-584.	1.7	53
3703	GeneFriends: a human RNA-seq-based gene and transcript co-expression database. Nucleic Acids Research, 2015, 43, D1124-D1132.	6.5	108
3704	Dynamic interactive events in gene regulation using E. coli dehydrogenase as a model. Functional and Integrative Genomics, 2015, 15, 175-188.	1.4	4
3705	Chronic Cardiovascular Disease-Associated Gene Network Analysis in Human Umbilical Vein Endothelial Cells Exposed to 2,3,7,8-Tetrachlorodibenzo-p-dioxin. Cardiovascular Toxicology, 2015, 15, 157-171.	1.1	10
3706	Experimental Strategies for Functional Annotation and Metabolism Discovery: Targeted Screening of Solute Binding Proteins and Unbiased Panning of Metabolomes. Biochemistry, 2015, 54, 909-931.	1.2	95
3707	Digital gene-expression of alfalfa saponin extract on laying hens. Genomics Data, 2015, 3, 97-99.	1.3	4

#	ARTICLE	IF	CITATIONS
3708	The KnownLeaf literature curation system captures knowledge about Arabidopsis leaf growth and development and facilitates integrated data mining. <i>Current Plant Biology</i> , 2015, 2, 1-11.	2.3	7
3709	Interactions of the Antiviral Factor Interferon Gamma-Inducible Protein 16 (IFI16) Mediate Immune Signaling and Herpes Simplex Virus-1 Immunosuppression. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2341-2356.	2.5	84
3710	Kinetics of glucosylated and non-glucosylated aryltetralin lignans in <i>Linum hairy</i> root cultures. <i>Phytochemistry</i> , 2015, 115, 70-78.	1.4	17
3711	A Comprehensive Membrane Interactome Mapping of Sho1p Reveals Fps1p as a Novel Key Player in the Regulation of the HOG Pathway in <i>S. cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2088-2103.	2.0	34
3712	Pantograph: A template-based method for genome-scale metabolic model reconstruction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550006.	0.3	29
3713	Incorporating computational resources in a cancer research program. <i>Human Genetics</i> , 2015, 134, 467-478.	1.8	2
3714	A look behind the screens: Characterization of the HSP70 family during osmotic stress in a non-model crop. <i>Journal of Proteomics</i> , 2015, 119, 10-20.	1.2	19
3715	Etiological treatment of Chagas disease patients with benznidazole lead to a sustained pro-inflammatory profile counterbalanced by modulatory events. <i>Immunobiology</i> , 2015, 220, 564-574.	0.8	22
3716	UDP-Arabinopyranose Mutase 3 is Required for Pollen Wall Morphogenesis in Rice ( <i>Oryza sativa</i> ). <i>Plant and Cell Physiology</i> , 2015, 56, 232-241.	1.5	45
3717	Temporal metabolomic responses of cultured HepG2 liver cells to high fructose and high glucose exposures. <i>Metabolomics</i> , 2015, 11, 707-721.	1.4	19
3718	Hierarchical organization of fluxes in <i>Escherichia coli</i> metabolic network: Using flux coupling analysis for understanding the physiological properties of metabolic genes. <i>Gene</i> , 2015, 561, 199-208.	1.0	6
3719	Relationship between honeybee nutrition and their microbial communities. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 921-933.	0.7	36
3720	Acetylome Analysis Reveals the Involvement of Lysine Acetylation in Photosynthesis and Carbon Metabolism in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Proteome Research</i> , 2015, 14, 1275-1286.	1.8	119
3721	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. <i>Proteomics</i> , 2015, 15, 1390-1404.	1.3	38
3722	Reconstructing the Roman London flavourscape: new insights into the exotic food plant trade using network and spatial analyses. <i>Journal of Archaeological Science</i> , 2015, 55, 244-252.	1.2	26
3723	Promises and Challenges of Big Data Computing in Health Sciences. <i>Big Data Research</i> , 2015, 2, 2-11.	2.6	185
3724	Genome-Wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2015, 8, 276-289.	3.9	16
3725	The immunological consequences of pasteurisation: Comparison of the response of human intestinally-derived cells to raw versus pasteurised milk. <i>International Dairy Journal</i> , 2015, 40, 67-72.	1.5	5



#	ARTICLE	IF	CITATIONS
3726	Molecular mechanisms of osteoarthritis using gene microarrays. <i>Acta Histochemica</i> , 2015, 117, 62-68.	0.9	20
3727	PhenomeExpress: A refined network analysis of expression datasets by inclusion of known disease phenotypes. <i>Scientific Reports</i> , 2015, 5, 8117.	1.6	25
3728	Chemomics: Network Reconstruction and Kinetics of Port Wine Aging. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 2576-2581.	2.4	18
3729	The Human Colostrum Whey Proteome Is Altered in Gestational Diabetes Mellitus. <i>Journal of Proteome Research</i> , 2015, 14, 512-520.	1.8	33
3730	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
3731	Recognition Mechanism between Lac Repressor and DNA with Correlation Network Analysis. <i>Journal of Physical Chemistry B</i> , 2015, 119, 2844-2856.	1.2	12
3732	Multi -omics and metabolic modelling pipelines: Challenges and tools for systems microbiology. <i>Microbiological Research</i> , 2015, 171, 52-64.	2.5	125
3733	Analysis of the hierarchical structure of the <i>B. subtilis</i> transcriptional regulatory network. <i>Molecular BioSystems</i> , 2015, 11, 930-941.	2.9	12
3734	Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. <i>Scientific Reports</i> , 2014, 4, 5576.	1.6	51
3735	Bacterial community shift in the coastal Gulf of Mexico salt-marsh sediment microcosm in vitro following exposure to the Mississippi Canyon Block 252 oil (MC252). <i>3 Biotech</i> , 2015, 5, 379-392.	1.1	40
3736	Proteome mining for drug target identification in <i>Listeria monocytogenes</i> strain EGD-e and structure-based virtual screening of a candidate drug target penicillin binding protein 4. <i>Journal of Microbiological Methods</i> , 2015, 111, 9-18.	0.7	23
3737	Succinylome Analysis Reveals the Involvement of Lysine Succinylation in Metabolism in Pathogenic <i>Mycobacterium tuberculosis</i> *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 796-811.	2.5	117
3738	MicroRNA expression profiling and functional annotation analysis of their targets associated with the malignant transformation of oral leukoplakia. <i>Gene</i> , 2015, 558, 271-277.	1.0	19
3739	Global correlation analysis for microRNA and gene expression profiles in human obesity. <i>Pathology Research and Practice</i> , 2015, 211, 361-368.	1.0	28
3740	Identification of rod- and cone-specific expression signatures to identify candidate genes for retinal disease. <i>Experimental Eye Research</i> , 2015, 132, 161-173.	1.2	5
3741	Chemotaxis by natural populations of coral reef bacteria. <i>ISME Journal</i> , 2015, 9, 1764-1777.	4.4	60
3742	Methylation of microRNA genes regulates gene expression in bisexual flower development in andromonoecious poplar. <i>Journal of Experimental Botany</i> , 2015, 66, 1891-1905.	2.4	55
3743	Transcriptional profiling analysis of individual kinase-deletion strains of fission yeast in response to nitrogen starvation. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1067-1083.	1.0	3

#	ARTICLE	IF	CITATIONS
3744	Integrative View of $\alpha$ 2,3-Sialyltransferases (ST3Gal) Molecular and Functional Evolution in Deuterostomes: Significance of Lineage-Specific Losses. <i>Molecular Biology and Evolution</i> , 2015, 32, 906-927.	3.5	40
3745	<scp>microRNAs</scp>: role in leukemia and their computational perspective. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 65-78.	3.2	12
3746	Bioaccumulation, Biotransformation, and Toxicity of BDE-47, 6-OH-BDE-47, and 6-MeO-BDE-47 in Early Life-Stages of Zebrafish (<i>Danio rerio</i>). <i>Environmental Science &amp; Technology</i> , 2015, 49, 1823-1833.	4.6	72
3747	Determining the Plasmodium vivax VCG-1 strain blood stage proteome. <i>Journal of Proteomics</i> , 2015, 113, 268-280.	1.2	32
3748	An association analysis between psychophysical characteristics and genome-wide gene expression changes in human adaptation to the extreme climate at the Antarctic Dome Argus. <i>Molecular Psychiatry</i> , 2015, 20, 536-544.	4.1	5
3749	Comprehensive analysis of genes, pathways, and TFs in nonsmoking Taiwan females with lung cancer. <i>Experimental Lung Research</i> , 2015, 41, 74-83.	0.5	9
3750	A bidirectional drug repositioning approach for Parkinson's disease through network-based inference. <i>Biochemical and Biophysical Research Communications</i> , 2015, 457, 280-287.	1.0	11
3751	Resistant Microbial Cooccurrence Patterns Inferred by Network Topology. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2090-2097.	1.4	104
3752	Divergence across diet, time and populations rules out parallel evolution in the gut microbiomes of Trinidadian guppies. <i>ISME Journal</i> , 2015, 9, 1508-1522.	4.4	133
3753	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. <i>Circulation</i> , 2015, 131, 536-549.	1.6	65
3754	The Product Space Revisited: China's Trade Profile. <i>World Economy</i> , 2015, 38, 1368-1386.	1.4	20
3755	FlowerNet: A Gene Expression Correlation Network for Anther and Pollen Development $\hat{A}$ . <i>Plant Physiology</i> , 2015, 167, 1717-1730.	2.3	48
3756	Potential microRNA-mediated oncogenic intercellular communication revealed by pan-cancer analysis. <i>Scientific Reports</i> , 2015, 4, 7097.	1.6	26
3757	The Role of Host Phylogeny Varies in Shaping Microbial Diversity in the Hindguts of Lower Termites. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1059-1070.	1.4	87
3758	Metabolomics and Diabetes: Analytical and Computational Approaches. <i>Diabetes</i> , 2015, 64, 718-732.	0.3	146
3759	Human Nek7-interactor RGS2 is required for mitotic spindle organization. <i>Cell Cycle</i> , 2015, 14, 656-667.	1.3	13
3760	Bacterial Diversity in the South Adriatic Sea during a Strong, Deep Winter Convection Year. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1715-1726.	1.4	40
3761	Myotubularin-related Proteins 3 and 4 Interact with Polo-like Kinase 1 and Centrosomal Protein of 55 kDa to Ensure Proper Abscission. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 946-960.	2.5	17

#	ARTICLE	IF	CITATIONS
3762	Basonuclin-1 modulates epithelial plasticity and TGF- $\beta$ 1-induced loss of epithelial cell integrity. <i>Oncogene</i> , 2015, 34, 1185-1195.	2.6	7
3763	Network analysis suggests a potentially "evil" alliance of opportunistic pathogens inhibited by a cooperative network in human milk bacterial communities. <i>Scientific Reports</i> , 2015, 5, 8275.	1.6	46
3764	The RNA helicase DDX6 regulates cell-fate specification in neural stem cells via miRNAs. <i>Nucleic Acids Research</i> , 2015, 43, 2638-2654.	6.5	48
3765	Recombinant mouse prion protein alone or in combination with lipopolysaccharide alters expression of innate immunity genes in the colon of mice. <i>Prion</i> , 2015, 9, 59-73.	0.9	6
3766	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 187-202.	1.5	17
3767	ocsESTdb: a database of oil crop seed EST sequences for comparative analysis and investigation of a global metabolic network and oil accumulation metabolism. <i>BMC Plant Biology</i> , 2015, 15, 19.	1.6	15
3768	Comparative RNA-Seq analysis reveals pervasive tissue-specific alternative polyadenylation in <i>Caenorhabditis elegans</i> intestine and muscles. <i>BMC Biology</i> , 2015, 13, 4.	1.7	70
3769	Inferring Ancestral Pueblo Social Networks from Simulation in the Central Mesa Verde. <i>Journal of Archaeological Method and Theory</i> , 2015, 22, 144-181.	1.4	30
3770	Diabetes associated metabolomic perturbations in NOD mice. <i>Metabolomics</i> , 2015, 11, 425-437.	1.4	33
3771	Identification of Differently Expressed Genes with Specific SNP Loci for Breast Cancer by the Integration of SNP and Gene Expression Profiling Analyses. <i>Pathology and Oncology Research</i> , 2015, 21, 469-475.	0.9	7
3772	A genome analysis based on repeat sharing gene networks. <i>Natural Computing</i> , 2015, 14, 403-420.	1.8	6
3773	Systems biologic analysis of T regulatory cells genetic pathways in murine primary biliary cirrhosis. <i>Journal of Autoimmunity</i> , 2015, 59, 26-37.	3.0	45
3774	Statistical model checking for biological systems. <i>International Journal on Software Tools for Technology Transfer</i> , 2015, 17, 351-367.	1.7	33
3775	Revealing the Strong Functional Association of adipor2 and cdh13 with adipog: A Gene Network Study. <i>Cell Biochemistry and Biophysics</i> , 2015, 71, 1445-1456.	0.9	6
3776	Unlocking proteomic heterogeneity in complex diseases through visual analytics. <i>Proteomics</i> , 2015, 15, 1405-1418.	1.3	12
3777	Genetic associations with brain cortical thickness in multiple sclerosis. <i>Genes, Brain and Behavior</i> , 2015, 14, 217-227.	1.1	31
3778	Evolutionary changes in promoter and enhancer activity during human corticogenesis. <i>Science</i> , 2015, 347, 1155-1159.	6.0	258
3779	A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. <i>Nucleic Acids Research</i> , 2015, 43, 1965-1984.	6.5	86

#	ARTICLE	IF	CITATIONS
3780	Can we trust untargeted metabolomics? Results of the metabo-ring initiative, a large-scale, multi-instrument inter-laboratory study. <i>Metabolomics</i> , 2015, 11, 807-821.	1.4	112
3781	Rheumatoid Arthritis Candidate Genes Identification by Investigating Core and Periphery Interaction Structures. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2015, , 87-96.	0.2	2
3782	Metabolic patterns associated with the seasonal rhythm of seed survival after dehydration in germinated seeds of <i>Schismus arabicus</i> . <i>BMC Plant Biology</i> , 2015, 15, 37.	1.6	1
3783	The shared microbiota of humans and companion animals as evaluated from <i>Staphylococcus</i> carriage sites. <i>Microbiome</i> , 2015, 3, 2.	4.9	95
3784	White adipose tissue reference network: a knowledge resource for exploring health-relevant relations. <i>Genes and Nutrition</i> , 2015, 10, 439.	1.2	9
3785	Genomic analysis of host " Peste des petits ruminants vaccine viral transcriptome uncovers transcription factors modulating immune regulatory pathways. <i>Veterinary Research</i> , 2015, 46, 15.	1.1	50
3786	Identification of Novel Long Noncoding RNAs Underlying Vertebrate Cardiovascular Development. <i>Circulation</i> , 2015, 131, 1278-1290.	1.6	185
3787	A web-tool for visualizing quantitative protein-protein interaction data. <i>Proteomics</i> , 2015, 15, 1432-1436.	1.3	30
3788	Exome sequencing identifies frequent mutation of MLL2 in non-small cell lung carcinoma from Chinese patients. <i>Scientific Reports</i> , 2014, 4, 6036.	1.6	33
3789	Mining Host-Pathogen Protein Interactions to Characterize <i>Burkholderia mallei</i> Infectivity Mechanisms. <i>PLoS Computational Biology</i> , 2015, 11, e1004088.	1.5	34
3790	Seedling development traits in <i>Brassica napus</i> examined by gene expression analysis and association mapping. <i>BMC Plant Biology</i> , 2015, 15, 136.	1.6	28
3791	Network reconstruction of platelet metabolism identifies metabolic signature for aspirin resistance. <i>Scientific Reports</i> , 2014, 4, 3925.	1.6	45
3792	Network Analyses Reveal Novel Aspects of ALS Pathogenesis. <i>PLoS Genetics</i> , 2015, 11, e1005107.	1.5	45
3793	Muscle Segment Homeobox Genes Direct Embryonic Diapause by Limiting Inflammation in the Uterus*. <i>Journal of Biological Chemistry</i> , 2015, 290, 15337-15349.	1.6	18
3794	Explanation in Systems Biology: Is It All About Mechanisms?. <i>History, Philosophy and Theory of the Life Sciences</i> , 2015, , 47-72.	0.4	8
3795	The trans-cis isomerization of Ni( $\dot{i}$ -2-TEMPO) <sub>2</sub> : Interconnections and conformational complexity. <i>Inorganica Chimica Acta</i> , 2015, 436, 220-229.	1.2	2
3796	Molecular and clinical disease of comorbidities in exacerbated COPD patients. <i>European Respiratory Journal</i> , 2015, 46, 1001-1010.	3.1	32
3797	Selective multifaceted E3 ubiquitin ligases barricade extreme defense: Potential therapeutic targets for neurodegeneration and ageing. <i>Ageing Research Reviews</i> , 2015, 24, 138-159.	5.0	19

#	ARTICLE	IF	CITATIONS
3798	Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. <i>Biophysical Journal</i> , 2015, 109, 1295-1306.	0.2	11
3799	MicroRNA expression profile of surgical removed mandibular bone tissues from patients with mandibular prognathism. <i>Journal of Surgical Research</i> , 2015, 198, 127-134.	0.8	11
3800	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. <i>Nature Communications</i> , 2015, 6, 7618.	5.8	361
3801	Lipidome and Transcriptome Profiling of Pneumolysin Intoxication Identifies Networks Involved in Statin-Conferred Protection of Airway Epithelial Cells. <i>Scientific Reports</i> , 2015, 5, 10624.	1.6	4
3802	Integrated in silico and experimental methods revealed that Arctigenin inhibited angiogenesis and HCT116 cell migration and invasion through regulating the H1F4A and Wnt/ $\beta$ -catenin pathway. <i>Molecular BioSystems</i> , 2015, 11, 2878-2884.	2.9	8
3803	Mistargeted mitochondrial proteins activate a proteostatic response in the cytosol. <i>Nature</i> , 2015, 524, 485-488.	13.7	348
3804	Influence of seawater intrusion on microbial communities in groundwater. <i>Science of the Total Environment</i> , 2015, 532, 337-343.	3.9	38
3805	Systematic discovery of cofactor motifs from ChIP-seq data by SIOMICS. <i>Methods</i> , 2015, 79-80, 47-51.	1.9	23
3806	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. <i>Journal of Proteomics</i> , 2015, 118, 49-62.	1.2	64
3807	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. <i>Autophagy</i> , 2015, 11, 1668-1687.	4.3	107
3808	Circulating microRNAs in obese and lean heart failure patients: A case-control study with computational target prediction analysis. <i>Gene</i> , 2015, 574, 1-10.	1.0	21
3809	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. <i>Scientific Reports</i> , 2015, 5, 12074.	1.6	0
3810	Functional Proteomics Identifies Acinus L as a Direct Insulin- and Amino Acid-Dependent Mammalian Target of Rapamycin Complex 1 (mTORC1) Substrate. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2042-2055.	2.5	18
3811	Medicinal plants used by Burundian traditional healers for the treatment of microbial diseases. <i>Journal of Ethnopharmacology</i> , 2015, 173, 338-351.	2.0	46
3812	Cellular Proteome Dynamics during Differentiation of Human Primary Myoblasts. <i>Journal of Proteome Research</i> , 2015, 14, 3348-3361.	1.8	30
3813	Diversification of memory B cells drives the continuous adaptation of secretory antibodies to gut microbiota. <i>Nature Immunology</i> , 2015, 16, 880-888.	7.0	192
3814	Application of RNAi to Genomic Drug Target Validation in Schistosomes. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003801.	1.3	33
3815	Quantifying MCMC Exploration of Phylogenetic Tree Space. <i>Systematic Biology</i> , 2015, 64, 472-491.	2.7	71

#	ARTICLE	IF	CITATIONS
3816	Ligand-Specific Transcriptional Mechanisms Underlie Aryl Hydrocarbon Receptor-Mediated Developmental Toxicity of Oxygenated PAHs. <i>Toxicological Sciences</i> , 2015, 147, 397-411.	1.4	54
3817	Identification of dysregulated miRNAs and their regulatory signature in glioma patients using the partial least squares method. <i>Experimental and Therapeutic Medicine</i> , 2015, 9, 167-171.	0.8	13
3818	Extension of three-dimensional activity cliff information through systematic mapping of active analogs. <i>RSC Advances</i> , 2015, 5, 43006-43015.	1.7	9
3819	Drug Repositioning for Diabetes Based on 'Omics' Data Mining. <i>PLoS ONE</i> , 2015, 10, e0126082.	1.1	74
3820	Genome-wide expression analyses of the stationary phase model of ageing in yeast. <i>Mechanisms of Ageing and Development</i> , 2015, 149, 65-74.	2.2	11
3821	In silico identification of AMPylating enzymes and study of their divergent evolution. <i>Scientific Reports</i> , 2015, 5, 10804.	1.6	32
3822	H7N9 T-cell epitopes that mimic human sequences are less immunogenic and may induce Treg-mediated tolerance. <i>Human Vaccines and Immunotherapeutics</i> , 2015, 11, 2241-2252.	1.4	40
3823	Hyperscape: visualization for complex biological networks. <i>Bioinformatics</i> , 2015, 31, 3390-3391.	1.8	7
3824	Microbial diversity associated with copepods in the North Atlantic subtropical gyre. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	55
3825	A knowledgebase resource for interleukin-17 family mediated signaling. <i>Journal of Cell Communication and Signaling</i> , 2015, 9, 291-296.	1.8	25
3826	Systems approach for the selection of micro-RNAs as therapeutic biomarkers of anti-EGFR monoclonal antibody treatment in colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 8013.	1.6	6
3827	Citrullination of myofilament proteins in heart failure. <i>Cardiovascular Research</i> , 2015, 108, 232-242.	1.8	64
3828	A knowledge driven supervised learning approach to identify gene network of differentially up-regulated genes during neuronal senescence in <i>Rattus norvegicus</i> . <i>BioSystems</i> , 2015, 135, 9-14.	0.9	2
3829	Regulatory MicroRNA Networks: Complex Patterns of Target Pathways for Disease-related and Housekeeping MicroRNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 159-168.	3.0	10
3830	Persistent effects of early infant diet and associated microbiota on the juvenile immune system. <i>Gut Microbes</i> , 2015, 6, 284-289.	4.3	26
3831	Bioinformatic analysis of specific genes in diabetic nephropathy. <i>Renal Failure</i> , 2015, 37, 1219-1224.	0.8	6
3832	OMICS for Tumor Biomarker Research. <i>Biomarkers in Disease</i> , 2015, , 3-30.	0.0	3
3833	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676

#	ARTICLE	IF	CITATIONS
3834	Inbreeding Affects Gene Expression Differently in Two Self-Incompatible <i>Arabidopsis lyrata</i> Populations with Similar Levels of Inbreeding Depression. <i>Molecular Biology and Evolution</i> , 2015, 32, 2036-2047.	3.5	15
3835	A prevalent peptide-binding domain guides ribosomal natural product biosynthesis. <i>Nature Chemical Biology</i> , 2015, 11, 564-570.	3.9	288
3836	MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. <i>Bioinformatics</i> , 2015, 31, i284-i292.	1.8	87
3837	Big Data Provenance Analysis and Visualization. , 2015, , .		8
3838	libRoadRunner: a high performance SBML simulation and analysis library. <i>Bioinformatics</i> , 2015, 31, 3315-3321.	1.8	130
3839	Dynamic Proteome Response of <i>Pseudomonas aeruginosa</i> to Tobramycin Antibiotic Treatment. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2126-2137.	2.5	37
3840	System-wide identification of wild-type SUMO-2 conjugation sites. <i>Nature Communications</i> , 2015, 6, 7289.	5.8	97
3841	Detecting pan-cancer conserved microRNA modules from microRNA expression profiles across multiple cancers. <i>Molecular BioSystems</i> , 2015, 11, 2227-2237.	2.9	6
3842	SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets. <i>Nucleic Acids Research</i> , 2015, 43, W276-W282.	6.5	24
3843	Plasma membrane-associated superstructure: Have we overlooked a new type of organelle in eukaryotic cells?. <i>Journal of Theoretical Biology</i> , 2015, 380, 346-358.	0.8	1
3844	semPlot: Unified Visualizations of Structural Equation Models. <i>Structural Equation Modeling</i> , 2015, 22, 474-483.	2.4	163
3845	Regulation of the transcriptional program by DNA methylation during human $\hat{1}\hat{2}$ T-cell development. <i>Nucleic Acids Research</i> , 2015, 43, 760-774.	6.5	43
3846	Analysis of the Human Adult Urinary Metabolome Variations with Age, Body Mass Index, and Gender by Implementing a Comprehensive Workflow for Univariate and OPLS Statistical Analyses. <i>Journal of Proteome Research</i> , 2015, 14, 3322-3335.	1.8	886
3847	Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. <i>Frontiers in Genetics</i> , 2015, 6, 117.	1.1	23
3848	An integrated RNA-Seq and network study reveals a complex regulation process of rice embryo during seed germination. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 176-181.	1.0	20
3849	Examining the Evolution of the Regulatory Circuit Controlling Secondary Metabolism and Development in the Fungal Genus <i>Aspergillus</i> . <i>PLoS Genetics</i> , 2015, 11, e1005096.	1.5	70
3850	CoVennTree: a new method for the comparative analysis of large datasets. <i>Frontiers in Genetics</i> , 2015, 6, 43.	1.1	8
3851	A Role for the Budding Yeast Separase, Esp1, in Ty1 Element Retrotransposition. <i>PLoS Genetics</i> , 2015, 11, e1005109.	1.5	16



#	ARTICLE	IF	CITATIONS
3852	Neural architecture underlying classification of face perception paradigms. <i>NeuroImage</i> , 2015, 119, 70-80.	2.1	28
3853	S100A4 and its role in metastasis – computational integration of data on biological networks. <i>Molecular BioSystems</i> , 2015, 11, 2238-2246.	2.9	14
3854	Evolutionary trends and functional anatomy of the human expanded autophagy network. <i>Autophagy</i> , 2015, 11, 1652-1667.	4.3	21
3855	Recent Coselection in Human Populations Revealed by Protein-Protein Interaction Network. <i>Genome Biology and Evolution</i> , 2015, 7, 136-153.	1.1	19
3856	3-way Networks: Application of Hypergraphs for Modelling Increased Complexity in Comparative Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004079.	1.5	29
3857	Systems Pharmacology Dissection of the Anti-Inflammatory Mechanism for the Medicinal Herb Folium <i>Eriobotryae</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 2913-2941.	1.8	41
3858	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human neuroblastoma cells. <i>Journal of Proteomics</i> , 2015, 123, 42-53.	1.2	62
3859	Identification of commonly dysregulated genes in colorectal cancer by integrating analysis of RNA-Seq data and qRT-PCR validation. <i>Cancer Gene Therapy</i> , 2015, 22, 278-284.	2.2	27
3860	The small RNA content of human sperm reveals pseudogene-derived piRNAs complementary to protein-coding genes. <i>Rna</i> , 2015, 21, 1085-1095.	1.6	83
3861	Shotgun analysis of plasma fibrin clot-bound proteins in patients with acute myocardial infarction. <i>Thrombosis Research</i> , 2015, 135, 754-759.	0.8	10
3862	A network pharmacology study of Sendeng-4, a Mongolian medicine. <i>Chinese Journal of Natural Medicines</i> , 2015, 13, 108-118.	0.7	6
3863	Interplay between copper and zinc homeostasis through the transcriptional regulator Zur in <i>Enterococcus faecalis</i> . <i>Metallomics</i> , 2015, 7, 1137-1145.	1.0	35
3864	Identifying functional gene regulatory network phenotypes underlying single cell transcriptional variability. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 87-98.	1.4	19
3865	Network decomposition based large-scale reverse engineering of gene regulatory network. <i>Neurocomputing</i> , 2015, 160, 213-227.	3.5	8
3866	Data integration reveals key homeostatic mechanisms following low dose radiation exposure. <i>Toxicology and Applied Pharmacology</i> , 2015, 285, 1-11.	1.3	13
3867	Development of a tandem affinity phosphoproteomic method with motif selectivity and its application in analysis of signal transduction networks. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 988, 166-174.	1.2	10
3868	Choose wisely: Network, ontology and annotation resources for the analysis of <i>Staphylococcus aureus</i> omics data. <i>International Journal of Medical Microbiology</i> , 2015, 305, 339-347.	1.5	3
3869	Enrichment pathway analysis. The inflammatory genetic background in Bipolar Disorder. <i>Journal of Affective Disorders</i> , 2015, 179, 88-94.	2.0	44

#	ARTICLE	IF	CITATIONS
3870	Mixed-effects model of epithelialâ€“mesenchymal transition reveals rewiring of signaling networks. <i>Cellular Signalling</i> , 2015, 27, 1413-1425.	1.7	25
3871	Systemic alterations in the metabolome of diabetic NOD mice delineate increased oxidative stress accompanied by reduced inflammation and hypertriglyceremia. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 308, E978-E989.	1.8	46
3872	Personalized microbial network inference via co-regularized spectral clustering. <i>Methods</i> , 2015, 83, 28-35.	1.9	16
3873	Coinheritance of COL4A5 and MYO1E mutations accentuate the severity of kidney disease. <i>Pediatric Nephrology</i> , 2015, 30, 1459-1465.	0.9	38
3874	Identification and isolation of a dermal lineage with intrinsic fibrogenic potential. <i>Science</i> , 2015, 348, aaa2151.	6.0	520
3875	Insights into protein interaction networks reveal non-receptor kinases as significant druggable targets for psoriasis. <i>Gene</i> , 2015, 566, 138-147.	1.0	8
3876	Identification of <i>Plasmodium falciparum</i> apicoplast-targeted tRNA-guanine transglycosylase and its potential inhibitors using comparative genomics, molecular modelling, docking and simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2404-2420.	2.0	8
3877	Analysis of swine fecal microbiota at various growth stages. <i>Archives of Microbiology</i> , 2015, 197, 753-759.	1.0	68
3878	MPTPâ€™s Pathway of Toxicity Indicates Central Role of Transcription Factor SP1. <i>Archives of Toxicology</i> , 2015, 89, 743-755.	1.9	33
3879	Whole transcriptome responses among females of the filariasis and arbovirus vector mosquito <i>Culex pipiens</i> implicate TGF- $\beta$ 2 signaling and chromatin modification as key drivers of diapause induction. <i>Functional and Integrative Genomics</i> , 2015, 15, 439-447.	1.4	35
3880	Anther proteomic characterization in temperature sensitive Bainong male sterile wheat. <i>Biologia Plantarum</i> , 2015, 59, 273-282.	1.9	3
3881	Phenome-Wide Association Studies: Leveraging Comprehensive Phenotypic and Genotypic Data for Discovery. <i>Current Genetic Medicine Reports</i> , 2015, 3, 92-100.	1.9	39
3882	Human cytomegalovirus pUL97 kinase induces global changes in the infected cell phosphoproteome. <i>Proteomics</i> , 2015, 15, 2006-2022.	1.3	39
3883	More than Skin Deep: Functional Genomic Basis for Resistance to Amphibian Chytridiomycosis. <i>Genome Biology and Evolution</i> , 2015, 7, 286-298.	1.1	110
3884	Comprehensive Profiling of the Rice Ubiquitome Reveals the Significance of Lysine Ubiquitination in Young Leaves. <i>Journal of Proteome Research</i> , 2015, 14, 2017-2025.	1.8	74
3885	Integrated miRNA and mRNA expression profiling to identify mRNA targets of dysregulated miRNAs in non-obstructive azoospermia. <i>Scientific Reports</i> , 2015, 5, 7922.	1.6	62
3887	Investigating the utility of clinical outcome-guided mutual information network in network-based Cox regression. <i>BMC Systems Biology</i> , 2015, 9, S8.	3.0	8
3888	Comparative functional pan-genome analyses to build connections between genomic dynamics and phenotypic evolution in polycyclic aromatic hydrocarbon metabolism in the genus <i>Mycobacterium</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 21.	3.2	38

#	ARTICLE	IF	CITATIONS
3889	Identification of gene co-expression clusters in liver tissues from multiple porcine populations with high and low backfat androstenone phenotype. <i>BMC Genetics</i> , 2015, 16, 21.	2.7	5
3890	Genome-wide detection and characterization of positive selection in Korean Native Black Pig from Jeju Island. <i>BMC Genetics</i> , 2015, 16, 3.	2.7	18
3891	Integromics network meta-analysis on cardiac aging offers robust multi-layer modular signatures and reveals micronome synergism. <i>BMC Genomics</i> , 2015, 16, 147.	1.2	19
3892	Comparative study of the protein profiles of Sunki mandarin and Rangpur lime plants in response to water deficit. <i>BMC Plant Biology</i> , 2015, 15, 69.	1.6	25
3893	New insights into the genetic networks affecting seed fatty acid concentrations in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2015, 15, 91.	1.6	73
3894	Effects of statin on circulating microRNAome and predicted function regulatory network in patients with unstable angina. <i>BMC Medical Genomics</i> , 2015, 8, 12.	0.7	19
3895	New interaction partners for Nek4.1 and Nek4.2 isoforms: from the DNA damage response to RNA splicing. <i>Proteome Science</i> , 2015, 13, 11.	0.7	22
3896	Constitutive activation of oncogenic PDGFR $\beta$ -mutant proteins occurring in GIST patients induces receptor mislocalisation and alters PDGFR $\beta$ signalling characteristics. <i>Cell Communication and Signaling</i> , 2015, 13, 21.	2.7	27
3897	Wormpath: searching for molecular interaction networks in <i>Caenorhabditis elegans</i> . <i>Source Code for Biology and Medicine</i> , 2015, 10, 5.	1.7	0
3898	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. <i>Genome Biology</i> , 2015, 16, 19.	3.8	60
3899	Characterization of the immunophenotypes and antigenomes of colorectal cancers reveals distinct tumor escape mechanisms and novel targets for immunotherapy. <i>Genome Biology</i> , 2015, 16, 64.	3.8	433
3900	Integrated analysis reveals microRNA networks coordinately expressed with key proteins in breast cancer. <i>Genome Medicine</i> , 2015, 7, 21.	3.6	34
3901	miREC: a database of miRNAs involved in the development of endometrial cancer. <i>BMC Research Notes</i> , 2015, 8, 104.	0.6	10
3902	Systems biology approaches for advancing the discovery of effective drug combinations. <i>Journal of Cheminformatics</i> , 2015, 7, 7.	2.8	109
3903	K-core decomposition of a protein domain co-occurrence network reveals lower cancer mutation rates for interior cores. <i>Journal of Clinical Bioinformatics</i> , 2015, 5, 1.	1.2	16
3904	The $d_{J/S}$ Ratio Test Reveals Hundreds of Novel Putative Cancer Drivers. <i>Molecular Biology and Evolution</i> , 2015, 32, 2181-2185.	3.5	7
3905	Characterization of Skin Aging-Associated Secreted Proteins (SAASP) Produced by Dermal Fibroblasts Isolated from Intrinsically Aged Human Skin. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1954-1968.	0.3	152
3906	Transposon mutagenesis identifies genetic drivers of BrafV600E melanoma. <i>Nature Genetics</i> , 2015, 47, 486-495.	9.4	61

#	ARTICLE	IF	CITATIONS
3907	Hsf and Hsp gene families in <i>Populus</i> : genome-wide identification, organization and correlated expression during development and in stress responses. <i>BMC Genomics</i> , 2015, 16, 181.	1.2	90
3908	Transcriptional events co-regulated by hypoxia and cold stresses in Zebrafish larvae. <i>BMC Genomics</i> , 2015, 16, 385.	1.2	92
3909	Systems biology approach reveals possible evolutionarily conserved moonlighting functions for enolase. <i>Computational Biology and Chemistry</i> , 2015, 58, 1-8.	1.1	18
3910	PqqD Is a Novel Peptide Chaperone That Forms a Ternary Complex with the Radical S-Adenosylmethionine Protein PqqE in the Pyrroloquinoline Quinone Biosynthetic Pathway. <i>Journal of Biological Chemistry</i> , 2015, 290, 12908-12918.	1.6	72
3911	Systems biology approaches to defining transcription regulatory networks in halophilic archaea. <i>Methods</i> , 2015, 86, 102-114.	1.9	16
3912	Visual Analytics of Signalling Pathways Using Time Profiles. <i>Advances in Experimental Medicine and Biology</i> , 2015, 823, 3-22.	0.8	0
3913	C<scp>o</scp>R<scp>eg</scp>N<scp>et</scp>: reconstruction and integrated analysis of co-regulatory networks. <i>Bioinformatics</i> , 2015, 31, 3066-3068.	1.8	46
3914	A molecular systems approach to modelling human skin pigmentation: identifying underlying pathways and critical components. <i>BMC Research Notes</i> , 2015, 8, 170.	0.6	9
3915	Genetic variation of transgenerational plasticity of offspring germination in response to salinity stress and the seed transcriptome of <i>Medicago truncatula</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 59.	3.2	56
3916	Resistant starch diet induces change in the swine microbiome and a predominance of beneficial bacterial populations. <i>Microbiome</i> , 2015, 3, 16.	4.9	132
3917	Identification of ncRNAs as potential therapeutic targets in multiple sclerosis through differential ncRNA â€“ mRNA network analysis. <i>BMC Genomics</i> , 2015, 16, 250.	1.2	17
3918	Latent Pathways Identification by Microarray Expression Profiles in Thyroid-Associated Ophthalmopathy Patients. <i>Endocrine Pathology</i> , 2015, 26, 200-210.	5.2	9
3919	Rv2031c of <i>Mycobacterium tuberculosis</i> : a master regulator of Rv2028â€“Rv2031 (HspX) operon. <i>Frontiers in Microbiology</i> , 2015, 6, 351.	1.5	20
3920	Vertical Distribution of Functional Potential and Active Microbial Communities in Meromictic Lake Kivu. <i>Microbial Ecology</i> , 2015, 70, 596-611.	1.4	52
3921	Dynamics of gene expression patterns during early development of the European seabass ( <i>Dicentrarchus labrax</i> ). <i>Physiological Genomics</i> , 2015, 47, 158-169.	1.0	23
3922	Are There Genetic Paths Common to Obesity, Cardiovascular Disease Outcomes, and Cardiovascular Risk Factors?. <i>Circulation Research</i> , 2015, 116, 909-922.	2.0	106
3923	Boolean network model for GPR142 against Type 2 diabetes and relative dynamic change ratio analysis using systems and biological circuits approach. <i>Systems and Synthetic Biology</i> , 2015, 9, 45-54.	1.0	21
3924	Potato leafroll virus structural proteins manipulate overlapping, yet distinct protein interaction networks during infection. <i>Proteomics</i> , 2015, 15, 2098-2112.	1.3	22

#	ARTICLE	IF	CITATIONS
3925	Identification of intrinsically disordered regions in PTEN and delineation of its function via a network approach. <i>Methods</i> , 2015, 77-78, 69-74.	1.9	14
3926	Human Disease Modeling Reveals Integrated Transcriptional and Epigenetic Mechanisms of NOTCH1 Haploinsufficiency. <i>Cell</i> , 2015, 160, 1072-1086.	13.5	173
3927	RNA Sequencing of Laser-Capture Microdissected Compartments of the Maize Kernel Identifies Regulatory Modules Associated with Endosperm Cell Differentiation. <i>Plant Cell</i> , 2015, 27, 513-531.	3.1	206
3928	CHCHD2 Is Coamplified with EGFR in NSCLC and Regulates Mitochondrial Function and Cell Migration. <i>Molecular Cancer Research</i> , 2015, 13, 1119-1129.	1.5	43
3929	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. <i>Genome Research</i> , 2015, 25, 655-666.	2.4	95
3930	Analysing human metabolic networks using metabolomics. , 2015, , 85-114.		1
3931	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. <i>Oncogene</i> , 2015, 34, 2764-2776.	2.6	63
3932	Metabolomics in chemical ecology. <i>Natural Product Reports</i> , 2015, 32, 937-955.	5.2	96
3933	Comparison of human cell signaling pathway databases’ evolution, drawbacks and challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	86
3934	Mass spectrometry tools and workflows for revealing microbial chemistry. <i>Analyst</i> , The, 2015, 140, 4949-4966.	1.7	39
3935	Molecular differences between stromal cell populations from deciduous and permanent human teeth. <i>Stem Cell Research and Therapy</i> , 2015, 6, 59.	2.4	19
3936	Genomic distribution and possible functional roles of putative G-quadruplex motifs in two subspecies of <i>Oryza sativa</i> . <i>Computational Biology and Chemistry</i> , 2015, 56, 122-130.	1.1	26
3937	Phosphoproteome Analysis Links Protein Phosphorylation to Cellular Remodeling and Metabolic Adaptation during <i>Magnaporthe oryzae</i> Appressorium Development. <i>Journal of Proteome Research</i> , 2015, 14, 2408-2424.	1.8	42
3938	Transcriptome profiling identifies p53 as a key player during calreticulin deficiency: Implications in lipid accumulation. <i>Cell Cycle</i> , 2015, 14, 2274-2284.	1.3	16
3939	Targets of drugs are generally and targets of drugs having side effects are specifically good spreaders of human interactome perturbations. <i>Scientific Reports</i> , 2015, 5, 10182.	1.6	22
3940	NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. <i>Nature Protocols</i> , 2015, 10, 823-844.	5.5	779
3941	The Transcriptome and Terpene Profile of <i>Eucalyptus grandis</i> Reveals Mechanisms of Defense Against the Insect Pest, <i>Leptocybe invasa</i> . <i>Plant and Cell Physiology</i> , 2015, 56, 1418-1428.	1.5	55
3942	Mechanism-Based Classification of PAH Mixtures to Predict Carcinogenic Potential. <i>Toxicological Sciences</i> , 2015, 146, 135-145.	1.4	23

#	ARTICLE	IF	CITATIONS
3943	Exploring the Molecular Mechanism and Biomarkers of Liver Cancer Based on Gene Expression Microarray. <i>Pathology and Oncology Research</i> , 2015, 21, 1077-1083.	0.9	9
3944	Molecular Cytotoxicity Mechanisms of Allyl Alcohol (Acrolein) in Budding Yeast. <i>Chemical Research in Toxicology</i> , 2015, 28, 1246-1264.	1.7	22
3945	Bioinformatics analyses of significant prognostic risk markers for thyroid papillary carcinoma. <i>Tumor Biology</i> , 2015, 36, 7457-7463.	0.8	14
3946	Quantitative Proteomics Analysis Reveals Novel Insights into Mechanisms of Action of Long Noncoding RNA Hox Transcript Antisense Intergenic RNA (HOTAIR) in HeLa Cells*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1447-1463.	2.5	44
3947	Gene expression profiling via bioinformatics analysis reveals biomarkers in laryngeal squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2015, 12, 2457-2464.	1.1	8
3948	Screening for characteristic microRNAs between pre-invasive and invasive stages of cervical cancer. <i>Molecular Medicine Reports</i> , 2015, 12, 55-62.	1.1	7
3949	Unravelling the architecture and dynamics of tropane alkaloid biosynthesis pathways using metabolite correlation networks. <i>Phytochemistry</i> , 2015, 116, 94-103.	1.4	17
3950	KAPPA, a simple algorithm for discovery and clustering of proteins defined by a key amino acid pattern: a case study of the cysteine-rich proteins. <i>Bioinformatics</i> , 2015, 31, 1716-1723.	1.8	6
3951	Plant Omics Data Center: An Integrated Web Repository for Interspecies Gene Expression Networks with NLP-Based Curation. <i>Plant and Cell Physiology</i> , 2015, 56, e9-e9.	1.5	55
3952	Identification of proteins responsible for adriamycin resistance in breast cancer cells using proteomics analysis. <i>Scientific Reports</i> , 2015, 5, 9301.	1.6	48
3953	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 815-822.	1.9	103
3954	CD11c+CD123Low Dendritic Cell Subset and the Triad TNF- $\alpha$ /IL-17A/IFN- $\gamma$ Integrate Mucosal and Peripheral Cellular Responses in HIV Patients With High-Grade Anal Intraepithelial Neoplasia. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2015, 68, 112-122.	0.9	17
3955	A pathway-based approach for identifying biomarkers of tumor progression to trastuzumab-resistant breast cancer. <i>Cancer Letters</i> , 2015, 356, 880-890.	3.2	31
3956	Identification of genes associated with disc degeneration using bioinformatics. <i>Biotechnic and Histochemistry</i> , 2015, 90, 353-360.	0.7	9
3957	Identification of potential therapeutic target genes, key miRNAs and mechanisms in acute myeloid leukemia based on bioinformatics analysis. <i>Medical Oncology</i> , 2015, 32, 152.	1.2	9
3958	Proteomics profiling of ethylene-induced tomato flower pedicel abscission. <i>Journal of Proteomics</i> , 2015, 121, 67-87.	1.2	27
3959	Copy number variability analysis of pharmacogenes in patients with lymphoma, leukemia, hepatocellular, and lung carcinoma using The Cancer Genome Atlas data. <i>Pharmacogenetics and Genomics</i> , 2015, 25, 1-7.	0.7	16
3960	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	1.8	38



#	ARTICLE	IF	CITATIONS
3961	Deciphering complex patterns of class II HLA peptide cross-reactivity via hierarchical grouping. <i>Immunology and Cell Biology</i> , 2015, 93, 522-532.	1.0	9
3962	Salivary microbiota reflects changes in gut microbiota in cirrhosis with hepatic encephalopathy. <i>Hepatology</i> , 2015, 62, 1260-1271.	3.6	272
3963	Identification of Commonly Dysregulated Genes in Non-small-cell Lung Cancer by Integrated Analysis of Microarray Data and qRT-PCR Validation. <i>Lung</i> , 2015, 193, 583-592.	1.4	27
3964	Multidimensional proteomics for cell biology. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 269-280.	16.1	375
3965	Anti-oxidative cellular protection effect of fasting-induced autophagy as a mechanism for hormesis. <i>Marine Environmental Research</i> , 2015, 107, 35-44.	1.1	31
3966	Sensory interaction between 3-mercaptohexan-1-ol, 3-isobutyl-2-methoxypyrazine and oxidation-related compounds. <i>Australian Journal of Grape and Wine Research</i> , 2015, 21, 179-188.	1.0	25
3967	Gut microbiome composition and metabolomic profiles of wild western lowland gorillas ( <i>Gorilla</i> ). <i>PLoS ONE</i> , 2015, 10, e0141171.	2.0	171
3968	Bridging topological and functional information in protein interaction networks by short loops profiling. <i>Scientific Reports</i> , 2015, 5, 8540.	1.6	19
3969	Involvement of multiple cellular pathways in regulating resistance to tamoxifen in BIK-suppressed MCF-7 cells. <i>Tumor Biology</i> , 2015, 36, 6991-7005.	0.8	3
3970	Network analysis of narrative content in large corpora. <i>Natural Language Engineering</i> , 2015, 21, 81-112.	2.1	27
3971	MetaMapR: pathway independent metabolomic network analysis incorporating unknowns. <i>Bioinformatics</i> , 2015, 31, 2757-2760.	1.8	101
3972	A network pharmacology approach to determine active ingredients and rationality of herb combinations of Modified-Simiaowan for treatment of gout. <i>Journal of Ethnopharmacology</i> , 2015, 168, 1-16.	2.0	67
3973	Integrative network-based analysis of mRNA and microRNA expression in 1,25-dihydroxyvitamin D3-treated cancer cells. <i>Genes and Nutrition</i> , 2015, 10, 35.	1.2	11
3974	Semi-supervised prediction of gene regulatory networks using machine learning algorithms. <i>Journal of Biosciences</i> , 2015, 40, 731-740.	0.5	32
3975	The close relation between <i>Lactococcus</i> and <i>Methanosaeta</i> is a keystone for stable methane production from molasses wastewater in a UASB reactor. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8271-8283.	1.7	28
3976	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
3977	Recognizing drug targets using evolutionary information: implications for repurposing FDA-approved drugs against <i>Mycobacterium tuberculosis</i> H37Rv. <i>Molecular BioSystems</i> , 2015, 11, 3316-3331.	2.9	20
3978	A systematic approach to prioritize drug targets using machine learning, a molecular descriptor-based classification model, and high-throughput screening of plant derived molecules: a case study in oral cancer. <i>Molecular BioSystems</i> , 2015, 11, 3362-3377.	2.9	8



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3979	Binary combination of epsilon-poly-l-lysine and isoeugenol affect progression of spoilage microbiota in fresh turkey meat, and delay onset of spoilage in <i>Pseudomonas putida</i> challenged meat. <i>International Journal of Food Microbiology</i> , 2015, 215, 131-142.	2.1	22
3980	Label-Free LC-MS/MS Proteomic Analysis of Cerebrospinal Fluid Identifies Protein/Pathway Alterations and Candidate Biomarkers for Amyotrophic Lateral Sclerosis. <i>Journal of Proteome Research</i> , 2015, 14, 4486-4501.	1.8	83
3981	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015, 12, 469-487.	1.3	70
3982	Global poplar root and leaf transcriptomes reveal links between growth and stress responses under nitrogen starvation and excess. <i>Tree Physiology</i> , 2015, 35, 1283-1302.	1.4	131
3983	Sequence-Structure-Function Classification of a Catalytically Diverse Oxidoreductase Superfamily in Mycobacteria. <i>Journal of Molecular Biology</i> , 2015, 427, 3554-3571.	2.0	67
3984	Navigating natural variation in herbivory-induced secondary metabolism in coyote tobacco populations using MS/MS structural analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4147-55.	3.3	67
3985	ncRDeathDB: A comprehensive bioinformatics resource for deciphering network organization of the ncRNA-mediated cell death system. <i>Autophagy</i> , 2015, 11, 1917-1926.	4.3	65
3986	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. <i>Human Molecular Genetics</i> , 2015, 24, ddv412.	1.4	14
3987	Cell cycle control, DNA damage repair, and apoptosis-related pathways control pre-ameloblasts differentiation during tooth development. <i>BMC Genomics</i> , 2015, 16, 592.	1.2	31
3988	Monitoring global growth of activity cliff information over time and assessing activity cliff frequencies and distributions. <i>Future Medicinal Chemistry</i> , 2015, 7, 1565-1579.	1.1	12
3989	Gene regulatory network in almond ( <i>Prunus dulcis</i> Mill.) in response to frost stress. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	20
3990	The Human Skin Double-Stranded DNA Virome: Topographical and Temporal Diversity, Genetic Enrichment, and Dynamic Associations with the Host Microbiome. <i>MBio</i> , 2015, 6, e01578-15.	1.8	232
3991	Biomarker-based drug safety assessment in the age of systems pharmacology: from foundational to regulatory science. <i>Biomarkers in Medicine</i> , 2015, 9, 1241-1252.	0.6	28
3992	Drug-target networks for Tanshinone IIA identified by data mining. <i>Chinese Journal of Natural Medicines</i> , 2015, 13, 751-759.	0.7	10
3993	The Human Endometrium-Specific Proteome Defined by Transcriptomics and Antibody-Based Profiling. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 659-668.	1.0	9
3994	Biochemical Studies of Mycobacterial Fatty Acid Methyltransferase: A Catalyst for the Enzymatic Production of Biodiesel. <i>Chemistry and Biology</i> , 2015, 22, 1480-1490.	6.2	17
3995	Reveal genes functionally associated with ACADS by a network study. <i>Gene</i> , 2015, 569, 294-302.	1.0	8
3996	A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. <i>BMC Plant Biology</i> , 2015, 15, 163.	1.6	55

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3997	Molecular analyses of juvenile granulosa cell tumors bearing <i>AKT1</i> mutations provide insights into tumor biology and therapeutic leads. <i>Human Molecular Genetics</i> , 2015, 24, 6687-6698.	1.4	51
3998	Visual analysis of biological data-knowledge networks. <i>BMC Bioinformatics</i> , 2015, 16, 135.	1.2	29
3999	Distribution of Bacteria and Archaea in meromictic tropical Lake Kivu (Africa). <i>Aquatic Microbial Ecology</i> , 2015, 74, 215-233.	0.9	28
4001	Microbiome interaction with sugar plays an important role in relapse of childhood caries. <i>Biochemical and Biophysical Research Communications</i> , 2015, 468, 294-299.	1.0	26
4002	The autism-associated gene chromodomain helicase DNA-binding protein 8 (CHD8) regulates noncoding RNAs and autism-related genes. <i>Translational Psychiatry</i> , 2015, 5, e568-e568.	2.4	104
4003	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. <i>Science Translational Medicine</i> , 2015, 7, 311ra174.	5.8	426
4005	Automatically visualise and analyse data on pathways using PathVisioRPC from any programming environment. <i>BMC Bioinformatics</i> , 2015, 16, 267.	1.2	13
4006	The gastrin and cholecystokinin receptors mediated signaling network: a scaffold for data analysis and new hypotheses on regulatory mechanisms. <i>BMC Systems Biology</i> , 2015, 9, 40.	3.0	46
4007	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	6.0	430
4008	Prediction of host - pathogen protein interactions between <i>Mycobacterium tuberculosis</i> and <i>Homo sapiens</i> using sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 100.	1.2	51
4009	Evaluation of BLAST-based edge-weighting metrics used for homology inference with the Markov Clustering algorithm. <i>BMC Bioinformatics</i> , 2015, 16, 218.	1.2	18
4010	A proteomic approach reveals integrin activation state-dependent control of microtubule cortical targeting. <i>Nature Communications</i> , 2015, 6, 6135.	5.8	71
4011	Causal Biological Network Database: A Comprehensive Platform of Causal Biological Network Models Focused on the Pulmonary and Vascular Systems. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 65-93.	0.1	8
4013	ZINC 15 “Ligand Discovery for Everyone. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 2324-2337.	2.5	2,194
4014	Integrative network analysis for survival-associated gene-gene interactions across multiple genomic profiles in ovarian cancer. <i>Journal of Ovarian Research</i> , 2015, 8, 42.	1.3	40
4015	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	3.8	50
4016	Computational Systems Biology of Psoriasis: Are We Ready for the Age of Omics and Systems Biomarkers?. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 669-687.	1.0	22
4017	Identification and characterization of long non-coding RNAs involved in osmotic and salt stress in <i>Medicago truncatula</i> using genome-wide high-throughput sequencing. <i>BMC Plant Biology</i> , 2015, 15, 131.	1.6	181

#	ARTICLE	IF	CITATIONS
4018	Divergent cerebrospinal fluid cytokine network induced by non-viral and different viral infections on the central nervous system. <i>BMC Infectious Diseases</i> , 2015, 15, 345.	1.3	17
4019	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	3.3	84
4020	Unique ability of pandemic influenza to downregulate the genes involved in neuronal disorders. <i>Molecular Biology Reports</i> , 2015, 42, 1377-1390.	1.0	27
4021	Systems Biology Approach Reveals a Calcium-Dependent Mechanism for Basal Toxicity in <i>Daphnia magna</i> . <i>Environmental Science &amp; Technology</i> , 2015, 49, 11132-11140.	4.6	28
4022	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , 2015, 5, 9156.	1.6	52
4023	Network analysis of temporal functionalities of the gut induced by perturbations in new-born piglets. <i>BMC Genomics</i> , 2015, 16, 556.	1.2	23
4024	Phytoplankton succession affects the composition of <i>Polynucleobacter</i> subtypes in humic lakes. <i>Environmental Microbiology</i> , 2015, 17, 816-828.	1.8	18
4025	Characterization of the rumen lipidome and microbiome of steers fed a diet supplemented with flax and echium oil. <i>Microbial Biotechnology</i> , 2015, 8, 331-341.	2.0	46
4026	Luzp4 defines a new mRNA export pathway in cancer cells. <i>Nucleic Acids Research</i> , 2015, 43, 2353-2366.	6.5	56
4027	Building Transcriptional Association Networks in Cytoscape with <i>RegNetC</i> . <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 823-824.	1.9	1
4028	Genome-wide identification of CCA1 targets uncovers an expanded clock network in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4802-10.	3.3	230
4029	Coexpression Network Analysis of Macronutrient Deficiency Response Genes in Rice. <i>Rice</i> , 2015, 8, 59.	1.7	43
4030	The nuclear localization pattern and interaction partners of GTF2IRD1 demonstrate a role in chromatin regulation. <i>Human Genetics</i> , 2015, 134, 1099-1115.	1.8	14
4031	Utilising established SDL-screening methods as a tool for the functional genomic characterisation of model and non-model organisms. <i>FEMS Yeast Research</i> , 2015, 15, fov091.	1.1	5
4032	Immunological signature of the different clinical stages of the HTLV-1 infection: establishing serum biomarkers for HTLV-1-associated disease morbidity. <i>Biomarkers</i> , 2015, 20, 502-512.	0.9	28
4033	Cytoscape.js: a graph theory library for visualisation and analysis. <i>Bioinformatics</i> , 2016, 32, 309-311.	1.8	531
4034	The expression profile of <i>Aedes albopictus</i> miRNAs is altered by dengue virus serotype-2 infection. <i>Cell and Bioscience</i> , 2015, 5, 16.	2.1	94
4035	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12628-12640.	4.6	72

#	ARTICLE	IF	CITATIONS
4036	The PfAlba1 RNA-binding protein is an important regulator of translational timing in Plasmodium falciparum blood stages. <i>Genome Biology</i> , 2015, 16, 212.	3.8	55
4037	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 495-506.	2.2	54
4038	Integrated network analysis and logistic regression modeling identify stage-specific genes in Oral Squamous Cell Carcinoma. <i>BMC Medical Genomics</i> , 2015, 8, 39.	0.7	12
4039	Correlation analysis of the transcriptome of growing leaves with mature leaf parameters in a maize RIL population. <i>Genome Biology</i> , 2015, 16, 168.	3.8	52
4040	Integrated analysis of gene expression and genomic aberration data in osteosarcoma (OS). <i>Cancer Gene Therapy</i> , 2015, 22, 524-529.	2.2	32
4041	Suboptimal cytoreduction in ovarian carcinoma is associated with molecular pathways characteristic of increased stromal activation. <i>Gynecologic Oncology</i> , 2015, 139, 394-400.	0.6	49
4042	Quantitative phosphoproteomics reveals new roles for the protein phosphatase PP6 in mitotic cells. <i>Science Signaling</i> , 2015, 8, rs12.	1.6	58
4043	Data for mitochondrial proteomic alterations in the aging mouse brain. <i>Data in Brief</i> , 2015, 4, 127-129.	0.5	5
4044	Integrative proteome analysis of Brachypodium distachyon roots and leaves reveals a synergetic responsive network under H <sub>2</sub> O <sub>2</sub> stress. <i>Journal of Proteomics</i> , 2015, 128, 388-402.	1.2	25
4045	Autophagic digestion of Leishmania major by host macrophages is associated with differential expression of BNIP3, CTSE, and the miRNAs miR-101c, miR-129, and miR-210. <i>Parasites and Vectors</i> , 2015, 8, 404.	1.0	92
4046	Analyzing maintainability and reliability of object-oriented software using weighted complex network. <i>Journal of Systems and Software</i> , 2015, 110, 28-53.	3.3	57
4048	Tripeptidyl Peptidase II Mediates Levels of Nuclear Phosphorylated ERK1 and ERK2. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2177-2193.	2.5	9
4049	Food Shortage Causes Differential Effects on Body Composition and Tissue-Specific Gene Expression in Salmon Modified for Increased Growth Hormone Production. <i>Marine Biotechnology</i> , 2015, 17, 753-767.	1.1	9
4050	Single-Cell RNA-Seq with Waterfall Reveals Molecular Cascades underlying Adult Neurogenesis. <i>Cell Stem Cell</i> , 2015, 17, 360-372.	5.2	680
4051	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. <i>Nature Genetics</i> , 2015, 47, 1179-1186.	9.4	330
4052	MPTP activates ASK1/p38 MAPK signaling pathway through TNF-dependent Trx1 oxidation in parkinsonism mouse model. <i>Free Radical Biology and Medicine</i> , 2015, 87, 312-325.	1.3	36
4053	Annual dynamics of North Sea bacterioplankton: seasonal variability superimposes short-term variation. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv099.	1.3	45
4054	Network analysis of S. aureus response to ramoplanin reveals modules for virulence factors and resistance mechanisms and characteristic novel genes. <i>Gene</i> , 2015, 574, 149-162.	1.0	15

#	ARTICLE	IF	CITATIONS
4055	The mRNA related ceRNAâ€œceRNA landscape and significance across 20 major cancer types. <i>Nucleic Acids Research</i> , 2015, 43, 8169-8182.	6.5	170
4056	The miR-146b-3p/PAX8/NIS Regulatory Circuit Modulates the Differentiation Phenotype and Function of Thyroid Cells during Carcinogenesis. <i>Cancer Research</i> , 2015, 75, 4119-4130.	0.4	90
4057	Identification of a PEAK1/ZEB1 signaling axis during TGFÎ²/fibronectin-induced EMT in breast cancer. <i>Biochemical and Biophysical Research Communications</i> , 2015, 465, 606-612.	1.0	38
4058	PARP1- and CTCF-Mediated Interactions between Active and Repressed Chromatin at the Lamina Promote Oscillating Transcription. <i>Molecular Cell</i> , 2015, 59, 984-997.	4.5	120
4059	Characterizing the Diverse Mutational Pathways Associated with R5-Tropic Maraviroc Resistance: HIV-1 That Uses the Drug-Bound CCR5 Coreceptor. <i>Journal of Virology</i> , 2015, 89, 11457-11472.	1.5	31
4060	Tissue-Specific Molecular Biomarker Signatures of Type 2 Diabetes: An Integrative Analysis of Transcriptomics and Proteinâ€œProtein Interaction Data. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 563-573.	1.0	70
4061	Large-scale models of signal propagation in human cells derived from discovery phosphoproteomic data. <i>Nature Communications</i> , 2015, 6, 8033.	5.8	79
4062	Methods and Techniques for miRNA Data Analysis. <i>Methods in Molecular Biology</i> , 2015, 1375, 11-23.	0.4	4
4063	Empowering biologists with multi-omics data: colorectal cancer as a paradigm. <i>Bioinformatics</i> , 2015, 31, 1436-1443.	1.8	22
4064	Allosteric Dynamic Control of Binding. <i>Biophysical Journal</i> , 2015, 109, 1190-1201.	0.2	19
4065	Transcriptional master regulator analysis in breast cancer genetic networks. <i>Computational Biology and Chemistry</i> , 2015, 59, 67-77.	1.1	53
4066	Age gene expression and coexpression progressive signatures in peripheral blood leukocytes. <i>Experimental Gerontology</i> , 2015, 72, 50-56.	1.2	14
4067	Identification and analysis of the currently available high-confidence three-dimensional activity cliffs. <i>RSC Advances</i> , 2015, 5, 43660-43668.	1.7	11
4068	The distribution pattern of genetic variation in the transcript isoforms of the alternatively spliced protein-coding genes in the human genome. <i>Molecular BioSystems</i> , 2015, 11, 1378-1388.	2.9	16
4069	Effects of Phosphorylation of Î² Subunits of Phycocyanins on State Transition in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Plant and Cell Physiology</i> , 2015, 56, 1997-2013.	1.5	37
4070	The Human Dental Pulp Proteome and N-Terminome: Levering the Unexplored Potential of Semitryptic Peptides Enriched by TAILS to Identify Missing Proteins in the Human Proteome Project in Underexplored Tissues. <i>Journal of Proteome Research</i> , 2015, 14, 3568-3582.	1.8	41
4071	Restoration of mesenchymal retinal pigmented epithelial cells by TGFÎ² pathway inhibitors: implications for age-related macular degeneration. <i>Genome Medicine</i> , 2015, 7, 58.	3.6	92
4072	Mixed effects of suberoylanilide hydroxamic acid (SAHA) on the host transcriptome and proteome and their implications for HIV reactivation from latency. <i>Antiviral Research</i> , 2015, 123, 78-85.	1.9	30

#	ARTICLE	IF	CITATIONS
4074	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. <i>Journal of Proteome Research</i> , 2015, 14, 4332-4341.	1.8	56
4075	Interplay among transcription factors Ets21c, Fos and Ftz-F1 drives JNK-mediated tumor malignancy. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1279-93.	1.2	69
4076	Antigenic variation of the human influenza A (H3N2) virus during the 2014â€“2015 winter season. <i>Science China Life Sciences</i> , 2015, 58, 882-888.	2.3	7
4077	An integrative approach to analyze microarray datasets for prioritization of genes relevant to lens biology and disease. <i>Genomics Data</i> , 2015, 5, 223-227.	1.3	27
4078	DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, W289-W294.	6.5	29
4079	Microbial population dynamics in response to increasing loadings of pre-hydrolyzed pig manure in an expanded granular sludge bed. <i>Water Research</i> , 2015, 87, 29-37.	5.3	30
4080	Targeted sequencing reveals clonal genetic changes in the progression of early lung neoplasms and paired circulating DNA. <i>Nature Communications</i> , 2015, 6, 8258.	5.8	129
4081	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 2743-2752.	1.6	32
4082	The microbiome of otitis media with effusion in Indigenous Australian children. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2015, 79, 1548-1555.	0.4	52
4083	Transcription Factor 7 Limits Regulatory T Cell Generation in the Thymus. <i>Journal of Immunology</i> , 2015, 195, 3058-3070.	0.4	27
4084	The spectrum of BRCA1 and BRCA2 alleles in Latin America and the Caribbean: a clinical perspective. <i>Breast Cancer Research and Treatment</i> , 2015, 154, 441-453.	1.1	63
4085	Identifying dense subgraphs in proteinâ€“protein interaction network for gene selection from microarray data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	7
4086	Evolutionarily Dynamic, but Robust, Targeting of Resistance Genes by the miR482/2118 Gene Family in the Solanaceae. <i>Genome Biology and Evolution</i> , 2015, 7, 3307-3321.	1.1	86
4087	Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. <i>Nucleic Acids Research</i> , 2015, 43, 10633-10654.	6.5	200
4088	Detecting protein complexes using connectivity among nodes in a PPI Network. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	2
4089	Automated analysis of the US presidential elections using Big Data and network analysis. <i>Big Data and Society</i> , 2015, 2, 205395171557291.	2.6	27
4090	Proteinâ€“protein interaction network analysis and identifying regulation microRNAs in asthmatic children. <i>Allergologia Et Immunopathologia</i> , 2015, 43, 584-592.	1.0	13
4091	Data for the characterization of the HSP70 family during osmotic stress in banana, a non-model crop. <i>Data in Brief</i> , 2015, 3, 78-84.	0.5	10



#	ARTICLE	IF	CITATIONS
4092	Quantitative analysis of PPT1 interactome in human neuroblastoma cells. <i>Data in Brief</i> , 2015, 4, 207-216.	0.5	11
4093	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. <i>Stem Cell Reports</i> , 2015, 4, 313-322.	2.3	38
4094	Beyond single modification: Reanalysis of the acetylproteome of human sperm reveals widespread multiple modifications. <i>Journal of Proteomics</i> , 2015, 126, 296-302.	1.2	11
4095	Diversity in protein domain superfamilies. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 40-49.	1.5	38
4096	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15084-15089.	3.3	126
4097	New genes drive the evolution of gene interaction networks in the human and mouse genomes. <i>Genome Biology</i> , 2015, 16, 202.	3.8	88
4098	Fast Activity Evoked by Intracranial 50 Hz Electrical Stimulation as a Marker of the Epileptogenic Zone. <i>International Journal of Neural Systems</i> , 2015, 25, 1550022.	3.2	5
4099	Capacitation-Related Lipid Remodeling of Mammalian Spermatozoa Membrane Determines the Final Fate of Male Gametes: A Computational Biology Study. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 712-721.	1.0	18
4100	Prediction of the anti-inflammatory mechanisms of curcumin by module-based protein interaction network analysis. <i>Acta Pharmaceutica Sinica B</i> , 2015, 5, 590-595.	5.7	29
4101	A potential signature of eight long non-coding RNAs predicts survival in patients with non-small cell lung cancer. <i>Journal of Translational Medicine</i> , 2015, 13, 231.	1.8	207
4102	Differential modulation of expression of nuclear receptor mediated genes by tris(2-butoxyethyl) phosphate (TBOEP) on early life stages of zebrafish ( <i>Danio rerio</i> ). <i>Aquatic Toxicology</i> , 2015, 169, 196-203.	1.9	21
4103	Integrated approaches to miRNAs target definition: time-series analysis in an osteosarcoma differentiative model. <i>BMC Medical Genomics</i> , 2015, 8, 34.	0.7	15
4104	A Chemical Proteomics Approach for Global Analysis of Lysine Monomethylome Profiling *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 329-339.	2.5	58
4105	LC-MS Metabolomics of Psoriasis Patients Reveals Disease Severity-Dependent Increases in Circulating Amino Acids That Are Ameliorated by Anti-TNF $\alpha$ Treatment. <i>Journal of Proteome Research</i> , 2015, 14, 557-566.	1.8	84
4106	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.4	173
4107	Transcriptome organization for chronic alcohol abuse in human brain. <i>Molecular Psychiatry</i> , 2015, 20, 1438-1447.	4.1	111
4108	3'UTR shortening identifies high-risk cancers with targeted dysregulation of the ceRNA network. <i>Scientific Reports</i> , 2014, 4, 5406.	1.6	52
4109	Analysis of Protein Interaction Networks for the Detection of Candidate Hepatitis B and C Biomarkers. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2015, 19, 181-189.	3.9	16



#	ARTICLE	IF	CITATIONS
4110	Converging Evidence Implicates the Abnormal MicroRNA System in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2015, 41, 728-735.	2.3	32
4111	Nutriproteomics: Facts, concepts, and perspectives. <i>Proteomics</i> , 2015, 15, 997-1013.	1.3	26
4112	Viewing the proteome: How to visualize proteomics data?. <i>Proteomics</i> , 2015, 15, 1341-1355.	1.3	32
4113	Cardiac steatosis potentiates angiotensin II effects in the heart. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2015, 308, H339-H350.	1.5	30
4114	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015, 347, 431-435.	6.0	362
4115	Physiological and Transcriptional Responses to High Temperature in <i>Arthrospira (Spirulina) platensis</i> C1. <i>Plant and Cell Physiology</i> , 2015, 56, 481-496.	1.5	30
4116	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of <i>Arabidopsis</i> protein complexes. <i>Nature Protocols</i> , 2015, 10, 169-187.	5.5	160
4117	The Cyni framework for network inference in Cytoscape. <i>Bioinformatics</i> , 2015, 31, 1499-1501.	1.8	9
4118	Characterizing the pocketome of <i>Mycobacterium tuberculosis</i> and application in rationalizing polypharmacological target selection. <i>Scientific Reports</i> , 2014, 4, 6356.	1.6	25
4119	Neuroproteomics in the auditory brainstem: Candidate proteins for ultrafast and precise information processing. <i>Molecular and Cellular Neurosciences</i> , 2015, 64, 9-23.	1.0	12
4120	Systematic assessment of coordinated activity cliffs formed by kinase inhibitors and detailed characterization of activity cliff clusters and associated SAR information. <i>European Journal of Medicinal Chemistry</i> , 2015, 90, 414-427.	2.6	9
4121	Deep sequencing analysis of the <i>Kineococcus radiotolerans</i> transcriptome in response to ionizing radiation. <i>Microbiological Research</i> , 2015, 170, 248-254.	2.5	8
4122	Fruits from ripening impaired, chlorophyll degraded and jasmonate insensitive tomato mutants have altered tocopherol content and composition. <i>Phytochemistry</i> , 2015, 111, 72-83.	1.4	34
4123	Proteome Profiling of Human Cutaneous Leishmaniasis Lesion. <i>Journal of Investigative Dermatology</i> , 2015, 135, 400-410.	0.3	40
4125	Genomic expression profiling of NK cells in health and disease. <i>European Journal of Immunology</i> , 2015, 45, 661-678.	1.6	13
4126	Integrating Proteomics Profiling Data Sets: A Network Perspective. <i>Methods in Molecular Biology</i> , 2015, 1243, 237-253.	0.4	5
4127	Plasma Metabolite Biomarkers for the Detection of Pancreatic Cancer. <i>Journal of Proteome Research</i> , 2015, 14, 1195-1202.	1.8	70
4128	Exploring the genes associated with the response to intravenous immunoglobulin in patients with Kawasaki disease using DNA microarray analysis. <i>Experimental and Molecular Pathology</i> , 2015, 98, 7-12.	0.9	4

#	ARTICLE	IF	CITATIONS
4129	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. <i>BioSystems</i> , 2015, 127, 67-72.	0.9	813
4130	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. <i>Proteomics</i> , 2015, 15, 981-996.	1.3	27
4131	MarVis-Pathway: integrative and exploratory pathway analysis of non-targeted metabolomics data. <i>Metabolomics</i> , 2015, 11, 764-777.	1.4	72
4132	Affinity chromatography revealed insights into unique functionality of two 14-3-3 protein species in developing maize kernels. <i>Journal of Proteomics</i> , 2015, 114, 274-286.	1.2	20
4133	Molecular principles of human virus protein-protein interactions. <i>Bioinformatics</i> , 2015, 31, 1025-1033.	1.8	41
4134	Unbiased classification of sensory neuron types by large-scale single-cell RNA sequencing. <i>Nature Neuroscience</i> , 2015, 18, 145-153.	7.1	1,710
4135	Transcription factor and microRNA co-regulatory loops: important regulatory motifs in biological processes and diseases. <i>Briefings in Bioinformatics</i> , 2015, 16, 45-58.	3.2	175
4136	Proteomics of extracellular vesicles: Exosomes and ectosomes. <i>Mass Spectrometry Reviews</i> , 2015, 34, 474-490.	2.8	336
4137	Genome wide identification and expression profile in epithelial cells exposed to TiO <sub>2</sub> particles. <i>Environmental Toxicology</i> , 2015, 30, 293-300.	2.1	17
4138	Metabolic Cancer Biology: Structural-based analysis of cancer as a metabolic disease, new sights and opportunities for disease treatment. <i>Seminars in Cancer Biology</i> , 2015, 30, 21-29.	4.3	38
4139	Effect of curcumin on aged <i>Drosophila Melanogaster</i> : A pathway prediction analysis. <i>Chinese Journal of Integrative Medicine</i> , 2015, 21, 115-122.	0.7	10
4140	Bacterial community shift is induced by dynamic environmental parameters in a changing coastal ecosystem (northern Adriatic, northeastern Mediterranean Sea) – a 2-year time-series study. <i>Environmental Microbiology</i> , 2015, 17, 3581-3596.	1.8	81
4141	Identification of disease-related miRNAs based on co-expression network in spinal cord injury. <i>International Journal of Neuroscience</i> , 2015, 125, 270-276.	0.8	9
4142	Combined experimental and bioinformatics analysis for the prediction and identification of VHR/DUSP3 nuclear targets related to DNA damage and repair. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 73-89.	0.6	11
4143	The discovery of integrated gene networks for autism and related disorders. <i>Genome Research</i> , 2015, 25, 142-154.	2.4	259
4144	Comprehensive characterization of cancer subtype associated long non-coding RNAs and their clinical implications. <i>Scientific Reports</i> , 2014, 4, 6591.	1.6	106
4145	Functional annotation and biological interpretation of proteomics data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 46-54.	1.1	45
4146	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. <i>Schizophrenia Bulletin</i> , 2015, 41, 715-727.	2.3	15

#	ARTICLE	IF	CITATIONS
4147	SAMNetWeb: identifying condition-specific networks linking signaling and transcription. <i>Bioinformatics</i> , 2015, 31, 1124-1126.	1.8	14
4148	Bioinformatics: The Next Frontier of Metabolomics. <i>Analytical Chemistry</i> , 2015, 87, 147-156.	3.2	112
4149	Genome-wide analysis of the MADS-box gene family in <i>Brassica rapa</i> (Chinese cabbage). <i>Molecular Genetics and Genomics</i> , 2015, 290, 239-255.	1.0	80
4150	A guide for building biological pathways along with two case studies: hair and breast development. <i>Methods</i> , 2015, 74, 16-35.	1.9	5
4151	Gene and Protein Network Analysis of AmpC $\beta$ -Lactamase. <i>Cell Biochemistry and Biophysics</i> , 2015, 71, 1553-1567.	0.9	18
4152	Substrate Trapping Proteomics Reveals Targets of the $\beta$ -TrCP2/FBXW1 Ubiquitin Ligase. <i>Molecular and Cellular Biology</i> , 2015, 35, 167-181.	1.1	55
4153	Biological ingredient analysis of traditional Chinese medicine preparation based on high-throughput sequencing: the story for Liuwei Dihuang Wan. <i>Scientific Reports</i> , 2014, 4, 5147.	1.6	132
4154	Translational research platforms integrating clinical and omics data: a review of publicly available solutions. <i>Briefings in Bioinformatics</i> , 2015, 16, 280-290.	3.2	84
4155	Genome-wide survey of tissue-specific microRNA and transcription factor regulatory networks in 12 tissues. <i>Scientific Reports</i> , 2014, 4, 5150.	1.6	175
4156	Exploring the Scaffold Universe of Kinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 315-332.	2.9	21
4157	Serum Metabolite Signatures of Type 2 Diabetes Mellitus Complications. <i>Journal of Proteome Research</i> , 2015, 14, 447-456.	1.8	32
4158	Phage-bacteria network analysis and its implication for the understanding of coral disease. <i>Environmental Microbiology</i> , 2015, 17, 1203-1218.	1.8	84
4159	Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. <i>ISME Journal</i> , 2015, 9, 683-695.	4.4	393
4160	Comprehensive Analysis of Three-Dimensional Activity Cliffs Formed by Kinase Inhibitors with Different Binding Modes and Cliff Mapping of Structural Analogues. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 252-264.	2.9	21
4161	Quantitative scoring of differential drug sensitivity for individually optimized anticancer therapies. <i>Scientific Reports</i> , 2014, 4, 5193.	1.6	243
4162	From pathways to networks: Connecting dots by establishing protein-protein interaction networks in signaling pathways using affinity purification and mass spectrometry. <i>Proteomics</i> , 2015, 15, 188-202.	1.3	20
4163	Proteomic analysis and prediction of human phosphorylation sites in subcellular level reveal subcellular specificity. <i>Bioinformatics</i> , 2015, 31, 194-200.	1.8	19
4164	An introduction to systems toxicology. <i>Toxicology Research</i> , 2015, 4, 9-22.	0.9	21

#	ARTICLE	IF	CITATIONS
4165	Network analysis reveals that bacteria and fungi form modules that correlate independently with soil parameters. <i>Environmental Microbiology</i> , 2015, 17, 2677-2689.	1.8	166
4166	miRNA functional synergistic network analysis of mice with ischemic stroke. <i>Neurological Sciences</i> , 2015, 36, 143-148.	0.9	23
4167	PINBPA: Cytoscape app for network analysis of GWAS data. <i>Bioinformatics</i> , 2015, 31, 262-264.	1.8	29
4168	Comparative metabolomics and transcriptomics of plant response to Tomato yellow leaf curl virus infection in resistant and susceptible tomato cultivars. <i>Metabolomics</i> , 2015, 11, 81-97.	1.4	77
4169	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. <i>ISME Journal</i> , 2015, 9, 207-216.	4.4	540
4170	BioVLAB-MMIA-NGS: microRNA-mRNA integrated analysis using high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, 265-267.	1.8	38
4171	fabp4 is central to eight obesity associated genes: A functional gene network-based polymorphic study. <i>Journal of Theoretical Biology</i> , 2015, 364, 344-354.	0.8	33
4172	Organellar proteome analyses of ricin toxin-treated HeLa cells. <i>Toxicology and Industrial Health</i> , 2016, 32, 1166-1178.	0.6	2
4173	Using gene networks to identify genes and pathways involved in milk production traits in Polish Holstein dairy cattle. <i>Czech Journal of Animal Science</i> , 2016, 61, 526-538.	0.5	21
4174	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. <i>Oncotarget</i> , 2016, 7, 55249-55263.	0.8	14
4175	Systems biology analysis reveals role of MDM2 in diabetic nephropathy. <i>JCI Insight</i> , 2016, 1, e87877.	2.3	34
4176	Proteomics of Schizophrenia. , 2016, , 195-209.		0
4177	Divergent Expression Patterns in Two Vernicia Species Revealed the Potential Role of the Hub Gene VmAP2/ERF036 in Resistance to Fusarium oxysporum in Vernicia montana. <i>Genes</i> , 2016, 7, 109.	1.0	8
4178	Metaviromics of Namib Desert Salt Pans: A Novel Lineage of Haloarchaeal Salterproviruses and a Rich Source of ssDNA Viruses. <i>Viruses</i> , 2016, 8, 14.	1.5	24
4179	Metformin increases PDH and suppresses HIF-1 $\alpha$ under hypoxic conditions and induces cell death in oral squamous cell carcinoma. <i>Oncotarget</i> , 2016, 7, 55057-55068.	0.8	81
4180	<i>Cis-</i> Natural Antisense Transcripts Are Mainly Co-expressed with Their Sense Transcripts and Primarily Related to Energy Metabolic Pathways during Muscle Development. <i>International Journal of Biological Sciences</i> , 2016, 12, 1010-1021.	2.6	6
4181	miR-27b shapes the presynaptic transcriptome and influences neurotransmission by silencing the polycomb group protein Bmi1. <i>BMC Genomics</i> , 2016, 17, 777.	1.2	16
4182	RNA-seq based transcriptomic map reveals new insights into mouse salivary gland development and maturation. <i>BMC Genomics</i> , 2016, 17, 923.	1.2	35

#	ARTICLE	IF	CITATIONS
4183	Knowledge Discovery from Biomedical Ontologies in Cross Domains. PLoS ONE, 2016, 11, e0160005.	1.1	23
4184	Transcriptome sequencing identified hub genes for hepatocellular carcinoma by weighted-gene co-expression analysis. Oncotarget, 2016, 7, 38487-38499.	0.8	22
4185	Prediction and Analysis of the Protein-Protein Interaction Networks for Chickens, Cattle, Dogs, Horses and Rabbits. Current Bioinformatics, 2016, 11, 131-142.	0.7	5
4186	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. Genetics and Molecular Biology, 2016, 39, 589-599.	0.6	8
4187	Iterative Multi Level Calibration of Metabolic Networks. Current Bioinformatics, 2016, 11, 93-105.	0.7	4
4188	Application of computational methods in genetic study of inflammatory bowel disease. World Journal of Gastroenterology, 2016, 22, 949.	1.4	6
4189	Disease-Phenotype Deconvolution in Genetic Eye Diseases Using Online Mendelian Inheritance in Man. , 2016, 57, 2895.		2
4190	Network analysis reveals potential markers for pediatric adrenocortical carcinoma. OncoTargets and Therapy, 2016, Volume 9, 4569-4581.	1.0	33
4191	Integrated miRNA-risk gene-pathway pair network analysis provides prognostic biomarkers for gastric cancer. OncoTargets and Therapy, 2016, 9, 2975.	1.0	7
4192	CoSpliceNet: a framework for co-splicing network inference from transcriptomics data. BMC Genomics, 2016, 17, 845.	1.2	10
4193	Glucose or Altered Ceramide Biosynthesis Mediate Oxygen Deprivation Sensitivity Through Novel Pathways Revealed by Transcriptome Analysis in <i>Caenorhabditis elegans</i> . G3: Genes, Genomes, Genetics, 2016, 6, 3149-3160.	0.8	15
4194	Lower expressed miR-198 and its potential targets in hepatocellular carcinoma: a clinicopathological and in silico study. OncoTargets and Therapy, 2016, Volume 9, 5163-5180.	1.0	33
4195	Genome sequencing and systems biology analysis of a lipase-producing bacterial strain. Genetics and Molecular Research, 2016, 15, .	0.3	0
4196	Extracellular Matrix Proteome and Phosphoproteome of Potato Reveals Functionally Distinct and Diverse Canonical and Non-Canonical Proteoforms. Proteomes, 2016, 4, 20.	1.7	9
4197	Computation in Analyzing Inflammation: A General Perspective. Interdisciplinary Journal of Microinflammation, 2016, 3, .	0.1	2
4198	Comprehensive analysis of aberrantly expressed profiles of lncRNAs and miRNAs with associated ceRNA network in muscle-invasive bladder cancer. Oncotarget, 2016, 7, 86174-86185.	0.8	87
4199	Identification of novel pathways linking epithelial-to-mesenchymal transition with resistance to HER2-targeted therapy. Oncotarget, 2016, 7, 11539-11552.	0.8	27
4200	How Hepatitis C Virus Leads to Hepatocellular Carcinoma: A Network-Based Study. Hepatitis Monthly, 2016, 16, e36005.	0.1	17

#	ARTICLE	IF	CITATIONS
4201	Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. <i>PeerJ</i> , 2016, 4, e1762.	0.9	87
4202	Identification of candidate anti-cancer molecular mechanisms of Compound Kushen Injection using functional genomics. <i>Oncotarget</i> , 2016, 7, 66003-66019.	0.8	87
4203	Practical aspects of NGS-based pathways analysis for personalized cancer science and medicine. <i>Oncotarget</i> , 2016, 7, 52493-52516.	0.8	15
4204	Integrated analysis miRNA and mRNA profiling in patients with severe oligozoospermia reveals miR-34c-3p downregulates PLCXD3 expression. <i>Oncotarget</i> , 2016, 7, 52781-52796.	0.8	22
4205	Metformin treatment reduces temozolomide resistance of glioblastoma cells. <i>Oncotarget</i> , 2016, 7, 78787-78803.	0.8	56
4206	<i>Mycoplasma pneumoniae</i> and <i>Streptococcus pneumoniae</i> caused different microbial structure and correlation network in lung microbiota. <i>Journal of Thoracic Disease</i> , 2016, 8, 1316-1322.	0.6	23
4207	Identification of Molecular Targets for Predicting Colon Adenocarcinoma. <i>Medical Science Monitor</i> , 2016, 22, 460-468.	0.5	13
4208	Organizational principles of the Reactome human BioPAX model using graph theory methods. <i>Journal of Complex Networks</i> , 2016, , cnw003.	1.1	1
4209	DNA Microarray Analysis in Screening Features of Genes Involved in Spinal Cord Injury. <i>Medical Science Monitor</i> , 2016, 22, 1571-1581.	0.5	4
4210	Analyzing and Visualizing Genomic Complexity for the Derivation of the Emergent Molecular Networks. <i>International Journal of Monitoring and Surveillance Technologies Research</i> , 2016, 4, 30-49.	0.3	18
4211	TGF- $\beta$ 2 and VEGF cooperatively control the immunotolerant tumor environment and the efficacy of cancer immunotherapies. <i>JCI Insight</i> , 2016, 1, e85974.	2.3	91
4212	Correlation-Based Network Generation, Visualization, and Analysis as a Powerful Tool in Biological Studies: A Case Study in Cancer Cell Metabolism. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	68
4213	Networks Models of Actin Dynamics during Spermatozoa Postejaculatory Life: A Comparison among Human-Made and Text Mining-Based Models. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	5
4214	Identification of the Key Genes and Pathways in Esophageal Carcinoma. <i>Gastroenterology Research and Practice</i> , 2016, 2016, 1-11.	0.7	19
4215	Comparison of FDA Approved Kinase Targets to Clinical Trial Ones: Insights from Their System Profiles and Drug-Target Interaction Networks. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	36
4216	Gene Prioritization by Integrated Analysis of Protein Structural and Network Topological Properties for the Protein-Protein Interaction Network of Neurological Disorders. <i>Scientifica</i> , 2016, 2016, 1-10.	0.6	0
4217	System Review about Function Role of ESCC Driver Gene KDM6A by Network Biology Approach. <i>Scientific World Journal</i> , The, 2016, 2016, 1-6.	0.8	1
4218	Analyzing the miRNA-Gene Networks to Mine the Important miRNAs under Skin of Human and Mouse. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	5

#	ARTICLE	IF	CITATIONS
4219	<i>Asparagus cochinchinensis</i> Extract Alleviates Metal Ion-Induced Gut Injury in <i>Drosophila</i> : An In Silico Analysis of Potential Active Constituents. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-9.	0.5	3
4220	Integrated Approaches to Drug Discovery for Oxidative Stress-Related Retinal Diseases. Oxidative Medicine and Cellular Longevity, 2016, 2016, 1-9.	1.9	12
4221	Leaf Proteome Analysis Reveals Prospective Drought and Heat Stress Response Mechanisms in Soybean. BioMed Research International, 2016, 2016, 1-23.	0.9	105
4222	Reconstruction of the Fatty Acid Biosynthetic Pathway of <i>Exiguobacterium antarcticum</i> B7 Based on Genomic and Bibliomic Data. BioMed Research International, 2016, 2016, 1-9.	0.9	5
4223	Genome-Wide Analysis of the Lysine Biosynthesis Pathway Network during Maize Seed Development. PLoS ONE, 2016, 11, e0148287.	1.1	5
4224	Systems Pharmacology Uncovers the Multiple Mechanisms of Xijiao Dihuang Decoction for the Treatment of Viral Hemorrhagic Fever. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-17.	0.5	31
4225	16S rRNA amplicon sequencing identifies microbiota associated with oral cancer, human papilloma virus infection and surgical treatment. Oncotarget, 2016, 7, 51320-51334.	0.8	237
4226	Biomarker and competing endogenous RNA potential of tumor-specific long noncoding RNA in chromophobe renal cell carcinoma. OncoTargets and Therapy, 2016, Volume 9, 6399-6406.	1.0	50
4227	The founder-cell transcriptome in the <i>Arabidopsis apetala1</i> cauliflower inflorescence meristem. BMC Genomics, 2016, 17, 855.	1.2	13
4228	Co-occurrence patterns in aquatic bacterial communities across changing permafrost landscapes. Biogeosciences, 2016, 13, 175-190.	1.3	64
4229	Construction of a protein-protein interaction network of Wilms's tumor and pathway prediction of molecular complexes. Genetics and Molecular Research, 2016, 15, .	0.3	2
4230	Lamina Associated Polypeptide 1 (LAP1) Interactome and Its Functional Features. Membranes, 2016, 6, 8.	1.4	19
4231	Regulatory complexity revealed by integrated cytological and RNA-seq analyses of meiotic substages in mouse spermatocytes. BMC Genomics, 2016, 17, 628.	1.2	35
4232	Identification of feature genes for smoking-related lung adenocarcinoma based on gene expression profile data. OncoTargets and Therapy, 2016, Volume 9, 7397-7407.	1.0	18
4233	Relapse-related long non-coding RNA signature to improve prognosis prediction of lung adenocarcinoma. Oncotarget, 2016, 7, 29720-29738.	0.8	80
4234	<i>Aspergillus</i> Secretome. , 2016, , 69-77.		1
4235	Proteome-Wide Effect of 17- $\beta$ -Estradiol and Lipoxin A4 in an Endometriotic Epithelial Cell Line. Frontiers in Endocrinology, 2015, 6, 192.	1.5	3
4236	Using Whole-Genome Sequence Information to Foster Conservation Efforts for the European Dark Honey Bee, <i>Apis mellifera mellifera</i> . Frontiers in Ecology and Evolution, 2016, 4, .	1.1	34



#	ARTICLE	IF	CITATIONS
4237	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. <i>Frontiers in Genetics</i> , 2016, 7, 116.	1.1	10
4238	Genome-Wide Association Study for Identifying Loci that Affect Fillet Yield, Carcass, and Body Weight Traits in Rainbow Trout ( <i>Oncorhynchus mykiss</i> ). <i>Frontiers in Genetics</i> , 2016, 7, 203.	1.1	124
4239	A Network Approach of Gene Co-expression in the <i>Zea mays</i> / <i>Aspergillus flavus</i> Pathosystem to Map Host/Pathogen Interaction Pathways. <i>Frontiers in Genetics</i> , 2016, 7, 206.	1.1	32
4240	Metabolomics and Its Application to Acute Lung Diseases. <i>Frontiers in Immunology</i> , 2016, 7, 44.	2.2	94
4241	Immunosenescence-Related Transcriptomic and Immunologic Changes in Older Individuals Following Influenza Vaccination. <i>Frontiers in Immunology</i> , 2016, 7, 450.	2.2	40
4242	Worldwide Analysis of Sedimentary DNA Reveals Major Gaps in Taxonomic Knowledge of Deep-Sea Benthos. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	138
4243	Methanotrophic Community Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	17
4245	Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. <i>Frontiers in Microbiology</i> , 2015, 6, 1438.	1.5	98
4246	Exploration of Microbial Diversity and Community Structure of Lonar Lake: The Only Hypersaline Meteorite Crater Lake within Basalt Rock. <i>Frontiers in Microbiology</i> , 2015, 6, 1553.	1.5	100
4247	Ecophysiology of Zetaproteobacteria Associated with Shallow Hydrothermal Iron-Oxyhydroxide Deposits in Nagahama Bay of Satsuma Iwo-Jima, Japan. <i>Frontiers in Microbiology</i> , 2015, 6, 1554.	1.5	20
4248	Using “Omics” and Integrated Multi-Omics Approaches to Guide Probiotic Selection to Mitigate Chytridiomycosis and Other Emerging Infectious Diseases. <i>Frontiers in Microbiology</i> , 2016, 7, 68.	1.5	135
4249	Short-Term Rhizosphere Effect on Available Carbon Sources, Phenanthrene Degradation, and Active Microbiome in an Aged-Contaminated Industrial Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 92.	1.5	69
4250	Understanding the Role of the Master Regulator XYR1 in <i>Trichoderma reesei</i> by Global Transcriptional Analysis. <i>Frontiers in Microbiology</i> , 2016, 7, 175.	1.5	91
4251	Short-Term Dynamics of North Sea Bacterioplankton-Dissolved Organic Matter Coherence on Molecular Level. <i>Frontiers in Microbiology</i> , 2016, 7, 321.	1.5	48
4252	Community Structure in Methanogenic Enrichments Provides Insight into Syntrophic Interactions in Hydrocarbon-Impacted Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 562.	1.5	52
4253	Co-occurrence Analysis of Microbial Taxa in the Atlantic Ocean Reveals High Connectivity in the Free-Living Bacterioplankton. <i>Frontiers in Microbiology</i> , 2016, 7, 649.	1.5	152
4254	Networks of Host Factors that Interact with NS1 Protein of Influenza A Virus. <i>Frontiers in Microbiology</i> , 2016, 7, 654.	1.5	27
4255	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	1.5	61

#	ARTICLE	IF	CITATIONS
4256	Bacterial Diversity and Community Structure of Supragingival Plaques in Adults with Dental Health or Caries Revealed by 16S Pyrosequencing. <i>Frontiers in Microbiology</i> , 2016, 7, 1145.	1.5	166
4257	<i>Salicornia strobilacea</i> (Synonym of <i>Halocnemum strobilaceum</i> ) Grown under Different Tidal Regimes Selects Rhizosphere Bacteria Capable of Promoting Plant Growth. <i>Frontiers in Microbiology</i> , 2016, 7, 1286.	1.5	51
4258	Transcriptional and Physiological Changes during <i>Mycobacterium tuberculosis</i> Reactivation from Non-replicating Persistence. <i>Frontiers in Microbiology</i> , 2016, 7, 1346.	1.5	63
4259	Fungal Assemblages in Different Habitats in an Ermanâ€™s Birch Forest. <i>Frontiers in Microbiology</i> , 2016, 7, 1368.	1.5	30
4260	Analysis of the Core Genome and Pan-Genome of Autotrophic Acetogenic Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1531.	1.5	68
4261	Bacterial Communities Associated with Four Cyanobacterial Genera Display Structural and Functional Differences: Evidence from an Experimental Approach. <i>Frontiers in Microbiology</i> , 2016, 7, 1662.	1.5	57
4262	Seasonal Succession of Free-Living Bacterial Communities in Coastal Waters of the Western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2016, 7, 1731.	1.5	53
4263	The Mutational Landscape of the Oncogenic MZF1 SCAN Domain in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 78.	1.6	34
4264	Algorithms for Drug Sensitivity Prediction. <i>Algorithms</i> , 2016, 9, 77.	1.2	41
4265	Integrative Systems Biology Investigation of Fabry Disease. <i>Diseases (Basel, Switzerland)</i> , 2016, 4, 35.	1.0	11
4266	Transcriptomic Insights into the Response of Placenta and Decidua Basalis to the CpG Oligodeoxynucleotide Stimulation in Non-Obese Diabetic Mice and Wild-Type Controls. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1281.	1.8	1
4267	Phylogenetic-Derived Insights into the Evolution of Sialylation in Eukaryotes: Comprehensive Analysis of Vertebrate Î²-2,3/6-Sialyltransferases (ST3Gal and ST6Gal). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1286.	1.8	25
4268	MicroRNA Transcriptome of Poly I:C-Stimulated Peripheral Blood Mononuclear Cells Reveals Evidence for MicroRNAs in Regulating Host Response to RNA Viruses in Pigs. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1601.	1.8	5
4269	iTRAQ-Based Quantitative Proteomic Analysis of the Potentiated and Dormant Antler Stem Cells. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1778.	1.8	32
4270	Systematic Understanding of Mechanisms of a Chinese Herbal Formula in Treatment of Metabolic Syndrome by an Integrated Pharmacology Approach. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2114.	1.8	30
4271	Direct Visual Editing of Node Attributes in Graphs. <i>Informatics</i> , 2016, 3, 17.	2.4	6
4272	Functional Annotations of Paralogs: A Blessing and a Curse. <i>Life</i> , 2016, 6, 39.	1.1	45
4273	Structure Identification and Anti-Cancer Pharmacological Prediction of Triterpenes from <i>Ganoderma lucidum</i> . <i>Molecules</i> , 2016, 21, 678.	1.7	27

#	ARTICLE	IF	CITATIONS
4274	Comparison of molecular signatures in large-scale protein interaction networks in normal and cancer conditions of brain, cervix, lung, ovary and prostate. <i>Biomedical Research and Therapy</i> , 2016, 3, .	0.3	1
4275	Mining kidney toxicogenomic data by using gene co-expression modules. <i>BMC Genomics</i> , 2016, 17, 790.	1.2	44
4276	Clinical significance of mitofusin-2 and its signaling pathways in hepatocellular carcinoma. <i>World Journal of Surgical Oncology</i> , 2016, 14, 179.	0.8	20
4277	Analysis of coevolution in nonstructural proteins of chikungunya virus. <i>Virology Journal</i> , 2016, 13, 86.	1.4	9
4278	Mash: fast genome and metagenome distance estimation using MinHash. <i>Genome Biology</i> , 2016, 17, 132.	3.8	2,099
4279	Identification of therapeutic targets for Alzheimer's disease via differentially expressed gene and weighted gene co-expression network analyses. <i>Molecular Medicine Reports</i> , 2016, 14, 4844-4848.	1.1	12
4280	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. <i>PLoS ONE</i> , 2016, 11, e0164036.	1.1	102
4281	APP Is a Context-Sensitive Regulator of the Hippocampal Presynaptic Active Zone. <i>PLoS Computational Biology</i> , 2016, 12, e1004832.	1.5	22
4282	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	1.5	105
4283	Structural and Functional Characterization of a <i>Caenorhabditis elegans</i> Genetic Interaction Network within Pathways. <i>PLoS Computational Biology</i> , 2016, 12, e1004738.	1.5	3
4284	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004892.	1.5	36
4285	Integrating Transcriptomic and Proteomic Data Using Predictive Regulatory Network Models of Host Response to Pathogens. <i>PLoS Computational Biology</i> , 2016, 12, e1005013.	1.5	24
4286	Large-Scale Off-Target Identification Using Fast and Accurate Dual Regularized One-Class Collaborative Filtering and Its Application to Drug Repurposing. <i>PLoS Computational Biology</i> , 2016, 12, e1005135.	1.5	65
4287	Parallel Mapping of Antibiotic Resistance Alleles in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0146916.	1.1	15
4288	Identification of Crowding Stress Tolerance Co-Expression Networks Involved in Sweet Corn Yield. <i>PLoS ONE</i> , 2016, 11, e0147418.	1.1	12
4289	Comparative Analysis of Genome Diversity in Bullmastiff Dogs. <i>PLoS ONE</i> , 2016, 11, e0147941.	1.1	26
4290	Low Dose Iron Treatments Induce a DNA Damage Response in Human Endothelial Cells within Minutes. <i>PLoS ONE</i> , 2016, 11, e0147990.	1.1	39
4291	Vikodak - A Modular Framework for Inferring Functional Potential of Microbial Communities from 16S Metagenomic Datasets. <i>PLoS ONE</i> , 2016, 11, e0148347.	1.1	85

#	ARTICLE	IF	CITATIONS
4292	Comprehensive Expression Profiling and Functional Network Analysis of p53-Regulated MicroRNAs in HepG2 Cells Treated with Doxorubicin. PLoS ONE, 2016, 11, e0149227.	1.1	23
4293	Genome-Wide Investigation Using sRNA-Seq, Degradome-Seq and Transcriptome-Seq Reveals Regulatory Networks of microRNAs and Their Target Genes in Soybean during Soybean mosaic virus Infection. PLoS ONE, 2016, 11, e0150582.	1.1	30
4294	Immune-Mediated Inflammation May Contribute to the Pathogenesis of Cardiovascular Disease in Mucopolysaccharidosis Type I. PLoS ONE, 2016, 11, e0150850.	1.1	20
4295	MiRComb: An R Package to Analyse miRNA-mRNA Interactions. Examples across Five Digestive Cancers. PLoS ONE, 2016, 11, e0151127.	1.1	41
4296	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. PLoS ONE, 2016, 11, e0152034.	1.1	53
4297	Mining Temporal Protein Complex Based on the Dynamic PIN Weighted with Connected Affinity and Gene Co-Expression. PLoS ONE, 2016, 11, e0153967.	1.1	14
4298	Gene Expression Differences in Peripheral Blood of Parkinson's Disease Patients with Distinct Progression Profiles. PLoS ONE, 2016, 11, e0157852.	1.1	36
4299	The Impact of a Researcher's Structural Position on Scientific Performance: An Empirical Analysis. PLoS ONE, 2016, 11, e0161281.	1.1	23
4300	Protein Co-Expression Analysis as a Strategy to Complement a Standard Quantitative Proteomics Approach: Case of a Glioblastoma Multiforme Study. PLoS ONE, 2016, 11, e0161828.	1.1	9
4301	Quantitative Proteomic Analysis of Wheat Seeds during Artificial Ageing and Priming Using the Isobaric Tandem Mass Tag Labeling. PLoS ONE, 2016, 11, e0162851.	1.1	40
4302	Graphlet Based Metrics for the Comparison of Gene Regulatory Networks. PLoS ONE, 2016, 11, e0163497.	1.1	17
4303	MicroRNA Expression for Early Prediction of Late Occurring Hematologic Acute Radiation Syndrome in Baboons. PLoS ONE, 2016, 11, e0165307.	1.1	23
4304	Gene Expression Dynamics Accompanying the Sponge Thermal Stress Response. PLoS ONE, 2016, 11, e0165368.	1.1	57
4305	Identification of Genes Discriminating Multiple Sclerosis Patients from Controls by Adapting a Pathway Analysis Method. PLoS ONE, 2016, 11, e0165543.	1.1	4
4306	Human Lung Tissue Transcriptome: Influence of Sex and Age. PLoS ONE, 2016, 11, e0167460.	1.1	14
4307	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. PLoS ONE, 2016, 11, e0167519.	1.1	21
4308	IFNs Modify the Proteome of Legionella-Containing Vacuoles and Restrict Infection Via IRG1-Derived Itaconic Acid. PLoS Pathogens, 2016, 12, e1005408.	2.1	195
4309	Quantitative Trait Locus Based Virulence Determinant Mapping of the HSV-1 Genome in Murine Ocular Infection: Genes Involved in Viral Regulatory and Innate Immune Networks Contribute to Virulence. PLoS Pathogens, 2016, 12, e1005499.	2.1	30

#	ARTICLE	IF	CITATIONS
4310	DNA Damage Response Is Involved in the Developmental Toxicity of Mebendazole in Zebrafish Retina. <i>Frontiers in Pharmacology</i> , 2016, 7, 57.	1.6	31
4311	E2F4 Promotes Neuronal Regeneration and Functional Recovery after Spinal Cord Injury in Zebrafish. <i>Frontiers in Pharmacology</i> , 2016, 7, 119.	1.6	16
4312	EP300 Protects from Light-Induced Retinopathy in Zebrafish. <i>Frontiers in Pharmacology</i> , 2016, 7, 126.	1.6	13
4313	Downregulation of GSTK1 Is a Common Mechanism Underlying Hypertrophic Cardiomyopathy. <i>Frontiers in Pharmacology</i> , 2016, 7, 162.	1.6	42
4314	Activation of Sterol Regulatory Element Binding Factors by Fenofibrate and Gemfibrozil Stimulates Myelination in Zebrafish. <i>Frontiers in Pharmacology</i> , 2016, 7, 206.	1.6	17
4315	Transcriptional Network Architecture of Breast Cancer Molecular Subtypes. <i>Frontiers in Physiology</i> , 2016, 7, 568.	1.3	48
4316	Crossing the Boundaries of Our Current Healthcare System by Integrating Ultra-Weak Photon Emissions with Metabolomics. <i>Frontiers in Physiology</i> , 2016, 7, 611.	1.3	6
4317	Network Analysis-Based Approach for Exploring the Potential Diagnostic Biomarkers of Acute Myocardial Infarction. <i>Frontiers in Physiology</i> , 2016, 7, 615.	1.3	49
4318	Genome-Wide Identification of VQ Motif-Containing Proteins and their Expression Profiles Under Abiotic Stresses in Maize. <i>Frontiers in Plant Science</i> , 2015, 6, 1177.	1.7	59
4319	Commentary: Comparative Transcriptome Analysis of <i>Raphanus sativus</i> Tissues. <i>Frontiers in Plant Science</i> , 2015, 6, 1191.	1.7	2
4320	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015, 6, 1194.	1.7	93
4321	Evolution and Functional Insights of Different Ancestral Orthologous Clades of Chitin Synthase Genes in the Fungal Tree of Life. <i>Frontiers in Plant Science</i> , 2016, 7, 37.	1.7	15
4322	Regulation of WRKY46 Transcription Factor Function by Mitogen-Activated Protein Kinases in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 61.	1.7	54
4323	Dual RNA-Sequencing of <i>Eucalyptus nitens</i> during <i>Phytophthora cinnamomi</i> Challenge Reveals Pathogen and Host Factors Influencing Compatibility. <i>Frontiers in Plant Science</i> , 2016, 7, 191.	1.7	54
4324	An Inventory of Nutrient-Responsive Genes in <i>Arabidopsis</i> Root Hairs. <i>Frontiers in Plant Science</i> , 2016, 7, 237.	1.7	32
4325	Relevance of the Axis Spermidine/EIF5A for Plant Growth and Development. <i>Frontiers in Plant Science</i> , 2016, 7, 245.	1.7	14
4326	Proteomic Responses of Switchgrass and Prairie Cordgrass to Senescence. <i>Frontiers in Plant Science</i> , 2016, 7, 293.	1.7	8
4327	Learning from Co-expression Networks: Possibilities and Challenges. <i>Frontiers in Plant Science</i> , 2016, 7, 444.	1.7	268

#	ARTICLE	IF	CITATIONS
4328	Genome-Wide Identification and Function Analyses of Heat Shock Transcription Factors in Potato. <i>Frontiers in Plant Science</i> , 2016, 7, 490.	1.7	70
4329	Identification of Novel Components of the Unfolded Protein Response in Arabidopsis. <i>Frontiers in Plant Science</i> , 2016, 7, 650.	1.7	18
4330	Conservation and Expression Patterns Divergence of Ascorbic Acid d-mannose/l-galactose Pathway Genes in Brassica rapa. <i>Frontiers in Plant Science</i> , 2016, 7, 778.	1.7	14
4331	Correlation-Based Network Analysis of Metabolite and Enzyme Profiles Reveals a Role of Citrate Biosynthesis in Modulating N and C Metabolism in Zea mays. <i>Frontiers in Plant Science</i> , 2016, 7, 1022.	1.7	20
4332	Proteometabolomic Study of Compatible Interaction in Tomato Fruit Challenged with Sclerotinia rolfsii Illustrates Novel Protein Network during Disease Progression. <i>Frontiers in Plant Science</i> , 2016, 7, 1034.	1.7	7
4333	Circadian Oscillation of the Lettuce Transcriptome under Constant Light and Light“Dark Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1114.	1.7	23
4334	Comparative Proteomics of Oxalate Downregulated Tomatoes Points toward Cross Talk of Signal Components and Metabolic Consequences during Post-harvest Storage. <i>Frontiers in Plant Science</i> , 2016, 7, 1147.	1.7	7
4335	Genome-Wide Characterization of the MADS-Box Gene Family in Radish (Raphanus sativus L.) and Assessment of Its Roles in Flowering and Floral Organogenesis. <i>Frontiers in Plant Science</i> , 2016, 07, 1390.	1.7	41
4336	Genome-Wide Identification, Evolution, and Co-expression Network Analysis of Mitogen-Activated Protein Kinase Kinase Kinases in Brachypodium distachyon. <i>Frontiers in Plant Science</i> , 2016, 7, 1400.	1.7	25
4337	Transcriptome Analysis of Stem and Globally Comparison with Other Tissues in Brassica napus. <i>Frontiers in Plant Science</i> , 2016, 7, 1403.	1.7	49
4338	Comparative Transcriptomic Analysis of Two Brassica napus Near-Isogenic Lines Reveals a Network of Genes That Influences Seed Oil Accumulation. <i>Frontiers in Plant Science</i> , 2016, 7, 1498.	1.7	10
4339	High-Throughput Sequencing Reveals H2O2 Stress-Associated MicroRNAs and a Potential Regulatory Network in Brachypodium distachyon Seedlings. <i>Frontiers in Plant Science</i> , 2016, 7, 1567.	1.7	16
4340	Interactive Effects of Elevated [CO2] and Water Stress on Physiological Traits and Gene Expression during Vegetative Growth in Four Durum Wheat Genotypes. <i>Frontiers in Plant Science</i> , 2016, 7, 1738.	1.7	54
4341	Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean (Vigna radiata [L.] R. Wilczek). <i>Frontiers in Plant Science</i> , 2016, 7, 1921.	1.7	23
4342	Global Lysine Acetylome Analysis of Desiccated Somatic Embryos of Picea asperata. <i>Frontiers in Plant Science</i> , 2016, 7, 1927.	1.7	14
4343	Comparative Temporal Transcriptome Profiling of Wheat near Isogenic Line Carrying Lr57 under Compatible and Incompatible Interactions. <i>Frontiers in Plant Science</i> , 2016, 7, 1943.	1.7	34
4344	Identification of Differentially Expressed Genes in Pelvic Organ Prolapse by RNA-Seq. <i>Medical Science Monitor</i> , 2016, 22, 4218-4225.	0.5	7
4345	A Group of Novel Serum Diagnostic Biomarkers for Multidrug-Resistant Tuberculosis by iTRAQ-2D LC-MS/MS and Solexa Sequencing. <i>International Journal of Biological Sciences</i> , 2016, 12, 246-256.	2.6	55



#	ARTICLE	IF	CITATIONS
4346	Hypoxia enhances the malignant nature of bladder cancer cells and concomitantly antagonizes protein glycosylation extension. <i>Oncotarget</i> , 2016, 7, 63138-63157.	0.8	58
4347	Clinical Genomics: Challenges and Opportunities. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2016, 26, 97-113.	0.4	12
4348	Surface Biofilm Interactions in Epizootic Shell Disease of the American Lobster ( <i>Homarus americanus</i> ). , 0, , .		5
4349	Calcineurin complex isolated from T-cell acute lymphoblastic leukemia (T-ALL) cells identifies new signaling pathways including mTOR/AKT/S6K whose inhibition synergize with calcineurin inhibition to promote T-ALL cell death. <i>Oncotarget</i> , 2016, 7, 45715-45729.	0.8	16
4350	Identification of miRNA/mRNA-Negative Regulation Pairs in Nasopharyngeal Carcinoma. <i>Medical Science Monitor</i> , 2016, 22, 2215-2234.	0.5	20
4351	Pathway-based Genome-wide Association Studies Reveal the Association Between Growth Factor Activity and Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 1540-1551.	0.9	8
4352	Reversal of dendritic phenotypes in 16p11.2 microduplication mouse model neurons by pharmacological targeting of a network hub. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8520-8525.	3.3	61
4353	Network Explorer. , 2016, , .		8
4354	Role of Altered Expression of miR-146a, miR-155, and miR-122 in Pediatric Patients with Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 327-335.	0.9	63
4355	Discoidin Domains as Emerging Therapeutic Targets. <i>Trends in Pharmacological Sciences</i> , 2016, 37, 641-659.	4.0	21
4356	BioNSi: A Discrete Biological Network Simulator Tool. <i>Journal of Proteome Research</i> , 2016, 15, 2871-2880.	1.8	16
4357	Chemokine (CXC motif) receptor 2 <sup>+</sup> positive monocytes aggravate the early phase of acetaminophen-induced acute liver injury. <i>Hepatology</i> , 2016, 64, 1667-1682.	3.6	271
4358	Protein turnover analysis in <i>Salmonella</i> Typhimurium during infection by dynamic SILAC, Topograph, and quantitative proteomics. <i>Journal of Basic Microbiology</i> , 2016, 56, 801-811.	1.8	8
4359	An overview of innovations and industrial solutions in Protein Microarray Technology. <i>Proteomics</i> , 2016, 16, 1297-1308.	1.3	34
4360	Data science: Accelerating innovation and discovery in chemical engineering. <i>AIChE Journal</i> , 2016, 62, 1402-1416.	1.8	63
4361	MPLEX: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. <i>MSystems</i> , 2016, 1, .	1.7	166
4362	Transcriptome analysis reveals physiological characteristics required for magnetosome formation in <i>Magnetospirillum gryphiswaldense</i> MSR-1. <i>Environmental Microbiology Reports</i> , 2016, 8, 371-381.	1.0	22
4363	Systems genetics reveals key genetic elements of drought induced gene regulation in diploid potato. <i>Plant, Cell and Environment</i> , 2016, 39, 1895-1908.	2.8	14



#	ARTICLE	IF	CITATIONS
4364	Systematic Assessment of Molecular Selectivity at the Level of Targets, Bioactive Compounds, and Structural Analogues. <i>ChemMedChem</i> , 2016, 11, 1362-1370.	1.6	6
4365	Dynamic metabolic and transcriptomic profiling of methyl jasmonate-treated hairy roots reveals synthetic characters and regulators of lignan biosynthesis in <i>Isatis indigotica</i> Fort. <i>Plant Biotechnology Journal</i> , 2016, 14, 2217-2227.	4.1	51
4366	Gene coexpression network analysis of oil biosynthesis in an interspecific backcross of oil palm. <i>Plant Journal</i> , 2016, 87, 423-441.	2.8	50
4367	Transcriptome analysis of bovine oocytes from distinct follicle sizes: Insights from correlation network analysis. <i>Molecular Reproduction and Development</i> , 2016, 83, 558-569.	1.0	34
4368	The diversity of H <sub>3</sub> loops determines the antigen-binding tendencies of antibody CDR loops. <i>Protein Science</i> , 2016, 25, 815-825.	3.1	52
4369	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. <i>Blood Cancer Journal</i> , 2016, 6, e439-e439.	2.8	16
4370	Bioinformatics Analyses of Differentially Expressed Genes Associated with Acute Myocardial Infarction. <i>Cardiovascular Therapeutics</i> , 2016, 34, 67-75.	1.1	14
4371	Partitioning of fungal assemblages across different marine habitats. <i>Environmental Microbiology Reports</i> , 2016, 8, 235-238.	1.0	44
4372	Transcriptomic investigation of meat tenderness in two Italian cattle breeds. <i>Animal Genetics</i> , 2016, 47, 273-287.	0.6	37
4373	Variation in myogenic differentiation 1 mRNA abundance is associated with beef tenderness in Nelore cattle. <i>Animal Genetics</i> , 2016, 47, 491-494.	0.6	8
4374	Role of Fanconi anemia/BRCA pathway genes in hepatocellular carcinoma chemoresistance. <i>Hepatology Research</i> , 2016, 46, 1264-1274.	1.8	16
4375	Rapid label-free quantitative analysis of the <i>E. coli</i> BL21(DE3) inner membrane proteome. <i>Proteomics</i> , 2016, 16, 85-97.	1.3	24
4376	Protein C-terminal enzymatic labeling identifies novel caspase cleavages during the apoptosis of multiple myeloma cells induced by kinase inhibition. <i>Proteomics</i> , 2016, 16, 60-69.	1.3	13
4377	Identification of imine reductase-specific sequence motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 600-610.	1.5	36
4378	Gene Network Analysis of Metallo Beta Lactamase Family Proteins Indicates the Role of Gene Partners in Antibiotic Resistance and Reveals Important Drug Targets. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 1330-1339.	1.2	21
4379	Inherent structure versus geometric metric for state space discretization. <i>Journal of Computational Chemistry</i> , 2016, 37, 1251-1258.	1.5	2
4380	Influence of pre-harvest calcium, potassium and triazole application on the proteome of apple at harvest. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 4984-4993.	1.7	8
4381	Joint genetic and network analyses identify loci associated with root growth under NaCl stress in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 918-934.	2.8	53

#	ARTICLE	IF	CITATIONS
4382	A transcriptome-wide study on the microRNA and the Argonaute 1-enriched small RNA-mediated regulatory networks involved in plant leaf senescence. <i>Plant Biology</i> , 2016, 18, 197-205.	1.8	18
4383	The relationships between serum cytokine levels and tumor infiltrating immune cells and their clinical significance in colorectal cancer. <i>International Journal of Cancer</i> , 2016, 139, 112-121.	2.3	48
4384	Persistent alterations of gene expression profiling of human peripheral blood mononuclear cells from smokers. <i>Molecular Carcinogenesis</i> , 2016, 55, 1424-1437.	1.3	4
4385	Integrating transcriptome and proteome profiling: Strategies and applications. <i>Proteomics</i> , 2016, 16, 2533-2544.	1.3	147
4386	Temporal Regulation of the <i>Bacillus subtilis</i> Acetylome and Evidence for a Role of MreB Acetylation in Cell Wall Growth. <i>MSystems</i> , 2016, 1, .	1.7	35
4387	Investigation of potential molecular biomarkers and small molecule drugs for hepatocellular carcinoma transformed from cirrhosis. <i>Oncology Letters</i> , 2016, 12, 495-503.	0.8	1
4388	Lineage-Specific Effector Signatures of Invariant NKT Cells Are Shared amongst $\gamma\delta$ T, Innate Lymphoid, and Th Cells. <i>Journal of Immunology</i> , 2016, 197, 1460-1470.	0.4	114
4389	MetaPred2CS: a sequence-based meta-predictor for protein-protein interactions of prokaryotic two-component system proteins. <i>Bioinformatics</i> , 2016, 32, 3339-3341.	1.8	2
4390	Human glioblastoma-associated microglia/monocytes express a distinct RNA profile compared to human control and murine samples. <i>Glia</i> , 2016, 64, 1416-1436.	2.5	90
4391	Gut microbiota drive the development of neuroinflammatory response in cirrhosis in mice. <i>Hepatology</i> , 2016, 64, 1232-1248.	3.6	83
4392	The microbiome of otitis media with effusion. <i>Laryngoscope</i> , 2016, 126, 2844-2851.	1.1	62
4393	Modifications of fungal membrane proteins profile under pathogenicity induction: A proteomic analysis of <i>Botrytis cinerea</i> membranome. <i>Proteomics</i> , 2016, 16, 2363-2376.	1.3	8
4394	The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. <i>Ecology Letters</i> , 2016, 19, 926-936.	3.0	803
4395	Regions of variable DNA methylation in human placenta associated with newborn neurobehavior. <i>Epigenetics</i> , 2016, 11, 603-613.	1.3	91
4396	Determinants of bacterial communities in Canadian agroforestry systems. <i>Environmental Microbiology</i> , 2016, 18, 1805-1816.	1.8	202
4397	MicroRNA signatures characterizing caste-independent ovarian activity in queen and worker honeybees ( <i>Apis mellifera</i> L.). <i>Insect Molecular Biology</i> , 2016, 25, 216-226.	1.0	39
4398	Genome-Wide Analysis of the TORC1 and Osmotic Stress Signaling Network in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 463-474.	0.8	10
4399	Sexual Polyploidization in <i>Medicago sativa</i> L.: Impact on the Phenotype, Gene Transcription, and Genome Methylation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 925-938.	0.8	6

#	ARTICLE	IF	CITATIONS
4400	Drought and flooding have distinct effects on herbivore-induced responses and resistance in <i>Solanum dulcamara</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 1485-1499.	2.8	59
4401	Neural Stem Cells Derived from Human Parthenogenetic Stem Cells Engraft and Promote Recovery in a Nonhuman Primate Model of Parkinson's Disease. <i>Cell Transplantation</i> , 2016, 25, 1945-1966.	1.2	59
4402	Genes Involved in Neurodevelopment, Neuroplasticity, and Bipolar Disorder: CACNA1C, CHRNA1, and MAPK1. <i>Neuropsychobiology</i> , 2016, 74, 159-168.	0.9	23
4403	Identification of Genes in <i>Candida glabrata</i> Conferring Altered Responses to Caspofungin, a Cell Wall Synthesis Inhibitor. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2893-2907.	0.8	19
4404	A new bioinformatic insight into the associated proteins in psychiatric disorders. <i>SpringerPlus</i> , 2016, 5, 1967.	1.2	2
4405	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016, 171, 2586-2598.	2.3	39
4406	Nucleolin interacts with influenza A nucleoprotein and contributes to viral ribonucleoprotein complexes nuclear trafficking and efficient influenza viral replication. <i>Scientific Reports</i> , 2016, 6, 29006.	1.6	29
4407	Transcriptomic and behavioural characterisation of a mouse model of burn pain identify the cholecystokinin 2 receptor as an analgesic target. <i>Molecular Pain</i> , 2016, 12, 174480691666536.	1.0	58
4408	The polymyxin B-induced transcriptomic response of a clinical, multidrug-resistant <i>Klebsiella pneumoniae</i> involves multiple regulatory elements and intracellular targets. <i>BMC Genomics</i> , 2016, 17, 737.	1.2	32
4409	Construction of a large collection of small genome variations in French dairy and beef breeds using whole-genome sequences. <i>Genetics Selection Evolution</i> , 2016, 48, 87.	1.2	15
4410	Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma. <i>Genome Biology</i> , 2016, 17, 125.	3.8	83
4411	Comparative transcriptomic analysis identifies genes differentially expressed in human epicardial progenitors and hiPSC-derived cardiac progenitors. <i>Physiological Genomics</i> , 2016, 48, 771-784.	1.0	2
4412	Acquired resistance of pancreatic cancer cells to cisplatin is multifactorial with cell context-dependent involvement of resistance genes. <i>Cancer Gene Therapy</i> , 2016, 23, 446-453.	2.2	34
4413	Idiographic Network Visualizations. <i>Leonardo</i> , 2016, 49, 447-447.	0.2	1
4414	Global Transcriptomic Analysis of Interactions between <i>Pseudomonas aeruginosa</i> and Bacteriophage PaP3. <i>Scientific Reports</i> , 2016, 6, 19237.	1.6	38
4415	Large-scale gene co-expression network as a source of functional annotation for cattle genes. <i>BMC Genomics</i> , 2016, 17, 846.	1.2	18
4416	Transcriptome sequencing of the choroid plexus in schizophrenia. <i>Translational Psychiatry</i> , 2016, 6, e964-e964.	2.4	50
4417	Identification of candidate genes in osteoporosis by integrated microarray analysis. <i>Bone and Joint Research</i> , 2016, 5, 594-601.	1.3	18

#	ARTICLE	IF	CITATIONS
4418	Combined Secretomics and Transcriptomics Revealed Cancer-Derived GDF15 is Involved in Diffuse-Type Gastric Cancer Progression and Fibroblast Activation. <i>Scientific Reports</i> , 2016, 6, 21681.	1.6	25
4419	Systems pharmacology to investigate the interaction of berberine and other drugs in treating polycystic ovary syndrome. <i>Scientific Reports</i> , 2016, 6, 28089.	1.6	24
4420	Long intergenic non-coding RNA expression signature in human breast cancer. <i>Scientific Reports</i> , 2016, 6, 37821.	1.6	26
4421	Non-obvious correlations to disease management unraveled by Bayesian artificial intelligence analyses of CMS data. <i>Artificial Intelligence in Medicine</i> , 2016, 74, 1-8.	3.8	28
4422	Model System-Guided Protein Interaction Mapping for Virus Isolated from Phloem Tissue. <i>Journal of Proteome Research</i> , 2016, 15, 4601-4611.	1.8	12
4423	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
4424	In silico identification of anti-cancer compounds and plants from traditional Chinese medicine database. <i>Scientific Reports</i> , 2016, 6, 25462.	1.6	39
4425	Comprehensive Gene expression meta-analysis and integrated bioinformatic approaches reveal shared signatures between thrombosis and myeloproliferative disorders. <i>Scientific Reports</i> , 2016, 6, 37099.	1.6	31
4426	Using Multi-objective Optimization to Identify Dynamical Network Biomarkers as Early-warning Signals of Complex Diseases. <i>Scientific Reports</i> , 2016, 6, 22023.	1.6	18
4427	HydDB: A web tool for hydrogenase classification and analysis. <i>Scientific Reports</i> , 2016, 6, 34212.	1.6	372
4428	A three-gene expression-based risk score can refine the European LeukemiaNet AML classification. <i>Journal of Hematology and Oncology</i> , 2016, 9, 78.	6.9	21
4429	Bioinformatics analysis of molecular mechanisms involved in intervertebral disc degeneration induced by TNF- $\alpha$ and IL-1 $\beta$ . <i>Molecular Medicine Reports</i> , 2016, 13, 2925-2931.	1.1	13
4430	Network-based analysis of reverse phase protein array data. , 2016, , .		0
4431	AKT1 as the PageRank hub gene is associated with melanoma and its functional annotation is highly related to the estrogen signaling pathway that may regulate the growth of melanoma. <i>Oncology Reports</i> , 2016, 36, 2087-2093.	1.2	9
4432	Triptolide targets on MYC towards testis may induce male reproductive toxicity. , 2016, , .		3
4433	Triptolide regulates immune response network against systemic lupus erythematosus. , 2016, , .		0
4434	What could the entire cornstover contribute to the enhancement of waste activated sludge acidification? Performance assessment and microbial community analysis. <i>Biotechnology for Biofuels</i> , 2016, 9, 241.	6.2	30
4435	Dysfunctional gut microbiota and relative co-abundance network in infantile eczema. <i>Gut Pathogens</i> , 2016, 8, 36.	1.6	34

#	ARTICLE	IF	CITATIONS
4436	Transcriptional identification and characterization of differentially expressed genes associated with embryogenesis in radish ( <i>Raphanus sativus</i> L.). <i>Scientific Reports</i> , 2016, 6, 21652.	1.6	42
4437	The application of transcriptomic data in the authentication of beef derived from contrasting production systems. <i>BMC Genomics</i> , 2016, 17, 746.	1.2	7
4438	An interactomics overview of the human and bovine milk proteome over lactation. <i>Proteome Science</i> , 2016, 15, 1.	0.7	37
4439	Long non-coding RNAs and genes contributing to the generation of cancer stem cells in hepatocellular carcinoma identified by RNA sequencing analysis. <i>Oncology Reports</i> , 2016, 36, 2619-2624.	1.2	7
4440	Prediction and characterization of protein-protein interaction network in <i>Bacillus licheniformis</i> WX-02. <i>Scientific Reports</i> , 2016, 6, 19486.	1.6	12
4441	Identification of novel acid stress resistance genes and their roles in cancer cell growth. <i>DMM Disease Models and Mechanisms</i> , 2016, 9, 1039-49.	1.2	5
4442	Complement Factor D (CFD) bound by Saikosaponin D (SSD) extracted from <i>Bupleuri Radix</i> might drive the anti-depression network to function. , 2016, , .		0
4443	Overlapping signatures of chronic pain in the DNA methylation landscape of prefrontal cortex and peripheral T cells. <i>Scientific Reports</i> , 2016, 6, 19615.	1.6	78
4444	Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat. <i>Scientific Reports</i> , 2016, 6, 23805.	1.6	29
4445	The Zebrafish Equivalent of Alzheimer's Disease-Associated PRESENILIN Isoform PS2V Regulates Inflammatory and Other Responses to Hypoxic Stress. <i>Journal of Alzheimer's Disease</i> , 2016, 52, 581-608.	1.2	25
4446	Inference and differential analysis of Extended Core Networks: A way to study anti-sense regulation. , 2016, , .		3
4447	Systems-level effects of ectopic galectin-7 reconstitution in cervical cancer and its microenvironment. <i>BMC Cancer</i> , 2016, 16, 680.	1.1	26
4448	Structural elucidation of estrus urinary lipocalin protein (EULP) and evaluating binding affinity with pheromones using molecular docking and fluorescence study. <i>Scientific Reports</i> , 2016, 6, 35900.	1.6	9
4449	Protein profile and protein interaction network of <i>Moniliophthora perniciosa</i> basidiospores. <i>BMC Microbiology</i> , 2016, 16, 120.	1.3	13
4450	Gene expression profile of angiogenic factors in pulmonary arteries in COPD: relationship with vascular remodeling. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2016, 310, L583-L592.	1.3	13
4451	Sparse Tangibles. , 2016, , .		16
4452	Structure and flexibility: Investigating the relation between the structure of the mental lexicon, fluid intelligence, and creative achievement.. <i>Psychology of Aesthetics, Creativity, and the Arts</i> , 2016, 10, 377-388.	1.0	91
4453	Peptide affinity analysis of proteins that bind to an unstructured region containing the transactivating domain of the osmoprotective transcription factor NFAT5. <i>Physiological Genomics</i> , 2016, 48, 835-849.	1.0	1

#	ARTICLE	IF	CITATIONS
4454	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. <i>Scientific Reports</i> , 2016, 6, 18517.	1.6	143
4455	Microvesicles from brain-extract <sup>+</sup> treated mesenchymal stem cells improve neurological functions in a rat model of ischemic stroke. <i>Scientific Reports</i> , 2016, 6, 33038.	1.6	84
4456	Alternative splicing in tomato pollen in response to heat stress. <i>DNA Research</i> , 2017, 24, dsw051.	1.5	55
4457	Prediction of key genes and miRNAs responsible for loss of muscle force in patients during an acute exacerbation of chronic obstructive pulmonary disease. <i>International Journal of Molecular Medicine</i> , 2016, 38, 1450-1462.	1.8	15
4458	Population Dynamics of Bulking and Foaming Bacteria in a Full-scale Wastewater Treatment Plant over Five Years. <i>Scientific Reports</i> , 2016, 6, 24180.	1.6	30
4459	Kinase impact assessment in the landscape of fusion genes that retain kinase domains: a pan-cancer study. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw127.	3.2	19
4460	Strain Prioritization and Genome Mining for Eneidyne Natural Products. <i>MBio</i> , 2016, 7, .	1.8	89
4461	A new evolutionary microRNA marker selection using next-generation sequencing data. , 2016, , .		2
4462	Widespread occurrence of lysine methylation in <i>Plasmodium falciparum</i> proteins at asexual blood stages. <i>Scientific Reports</i> , 2016, 6, 35432.	1.6	18
4463	Chromatin remodeller SMARCA4 recruits topoisomerase 1 and suppresses transcription-associated genomic instability. <i>Nature Communications</i> , 2016, 7, 10549.	5.8	65
4464	Bridging the gap between clinicians and systems biologists: from network biology to translational biomedical research. <i>Journal of Translational Medicine</i> , 2016, 14, 324.	1.8	21
4465	Identification of potential candidate genes for hypertensive nephropathy based on gene expression profile. <i>BMC Nephrology</i> , 2016, 17, 149.	0.8	15
4466	Dynamics Correlation Network for Allosteric Switching of PreQ1 Riboswitch. <i>Scientific Reports</i> , 2016, 6, 31005.	1.6	24
4467	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <i>Scientific Reports</i> , 2016, 6, 38575.	1.6	4
4468	An investigation into blood microbiota and its potential association with Bacterial Chondronecrosis with Osteomyelitis (BCO) in Broilers. <i>Scientific Reports</i> , 2016, 6, 25882.	1.6	56
4469	bnstruct: an R package for Bayesian Network structure learning in the presence of missing data. <i>Bioinformatics</i> , 2017, 33, 1250-1252.	1.8	65
4470	Interactomic analysis of REST/NRSF and implications of its functional links with the transcription suppressor TRIM28 during neuronal differentiation. <i>Scientific Reports</i> , 2016, 6, 39049.	1.6	20
4471	Sodium selenate regulates the brain ionome in a transgenic mouse model of Alzheimer <sup>TM</sup> s disease. <i>Scientific Reports</i> , 2016, 6, 39290.	1.6	27

#	ARTICLE	IF	CITATIONS
4472	Deep sequencing of wheat sRNA transcriptome reveals distinct temporal expression pattern of miRNAs in response to heat, light and UV. <i>Scientific Reports</i> , 2016, 6, 39373.	1.6	51
4473	MetaboSignal: a network-based approach for topological analysis of metabolite regulation via metabolic and signaling pathways. <i>Bioinformatics</i> , 2017, 33, 773-775.	1.8	20
4474	Co-expression network analysis of duplicate genes in maize ( <i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016, 17, 875.	1.2	36
4476	Relative quantification of phosphoproteomic changes in grapevine ( <i>Vitis vinifera</i> L.) leaves in response to abscisic acid. <i>Horticulture Research</i> , 2016, 3, 16029.	2.9	15
4477	The non-canonical mitochondrial inner membrane presequence translocase of trypanosomatids contains two essential rhomboid-like proteins. <i>Nature Communications</i> , 2016, 7, 13707.	5.8	40
4478	Gene network analysis identifies rumen epithelial cell proliferation, differentiation and metabolic pathways perturbed by diet and correlated with methane production. <i>Scientific Reports</i> , 2016, 6, 39022.	1.6	68
4479	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations. <i>Journal of Animal Science</i> , 2016, 94, 1446-1458.	0.2	11
4480	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. <i>Journal of Animal Science</i> , 2016, 94, 3693-3702.	0.2	27
4481	Galectin-3 Induces a Pro-degradative/inflammatory Gene Signature in Human Chondrocytes, Teaming Up with Galectin-1 in Osteoarthritis Pathogenesis. <i>Scientific Reports</i> , 2016, 6, 39112.	1.6	47
4482	Differential DNA methylation in peripheral blood mononuclear cells in adolescents exposed to significant early but not later childhood adversity. <i>Development and Psychopathology</i> , 2016, 28, 1385-1399.	1.4	61
4483	Transcriptome analysis of human ageing in male skin shows mid-life period of variability and central role of NF- $\kappa$ B. <i>Scientific Reports</i> , 2016, 6, 26846.	1.6	52
4484	CASP3, TP53, and MYC Targeted by Triptolide towards Ovary Induce Female Reproductive Toxicity. , 2016, , .		0
4485	Application of Latent Semantic Analysis to Clustering of Cardiovascular Gene Ontology. , 2016, , .		1
4486	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	3.2	42
4487	Comparative Systems Analyses Reveal Molecular Signatures of Clinically tested Vaccine Adjuvants. <i>Scientific Reports</i> , 2016, 6, 39097.	1.6	53
4488	Increased burden of deleterious variants in essential genes in autism spectrum disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15054-15059.	3.3	68
4489	Mitotic phosphotyrosine network analysis reveals that tyrosine phosphorylation regulates Polo-like kinase 1 (PLK1). <i>Science Signaling</i> , 2016, 9, rs14.	1.6	26
4490	A biogeographic network reveals evolutionary links between deep-sea hydrothermal vent and methane seep faunas. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20162337.	1.2	47



#	ARTICLE	IF	CITATIONS
4491	Human lymphoid organ dendritic cell identity is predominantly dictated by ontogeny, not tissue microenvironment. <i>Science Immunology</i> , 2016, 1, .	5.6	145
4492	Systems analysis uncovers inflammatory Th/Tc17-driven modules during acute GVHD in monkey and human T cells. <i>Blood</i> , 2016, 128, 2568-2579.	0.6	46
4493	Microcystin-Leucine Arginine Causes Cytotoxic Effects in Sertoli Cells Resulting in Reproductive Dysfunction in Male Mice. <i>Scientific Reports</i> , 2016, 6, 39238.	1.6	35
4494	BiMat: a MATLAB package to facilitate the analysis of bipartite networks. <i>Methods in Ecology and Evolution</i> , 2016, 7, 127-132.	2.2	58
4495	System pharmacology: Application of network theory in predicting potential adverse drug reaction based on gene expression data. , 2016, , .		3
4496	Epigenetic profiling of human brain differential DNA methylation networks in schizophrenia. <i>BMC Medical Genomics</i> , 2016, 9, 68.	0.7	32
4497	Developing integrated crop knowledge networks to advance candidate gene discovery. <i>Applied &amp; Translational Genomics</i> , 2016, 11, 18-26.	2.1	66
4498	Identification and Validation of PCAT14 as Prognostic Biomarker in Prostate Cancer. <i>Neoplasia</i> , 2016, 18, 489-499.	2.3	55
4499	Gene expression and metabolism preceding soft scald, a chilling injury of "Honeycrisp" apple fruit. <i>BMC Genomics</i> , 2016, 17, 798.	1.2	28
4500	The Proteome of BLOC-1 Genetic Defects Identifies the Arp2/3 Actin Polymerization Complex to Function Downstream of the Schizophrenia Susceptibility Factor Dysbindin at the Synapse. <i>Journal of Neuroscience</i> , 2016, 36, 12393-12411.	1.7	26
4501	Single-cell sequencing maps gene expression to mutational phylogenies in PDGF- and EGF-driven gliomas. <i>Molecular Systems Biology</i> , 2016, 12, 889.	3.2	91
4502	Graph Theoretic Concepts in the Study of Biological Networks. <i>Springer Proceedings in Mathematics and Statistics</i> , 2016, , 187-200.	0.1	0
4503	Genome-wide identification and analysis of rice genes to elucidate morphological agronomic traits. <i>Journal of Plant Biology</i> , 2016, 59, 639-647.	0.9	5
4504	Network Based Linear Population Size Reduction in SHADE. , 2016, , .		16
4505	Analysis of Post-Traumatic Brain Injury Gene Expression Signature Reveals Tubulins, Nfe2l2, Nfkb, Cd44 and S100a4 as Treatment Targets. <i>Scientific Reports</i> , 2016, 6, 31570.	1.6	60
4506	Interaction of MDM33 with mitochondrial inner membrane homeostasis pathways in yeast. <i>Scientific Reports</i> , 2016, 5, 18344.	1.6	20
4507	Effect on Intermittent Hypoxia on Plasma Exosomal Micro RNA Signature and Endothelial Function in Healthy Adults. <i>Sleep</i> , 2016, 39, 2077-2090.	0.6	75
4508	Characterization of DWARF14 Genes in Populus. <i>Scientific Reports</i> , 2016, 6, 21593.	1.6	26

#	ARTICLE	IF	CITATIONS
4509	The genome sequence of Sea-Island cotton ( <i>Gossypium barbadense</i> ) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2016, 5, 17662.	1.6	294
4510	A land similarity approach to modeling complex ecological networks. , 2016, , .		1
4511	Identification of gene network motifs for cancer disease diagnosis. , 2016, , .		6
4512	Integrated network-diversity analyses suggest suppressive effect of Hodgkin's lymphoma and slightly relieving effect of chemotherapy on human milk microbiome. <i>Scientific Reports</i> , 2016, 6, 28048.	1.6	10
4513	Requirement for Dicer in Maintenance of Monosynaptic Sensory-Motor Circuits in the Spinal Cord. <i>Cell Reports</i> , 2016, 17, 2163-2172.	2.9	8
4514	Integrative approaches for data analysis in systems biology: Current advances. , 2016, , .		3
4515	Sig2GRN: a software tool linking signaling pathway with gene regulatory network for dynamic simulation. <i>BMC Systems Biology</i> , 2016, 10, 123.	3.0	3
4516	Discovering gene re-ranking efficiency and conserved gene-gene relationships derived from gene co-expression network analysis on breast cancer data. <i>Scientific Reports</i> , 2016, 6, 20518.	1.6	25
4517	An Integrative Genetic Study of Rice Metabolism, Growth and Stochastic Variation Reveals Potential C/N Partitioning Loci. <i>Scientific Reports</i> , 2016, 6, 30143.	1.6	17
4518	Undiscovered Physiology of Transcript and Protein Networks. , 2016, 6, 1851-1872.		0
4519	Modélisation logique et analyse intégrative des voies moléculaires impliquées dans la polyarthrite rhumatoïde. <i>Revue Du Rhumatisme (Edition Francaise)</i> , 2016, 83, A297.	0.0	0
4520	A transcriptome-wide, organ-specific regulatory map of <i>Dendrobium officinale</i> , an important traditional Chinese orchid herb. <i>Scientific Reports</i> , 2016, 6, 18864.	1.6	44
4521	Network Metamodeling: Effect of Correlation Metric Choice on Phylogenomic and Transcriptomic Network Topology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 143-183.	0.6	27
4522	DLG5 connects cell polarity and Hippo signaling protein networks by linking PAR-1 with MST1/2. <i>Genes and Development</i> , 2016, 30, 2696-2709.	2.7	67
4523	Total particulate matter concentration skews cigarette smoke's gene expression profile. <i>ERJ Open Research</i> , 2016, 2, 00029-2016.	1.1	10
4524	Integrating network, sequence and functional features using machine learning approaches towards identification of novel Alzheimer genes. <i>BMC Genomics</i> , 2016, 17, 807.	1.2	30
4525	Analysis of rumen microbial community in cattle through the integration of metagenomic and network-based approaches. , 2016, , .		3
4526	The chromatin-binding protein Smyd1 restricts adult mammalian heart growth. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2016, 311, H1234-H1247.	1.5	51

#	ARTICLE	IF	CITATIONS
4527	MetaMIS: a metagenomic microbial interaction simulator based on microbial community profiles. <i>BMC Bioinformatics</i> , 2016, 17, 488.	1.2	70
4528	Effects of light attenuation on the sponge holobiont- implications for dredging management. <i>Scientific Reports</i> , 2016, 6, 39038.	1.6	56
4529	Microbial profiles at baseline and not the use of antibiotics determine the clinical outcome of the treatment of chronic periodontitis. <i>Scientific Reports</i> , 2016, 6, 20205.	1.6	51
4530	Biocatalytic study of novel oleate hydratases. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2016, 133, S243-S249.	1.8	32
4531	Iterative segmented least square method for functional microRNA-mRNA module discovery in breast cancer. , 2016, , .		1
4532	Gene dysregulation is restored in the Parkinson's disease MPTP neurotoxic mice model upon treatment of the therapeutic drug Cull(atsm). <i>Scientific Reports</i> , 2016, 6, 22398.	1.6	14
4533	Toward Repurposing Metformin as a Precision Anti-Cancer Therapy Using Structural Systems Pharmacology. <i>Scientific Reports</i> , 2016, 6, 20441.	1.6	34
4534	Global quantitative proteomics reveal up-regulation of endoplasmic reticulum stress response proteins upon depletion of eIF5A in HeLa cells. <i>Scientific Reports</i> , 2016, 6, 25795.	1.6	43
4535	DMirNet: Inferring direct microRNA-mRNA association networks. <i>BMC Systems Biology</i> , 2016, 10, 125.	3.0	4
4536	Differential root transcriptomics in a polyploid non-model crop: the importance of respiration during osmotic stress. <i>Scientific Reports</i> , 2016, 6, 22583.	1.6	34
4537	Personalized Immunomonitoring Uncovers Molecular Networks that Stratify Lupus Patients. <i>Cell</i> , 2016, 165, 551-565.	13.5	524
4538	A network-based drug repositioning infrastructure for precision cancer medicine through targeting significantly mutated genes in the human cancer genomes. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016, 23, 681-691.	2.2	46
4539	Interaction between bound water molecules and local protein structures: A statistical analysis of the hydrogen bond structures around bound water molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 43-51.	1.5	14
4540	Transcriptional profiling and muscle cross-section analysis reveal signs of ischemia reperfusion injury following total knee arthroplasty with tourniquet. <i>Physiological Reports</i> , 2016, 4, e12671.	0.7	31
4541	Endemic plants harbour specific <i>Trichoderma</i> communities with an exceptional potential for biocontrol of phytopathogens. <i>Journal of Biotechnology</i> , 2016, 235, 162-170.	1.9	37
4542	An Atlas of the Human Kinome Reveals the Mutational Landscape Underlying Dysregulated Phosphorylation Cascades in Cancer. <i>Cancer Research</i> , 2016, 76, 1733-1745.	0.4	20
4543	Transcriptomic profiling of chemical exposure reveals roles of Yap1 in protecting yeast cells from oxidative and other types of stresses. <i>Yeast</i> , 2016, 33, 5-19.	0.8	8
4544	Clinical Epigenetics and Epigenomics. <i>Translational Bioinformatics</i> , 2016, , 269-293.	0.0	0

#	ARTICLE	IF	CITATIONS
4545	Biostatistics, Data Mining and Computational Modeling. <i>Translational Bioinformatics</i> , 2016, , 23-57.	0.0	2
4546	Gene Expression and Profiling. <i>Translational Bioinformatics</i> , 2016, , 59-82.	0.0	0
4547	Proteomic Profiling: Data Mining and Analyses. <i>Translational Bioinformatics</i> , 2016, , 133-173.	0.0	0
4548	Proteomic Analysis Reveals a Novel Mutator S (MutS) Partner Involved in Mismatch Repair Pathway. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1299-1308.	2.5	28
4549	The C-terminal motif of SiAGO1b is required for the regulation of growth, development and stress responses in foxtail millet ( <i>Setaria italica</i> (L.) P. Beauv). <i>Journal of Experimental Botany</i> , 2016, 67, 3237-3249.	2.4	33
4550	Connectivity to the surface determines diversity patterns in subsurface aquifers of the Fennoscandian shield. <i>ISME Journal</i> , 2016, 10, 2447-2458.	4.4	93
4551	Genetic architecture of wood properties based on association analysis and co-expression networks in white spruce. <i>New Phytologist</i> , 2016, 210, 240-255.	3.5	43
4552	A scientometric analysis of reproductive medicine. <i>Scientometrics</i> , 2016, 109, 103-120.	1.6	8
4553	PKC $\delta$ and HMGB1 antagonistically control hydrogen peroxide-induced poly-ADP-ribose formation. <i>Nucleic Acids Research</i> , 2016, 44, 7630-7645.	6.5	15
4554	Bioinformatics Based Approaches to Study Virus-Host Interactions During Chikungunya Virus Infection. <i>Methods in Molecular Biology</i> , 2016, 1426, 195-200.	0.4	1
4555	Differential Functional Analysis and Change Motifs in Gene Networks to Explore the Role of Anti-sense Transcription. <i>Lecture Notes in Computer Science</i> , 2016, , 117-126.	1.0	3
4556	Topological and Conceptual Complex Network Models for Environmental Planning. <i>Procedia Computer Science</i> , 2016, 83, 123-130.	1.2	1
4557	A Laser Dissection-RNAseq Analysis Highlights the Activation of Cytokinin Pathways by Nod Factors in the <i>Medicago truncatula</i> Root Epidermis. <i>Plant Physiology</i> , 2016, 171, 2256-2276.	2.3	128
4558	Age-related changes in gut microbiota composition from newborn to centenarian: a cross-sectional study. <i>BMC Microbiology</i> , 2016, 16, 90.	1.3	993
4559	Screening for genes and subnetworks associated with pancreatic cancer based on the gene expression profile. <i>Molecular Medicine Reports</i> , 2016, 13, 3779-3786.	1.1	4
4560	Synergistic Allosteric Mechanism of Fructose-1,6-bisphosphate and Serine for Pyruvate Kinase M2 via Dynamics Fluctuation Network Analysis. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1184-1192.	2.5	33
4561	A proteomic signature of ovarian cancer tumor fluid identified by highthroughput and verified by targeted proteomics. <i>Journal of Proteomics</i> , 2016, 145, 226-236.	1.2	33
4562	Computational analysis of fitness landscapes and evolutionary networks from in vitro evolution experiments. <i>Methods</i> , 2016, 106, 86-96.	1.9	10

#	ARTICLE	IF	CITATIONS
4563	Transcriptomic network analyses of leaf dehydration responses identify highly connected ABA and ethylene signaling hubs in three grapevine species differing in drought tolerance. <i>BMC Plant Biology</i> , 2016, 16, 118.	1.6	62
4564	BMPOS: a Flexible and User-Friendly Tool Sets for Microbiome Studies. <i>Microbial Ecology</i> , 2016, 72, 443-447.	1.4	45
4565	A comprehensive assessment of networks and pathways of hypoxia-associated proteins and identification of responsive protein modules. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2016, 5, 1.	1.2	4
4566	Construction of an immunorelated protein-protein interaction network for clarifying the mechanism of burn. <i>Burns</i> , 2016, 42, 405-413.	1.1	8
4567	Identifying a biomarker network for corticosteroid resistance in asthma from bronchoalveolar lavage samples. <i>Molecular Biology Reports</i> , 2016, 43, 697-710.	1.0	17
4568	High-rate activated sludge communities have a distinctly different structure compared to low-rate sludge communities, and are less sensitive towards environmental and operational variables. <i>Water Research</i> , 2016, 100, 137-145.	5.3	62
4569	Gene expression profiling during seed-filling process in peanut with emphasis on oil biosynthesis networks. <i>Plant Science</i> , 2016, 248, 116-127.	1.7	21
4570	Global <i>De Novo</i> Protein-Protein Interactome Elucidates Interactions of Drought-Responsive Proteins in Horse Gram ( <i>Macrotyloma uniflorum</i> ). <i>Journal of Proteome Research</i> , 2016, 15, 1794-1809.	1.8	17
4571	Global Profiling of Protein Lysine Malonylation in <i>Escherichia coli</i> Reveals Its Role in Energy Metabolism. <i>Journal of Proteome Research</i> , 2016, 15, 2060-2071.	1.8	63
4572	Tracing haematopoietic stem cell formation at single-cell resolution. <i>Nature</i> , 2016, 533, 487-492.	13.7	297
4573	Network Pharmacology-based Approaches Capture Essence of Chinese Herbal Medicines. <i>Chinese Herbal Medicines</i> , 2016, 8, 107-116.	1.2	61
4574	Monitoring light/dark association dynamics of multi-protein complexes in cyanobacteria using size exclusion chromatography-based proteomics. <i>Journal of Proteomics</i> , 2016, 142, 33-44.	1.2	12
4575	Skeletal muscle transcriptional profiles in two Italian beef breeds, Chianina and Maremmana, reveal breed specific variation. <i>Molecular Biology Reports</i> , 2016, 43, 253-268.	1.0	16
4576	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. <i>Journal of Proteomics</i> , 2016, 142, 45-52.	1.2	21
4577	The Proteasome Stress Regulon Is Controlled by a Pair of NAC Transcription Factors in Arabidopsis. <i>Plant Cell</i> , 2016, 28, 1279-1296.	3.1	72
4578	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. <i>BMC Genomics</i> , 2016, 17, 235.	1.2	31
4579	Explorations in genome-wide association studies and network analyses with dairy cattle fertility traits. <i>Journal of Dairy Science</i> , 2016, 99, 6420-6435.	1.4	59
4580	Computational approaches in target identification and drug discovery. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 177-184.	1.9	270

#	ARTICLE	IF	CITATIONS
4581	Environmental factors shaping cultured free-living amoebae and their associated bacterial community within drinking water network. <i>Water Research</i> , 2016, 100, 382-392.	5.3	60
4582	Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. <i>Journal of Experimental Medicine</i> , 2016, 213, 1061-1077.	4.2	45
4583	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. <i>BMC Bioinformatics</i> , 2016, 17, 3.	1.2	50
4584	<i>Bifidobacterium thermophilum</i> RBL67 impacts on growth and virulence gene expression of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhimurium. <i>BMC Microbiology</i> , 2016, 16, 46.	1.3	33
4585	A transcriptional miRNA-gene network associated with lung adenocarcinoma metastasis based on the TCGA database. <i>Oncology Reports</i> , 2016, 35, 2257-2269.	1.2	12
4586	Bioinformatics identification of the methylerythritol phosphate pathway associated genes in <i>Arabidopsis thaliana</i> with <i>ceh1</i> mutant. <i>Russian Journal of Plant Physiology</i> , 2016, 63, 293-299.	0.5	1
4587	p53 Pulses Diversify Target Gene Expression Dynamics in an mRNA Half-Life-Dependent Manner and Delineate Co-regulated Target Gene Subnetworks. <i>Cell Systems</i> , 2016, 2, 272-282.	2.9	68
4588	Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles. <i>Journal of Biomedical Informatics</i> , 2016, 61, 194-202.	2.5	6
4589	Regional features of northern Italian sparkling wines, identified using solid-phase micro extraction and comprehensive two-dimensional gas chromatography coupled with time-of-flight mass spectrometry. <i>Food Chemistry</i> , 2016, 208, 68-80.	4.2	56
4590	High richness of ectomycorrhizal fungi and low host specificity in a coastal sand dune ecosystem revealed by network analysis. <i>Ecology and Evolution</i> , 2016, 6, 349-362.	0.8	21
4591	MAGE-A1 promotes melanoma proliferation and migration through C-JUN activation. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 959-965.	1.0	23
4592	Gene expression profile analysis of pancreatic cancer based on microarray data. <i>Molecular Medicine Reports</i> , 2016, 13, 3913-3919.	1.1	16
4593	RNA-Seq analysis of non-small cell lung cancer in female never-smokers reveals candidate cancer-associated long non-coding RNAs. <i>Pathology Research and Practice</i> , 2016, 212, 549-554.	1.0	18
4594	Predicting Protein-Protein Interactions from the Molecular to the Proteome Level. <i>Chemical Reviews</i> , 2016, 116, 4884-4909.	23.0	289
4595	WikiPathways: capturing the full diversity of pathway knowledge. <i>Nucleic Acids Research</i> , 2016, 44, D488-D494.	6.5	380
4596	Tissue-overlapping response of half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ) to thermostressing based on transcriptome profiles. <i>Gene</i> , 2016, 586, 97-104.	1.0	37
4597	Evolutionary assembly patterns of prokaryotic genomes. <i>Genome Research</i> , 2016, 26, 826-833.	2.4	15
4598	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals the Meristematic Nature of <i>Arabidopsis</i> Gynoecial Medial Domain. <i>Plant Physiology</i> , 2016, 171, 42-61.	2.3	32

#	ARTICLE	IF	CITATIONS
4599	Sensory effect of acetaldehyde on the perception of 3-mercaptohexan-1-ol and 3-isobutyl-2-methoxy-pyrazine. <i>Australian Journal of Grape and Wine Research</i> , 2016, 22, 197-204.	1.0	17
4600	High Conservation in Transcriptomic and Proteomic Response of White Sturgeon to Equipotent Concentrations of 2,3,7,8-TCDD, PCB 77, and Benzo[a]pyrene. <i>Environmental Science &amp; Technology</i> , 2016, 50, 4826-4835.	4.6	35
4601	Comparative Phosphoproteomics Analysis of VEGF and Angiopoietin-1 Signaling Reveals ZO-1 as a Critical Regulator of Endothelial Cell Proliferation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1511-1525.	2.5	18
4602	Unique microbial-derived volatile organic compounds in portal venous circulation in murine non-alcoholic fatty liver disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1337-1344.	1.8	20
4603	Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4976-4981.	3.3	249
4604	Mass spectrometry analysis of adipose-derived stem cells reveals a significant effect of hypoxia on pathways regulating extracellular matrix. <i>Stem Cell Research and Therapy</i> , 2016, 7, 52.	2.4	49
4605	Bioinformatic exploration of MTA1-regulated gene networks in colon cancer. <i>Frontiers of Medicine</i> , 2016, 10, 178-182.	1.5	5
4606	Metabolites involved in glycolysis and amino acid metabolism are altered in short children born small for gestational age. <i>Pediatric Research</i> , 2016, 80, 299-305.	1.1	6
4607	G-quadruplexes as novel cis-elements controlling transcription during embryonic development. <i>Nucleic Acids Research</i> , 2016, 44, 4163-4173.	6.5	83
4608	Determination of antigenicity-altering patches on the major surface protein of human influenza A/H3N2 viruses. <i>Virus Evolution</i> , 2016, 2, vev025.	2.2	21
4609	HiQuant: Rapid Postquantification Analysis of Large-Scale MS-Generated Proteomics Data. <i>Journal of Proteome Research</i> , 2016, 15, 2072-2079.	1.8	7
4610	Chaperone-like protein HYPK and its interacting partners augment autophagy. <i>European Journal of Cell Biology</i> , 2016, 95, 182-194.	1.6	6
4611	Bioinformatics analysis of molecular mechanism of the expansion of hematopoietic stem cell transduced by HOXB4/HOXC4. <i>Hematology</i> , 2016, 21, 462-469.	0.7	3
4612	Comprehensive transcriptome analysis identifies novel molecular subtypes and subtype-specific RNAs of triple-negative breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 33.	2.2	176
4613	Genetic diversity of native and introduced populations of the invasive house crow ( <i>Corvus splendens</i> ) in Asia and Africa. <i>Biological Invasions</i> , 2016, 18, 1867-1881.	1.2	8
4614	mDCC_tools: characterizing multi-modal atomic motions in molecular dynamics trajectories. <i>Bioinformatics</i> , 2016, 32, 2531-2533.	1.8	3
4615	Neutrophil-Derived Exosomes: A New Mechanism Contributing to Airway Smooth Muscle Remodeling. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2016, 55, 450-461.	1.4	101
4616	Cathepsin L in tumor angiogenesis and its therapeutic intervention by the small molecule inhibitor KGP94. <i>Clinical and Experimental Metastasis</i> , 2016, 33, 461-473.	1.7	37



#	ARTICLE	IF	CITATIONS
4617	Brain in situ hybridization maps as a source for reverse-engineering transcriptional regulatory networks: Alzheimer's disease insights. <i>Gene</i> , 2016, 586, 77-86.	1.0	17
4618	Network analysis with PubChem BioAssay: Preliminary study on drug abuse. , 2016, , .		0
4619	Using biological networks to integrate, visualize and analyze genomics data. <i>Genetics Selection Evolution</i> , 2016, 48, 27.	1.2	86
4620	Zika Virus Depletes Neural Progenitors in Human Cerebral Organoids through Activation of the Innate Immune Receptor TLR3. <i>Cell Stem Cell</i> , 2016, 19, 258-265.	5.2	629
4621	Elucidation of tonic and activated B-cell receptor signaling in Burkitt's lymphoma provides insights into regulation of cell survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5688-5693.	3.3	44
4622	WeSME: uncovering mutual exclusivity of cancer drivers and beyond. <i>Bioinformatics</i> , 2017, 33, 814-821.	1.8	79
4623	NAPS: Network Analysis of Protein Structures. <i>Nucleic Acids Research</i> , 2016, 44, W375-W382.	6.5	150
4624	Generation of topic evolution trees from heterogeneous bibliographic networks. <i>Journal of Informetrics</i> , 2016, 10, 606-621.	1.4	19
4625	Combining complex networks and data mining: Why and how. <i>Physics Reports</i> , 2016, 635, 1-44.	10.3	139
4626	Transcriptome analysis of reproductive-stage <i>Arabidopsis</i> plants exposed gamma-ray irradiation at various doses. <i>International Journal of Radiation Biology</i> , 2016, 92, 451-465.	1.0	13
4627	PREDAC-H3: a user-friendly platform for antigenic surveillance of human influenza a(H3N2) virus based on hemagglutinin sequences. <i>Bioinformatics</i> , 2016, 32, 2526-2527.	1.8	5
4628	Application of single-cell RNA sequencing in optimizing a combinatorial therapeutic strategy in metastatic renal cell carcinoma. <i>Genome Biology</i> , 2016, 17, 80.	3.8	170
4629	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016, 1, .	1.7	53
4630	Metabolic and growth responses of maize to successive drought and re-watering cycles. <i>Agricultural Water Management</i> , 2016, 172, 62-73.	2.4	54
4631	Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1622-1641.	2.5	92
4632	Network analysis and cross species comparison of protein-protein interaction networks of human, mouse and rat cytochrome P450 proteins that degrade xenobiotics. <i>Molecular BioSystems</i> , 2016, 12, 2119-2134.	2.9	11
4633	Biological findings from the PheWAS catalog: focus on connective tissue-related disorders (pelvic) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 779-795.	1.8	14
4634	The Widening Sphere of Influence of HOXB7 in Solid Tumors. <i>Cancer Research</i> , 2016, 76, 2857-2862.	0.4	30

#	ARTICLE	IF	CITATIONS
4635	Single-cell profiling of human megakaryocyte-erythroid progenitors identifies distinct megakaryocyte and erythroid differentiation pathways. <i>Genome Biology</i> , 2016, 17, 83.	3.8	124
4636	Design of Visualizations for Human-Information Interaction: A Pattern-Based Framework. <i>Synthesis Lectures on Visualization</i> , 2016, 4, 1-185.	0.1	25
4637	Molecular Signatures of Membrane Protein Complexes Underlying Muscular Dystrophy. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2169-2185.	2.5	18
4638	Proteomic and phosphoproteomic analysis reveals the response and defense mechanism in leaves of diploid wheat <i>T. monococcum</i> under salt stress and recovery. <i>Journal of Proteomics</i> , 2016, 143, 93-105.	1.2	61
4639	A Gating Mechanism of the Serotonin 5-HT 3 Receptor. <i>Structure</i> , 2016, 24, 816-825.	1.6	43
4640	HsfA2 Controls the Activity of Developmentally and Stress-Regulated Heat Stress Protection Mechanisms in Tomato Male Reproductive Tissues. <i>Plant Physiology</i> , 2016, 170, 2461-2477.	2.3	148
4641	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. <i>Genetics Selection Evolution</i> , 2016, 48, 9.	1.2	68
4642	Network-driven plasma proteomics expose molecular changes in the Alzheimer's brain. <i>Molecular Neurodegeneration</i> , 2016, 11, 31.	4.4	34
4643	Identification of miRNAs and differentially expressed genes in early phase non-small cell lung cancer. <i>Oncology Reports</i> , 2016, 35, 2171-2176.	1.2	27
4644	Network analysis reveals functional redundancy and keystone taxa amongst bacterial and fungal communities during organic matter decomposition in an arable soil. <i>Soil Biology and Biochemistry</i> , 2016, 97, 188-198.	4.2	617
4645	HMGN proteins modulate chromatin regulatory sites and gene expression during activation of naïve B cells. <i>Nucleic Acids Research</i> , 2016, 44, gkw323.	6.5	11
4646	CompNet: a GUI based tool for comparison of multiple biological interaction networks. <i>BMC Bioinformatics</i> , 2016, 17, 185.	1.2	38
4647	The systems biology format converter. <i>BMC Bioinformatics</i> , 2016, 17, 154.	1.2	30
4648	High-throughput proteomics and the fight against pathogens. <i>Molecular BioSystems</i> , 2016, 12, 2373-2384.	2.9	12
4649	Circulating Plasma Extracellular Microvesicle MicroRNA Cargo and Endothelial Dysfunction in Children with Obstructive Sleep Apnea. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1116-1126.	2.5	109
4650	Identification of potential therapeutic targets for papillary thyroid carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 51-58.	0.8	15
4651	Screening genes associated with melanoma using a combined analysis of mRNA and methylation microarray. <i>Gene Reports</i> , 2016, 4, 53-59.	0.4	1
4652	Analysis of bHLH coding genes using gene co-expression network approach. <i>Molecular Biology Reports</i> , 2016, 43, 677-685.	1.0	5

#	ARTICLE	IF	CITATIONS
4653	Spatial Cross-Talk between Oxidative Stress and DNA Replication in Human Fibroblasts. <i>Journal of Proteome Research</i> , 2016, 15, 1907-1938.	1.8	4
4654	Genome-wide identification and functional prediction of nitrogen-responsive intergenic and intronic long non-coding RNAs in maize ( <i>Zea mays</i> L.). <i>BMC Genomics</i> , 2016, 17, 350.	1.2	107
4655	RNA-seq analysis of the transcriptional response to blue and red light in the extremophilic red alga, <i>Cyanidioschyzon merolae</i> . <i>Functional and Integrative Genomics</i> , 2016, 16, 657-669.	1.4	20
4656	Co-expression network analysis of Down's syndrome based on microarray data. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 1503-1508.	0.8	25
4657	Macrophage molecular signaling and inflammatory responses during ingestion of atherogenic lipoproteins are modulated by complement protein C1q. <i>Atherosclerosis</i> , 2016, 253, 38-46.	0.4	20
4658	Identification of promising plasma immune biomarkers to differentiate active pulmonary tuberculosis. <i>Cytokine</i> , 2016, 88, 99-107.	1.4	30
4659	An LC-MS based untargeted metabolomics study identified novel biomarkers for coronary heart disease. <i>Molecular BioSystems</i> , 2016, 12, 3425-3434.	2.9	17
4660	Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants ( <i>Cucumis sativus</i> ). <i>Plant Physiology</i> , 2016, 172, 603-618.	2.3	99
4661	Lack of Overt Genome Reduction in the Bryostatin-Producing Bryozoan Symbiont <i>Candidatus Endobugula sertula</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6573-6583.	1.4	41
4662	Network analysis reveals seasonal variation of co-occurrence correlations between Cyanobacteria and other bacterioplankton. <i>Science of the Total Environment</i> , 2016, 573, 817-825.	3.9	101
4663	A multifunctional AAV-CRISPR-Cas9 and its host response. <i>Nature Methods</i> , 2016, 13, 868-874.	9.0	506
4664	Fibrous nests in human hepatocellular carcinoma express a Wnt-induced gene signature associated with poor clinical outcome. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 81, 195-207.	1.2	32
4665	Early detection of aquatic invaders using metabarcoding reveals a high number of non-indigenous species in Canadian ports. <i>Diversity and Distributions</i> , 2016, 22, 1045-1059.	1.9	82
4666	Superclusteroid 2.0: A Web Tool for Processing Big Biological Networks. <i>IFIP Advances in Information and Communication Technology</i> , 2016, , 623-633.	0.5	0
4667	Influence of exposure to pesticides on telomere length in tobacco farmers: A biology system approach. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2016, 791-792, 19-26.	0.4	22
4668	Hypoxia-independent gene expression signature associated with radiosensitisation of prostate cancer cell lines by histone deacetylase inhibition. <i>British Journal of Cancer</i> , 2016, 115, 929-939.	2.9	28
4669	m6A RNA methylation promotes XIST-mediated transcriptional repression. <i>Nature</i> , 2016, 537, 369-373.	13.7	1,250
4670	PhenomeScape: a cytoscape app to identify differentially regulated sub-networks using known disease associations. <i>Bioinformatics</i> , 2016, 32, 3847-3849.	1.8	13

#	ARTICLE	IF	CITATIONS
4671	MYB107 and MYB9 Homologs Regulate Suberin Deposition in Angiosperms. <i>Plant Cell</i> , 2016, 28, 2097-2116.	3.1	151
4672	Predicting Rat and Human Pregnane X Receptor Activators Using Bayesian Classification Models. <i>Chemical Research in Toxicology</i> , 2016, 29, 1729-1740.	1.7	21
4673	Mapping the Regulatory Network for <i>Salmonella enterica</i> Serovar Typhimurium Invasion. <i>MBio</i> , 2016, 7, .	1.8	42
4674	MicroRNAs and oncogenic transcriptional regulatory networks controlling metabolic reprogramming in cancers. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 223-233.	1.9	62
4675	Analysis of soil eDNA functional genes: potential to increase profitability and sustainability of pastoral agriculture. <i>New Zealand Journal of Agricultural Research</i> , 2016, 59, 333-350.	0.9	10
4676	Simultaneous discovery of cancer subtypes and subtype features by molecular data integration. <i>Bioinformatics</i> , 2016, 32, i445-i454.	1.8	25
4677	The Network Library: a framework to rapidly integrate network biology resources. <i>Bioinformatics</i> , 2016, 32, i473-i478.	1.8	8
4678	Bacterial microbiota associated with flower pollen is influenced by pollination type, and shows a high degree of diversity and species-specificity. <i>Environmental Microbiology</i> , 2016, 18, 5161-5174.	1.8	132
4679	Classification and substrate head-group specificity of membrane fatty acid desaturases. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 341-349.	1.9	22
4680	Insulin stimulated MCF7 breast cancer cells: Proteome dataset. <i>Data in Brief</i> , 2016, 9, 579-584.	0.5	6
4681	Network analysis of transcriptomics expands regulatory landscapes in <i>Synechococcus</i> sp. PCC 7002. <i>Nucleic Acids Research</i> , 2016, 44, 8810-8825.	6.5	26
4682	The Visualisation of Ecological Networks, and Their Use as a Tool for Engagement, Advocacy and Management. <i>Advances in Ecological Research</i> , 2016, , 41-85.	1.4	45
4683	Tumor promoter PMA enhances kindlin-2 and decreases vimentin recruitment into cell adhesion sites. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 78, 22-30.	1.2	4
4684	MicroRNA expression signatures in lungs of mice infected with <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2016, 101, 151-159.	0.8	14
4685	Ribosome quality control is a central protection mechanism for yeast exposed to deoxynivalenol and trichothecin. <i>BMC Genomics</i> , 2016, 17, 417.	1.2	23
4686	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016, 17, 191.	3.8	120
4687	OxLDL receptor chromatography from live human U937 cells identifies SYK(L) that regulates phagocytosis of oxLDL. <i>Analytical Biochemistry</i> , 2016, 513, 7-20.	1.1	12
4688	XPO1-dependent nuclear export is a druggable vulnerability in KRAS-mutant lung cancer. <i>Nature</i> , 2016, 538, 114-117.	13.7	162

#	ARTICLE	IF	CITATIONS
4689	Ketamine suppresses hypoxia-induced inflammatory responses in the late-gestation ovine fetal kidney cortex. <i>Journal of Physiology</i> , 2016, 594, 1295-1310.	1.3	23
4690	Protein-coding genes combined with long non-coding RNAs predict prognosis in esophageal squamous cell carcinoma patients as a novel clinical multi-dimensional signature. <i>Molecular BioSystems</i> , 2016, 12, 3467-3477.	2.9	31
4691	The promises of quantitative systems pharmacology modelling for drug development. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 363-370.	1.9	77
4692	Discovery Proteomics Identifies a Molecular Link between the Coatomer Protein Complex I and Androgen Receptor-dependent Transcription. <i>Journal of Biological Chemistry</i> , 2016, 291, 18818-18842.	1.6	16
4693	Cetylpyridinium chloride mouth rinses alleviate experimental gingivitis by inhibiting dental plaque maturation. <i>International Journal of Oral Science</i> , 2016, 8, 182-190.	3.6	41
4694	The emerging role of lysine methyltransferase SETD8 in human diseases. <i>Clinical Epigenetics</i> , 2016, 8, 102.	1.8	77
4695	Integrative transcriptomic analysis of NAFLD animal model reveals dysregulated genes and pathways in metabolism. <i>Gene</i> , 2016, 595, 99-108.	1.0	9
4696	Screening of gene signatures for rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 14, 1587-1593.	1.1	36
4697	Identification of a gene expression signature in peripheral blood of multiple sclerosis patients treated with disease-modifying therapies. <i>Clinical Immunology</i> , 2016, 173, 133-146.	1.4	9
4698	Graph Models of Network Behavior in Environmental Planning. <i>Procedia Computer Science</i> , 2016, 96, 73-80.	1.2	3
4699	Changes in the detergent-insoluble brain proteome linked to amyloid and tau in Alzheimer's Disease progression. <i>Proteomics</i> , 2016, 16, 3042-3053.	1.3	69
4700	Development of a motif-based topology-independent structure comparison method to identify evolutionarily related folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1859-1874.	1.5	10
4701	A Guide to Genome-Wide In Vivo RNAi Applications in Drosophila. <i>Methods in Molecular Biology</i> , 2016, 1478, 117-143.	0.4	32
4702	The epichaperome is an integrated chaperome network that facilitates tumour survival. <i>Nature</i> , 2016, 538, 397-401.	13.7	233
4703	APOSTL: An Interactive Galaxy Pipeline for Reproducible Analysis of Affinity Proteomics Data. <i>Journal of Proteome Research</i> , 2016, 15, 4747-4754.	1.8	16
4704	Building and analysis of protein-protein interactions related to diabetes mellitus using support vector machine, biomedical text mining and network analysis. <i>Computational Biology and Chemistry</i> , 2016, 65, 37-44.	1.1	23
4705	Gene Co-Expression Network Analysis Reveals the Correlation Patterns Among Genes in Euryhaline Adaptation of <i>Crassostrea gigas</i> . <i>Marine Biotechnology</i> , 2016, 18, 535-544.	1.1	25
4706	Protein-protein interaction and molecular dynamics analysis for identification of novel inhibitors in <i>Burkholderia cepacia</i> GG4. <i>Computational Biology and Chemistry</i> , 2016, 65, 80-90.	1.1	7

#	ARTICLE	IF	CITATIONS
4707	Identification of 2-oxohistidine Interacting Proteins Using E. coli Proteome Chips. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3581-3593.	2.5	3
4708	Comparative Ploidy Proteomics of <i>Candida albicans</i> Biofilms Unraveled the Role of the AHP1 Gene in the Biofilm Persistence Against Amphotericin B. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3488-3500.	2.5	37
4709	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
4710	IDENTIFICATION OF NOVEL GENES RELATED TO DIABETIC RETINOPATHY USING PROTEIN-PROTEIN INTERACTION NETWORK AND GENE ONTOLOGIES. <i>Journal of Biological Systems</i> , 2016, 24, 117-127.	0.5	5
4713	Synergizing Proteomic and Metabolomic Data to Study Cardiovascular Systems. , 2016, , 365-388.		0
4714	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , 2016, 19, 1454-1462.	7.1	359
4715	Molecular dynamics simulations and modelling of the residue interaction networks in the BRAF kinase complexes with small molecule inhibitors: probing the allosteric effects of ligand-induced kinase dimerization and paradoxical activation. <i>Molecular BioSystems</i> , 2016, 12, 3146-3165.	2.9	25
4716	Comparison on the structure and function of the rhizosphere microbial community between healthy and root-rot <i>Panax notoginseng</i> . <i>Applied Soil Ecology</i> , 2016, 107, 99-107.	2.1	68
4717	Automating bibliometric analyses using Taverna scientific workflows: A tutorial on integrating Web Services. <i>Journal of Informetrics</i> , 2016, 10, 830-841.	1.4	25
4718	Different interactomes for p70-S6K1 and p54-S6K2 revealed by proteomic analysis. <i>Proteomics</i> , 2016, 16, 2650-2666.	1.3	23
4719	Intact polar diacylglycerol biomarker lipids isolated from suspended particulate organic matter accumulating in an ultraoligotrophic water column. <i>Organic Geochemistry</i> , 2016, 100, 29-41.	0.9	17
4720	Computational Method for the Systematic Identification of Analog Series and Key Compounds Representing Series and Their Biological Activity Profiles. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 7667-7676.	2.9	50
4721	A metabolomics guided exploration of marine natural product chemical space. <i>Metabolomics</i> , 2016, 12, 1.	1.4	43
4722	When pumpkin is closer to onion than to squash: The structure of the second language lexicon. <i>Cognition</i> , 2016, 156, 60-70.	1.1	86
4723	The full-scale anaerobic digestion microbiome is represented by specific marker populations. <i>Water Research</i> , 2016, 104, 101-110.	5.3	61
4724	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	9.4	2,802
4725	Application of IT in healthcare. <i>ACM SIGBioinformatics Record</i> , 2016, 6, 1-8.	0.3	4
4726	A human neurodevelopmental model for Williams syndrome. <i>Nature</i> , 2016, 536, 338-343.	13.7	166

#	ARTICLE	IF	CITATIONS
4727	In vivo tissue sampling using solid-phase microextraction for non-lethal exposome-wide association study of CYP1A1 induction in <i>Catostomus commersonii</i> . <i>Environmental Research</i> , 2016, 151, 216-223.	3.7	15
4728	High-throughput Tag-sequencing Analysis of Early Events Induced by Ochratoxin A in HepG2 Cells. <i>Journal of Biochemical and Molecular Toxicology</i> , 2016, 30, 29-36.	1.4	4
4729	Caspase-related apoptosis genes in gliomas by RNA-seq and bioinformatics analysis. <i>Journal of Clinical Neuroscience</i> , 2016, 33, 259-263.	0.8	6
4730	RNA sequencing provides insights into the toxicogenomic response of ZF4 cells to methyl methanesulfonate. <i>Journal of Applied Toxicology</i> , 2016, 36, 94-104.	1.4	8
4731	New insights on the mitochondrial proteome plasticity in Parkinson's disease. <i>Proteomics - Clinical Applications</i> , 2016, 10, 416-429.	0.8	11
4732	An antibiotic target ranking and prioritization pipeline combining sequence, structure and network-based approaches exemplified for <i>Serratia marcescens</i> . <i>Gene</i> , 2016, 591, 268-278.	1.0	17
4733	A regulatory gene network related to the porcine umami taste receptor ( <i>TAS1R1</i> / <i>TAS1R3</i> ). <i>Animal Genetics</i> , 2016, 47, 114-119.	0.6	5
4734	Construction of co-expression network based on natural expression variation of xylogenesis-related transcripts in <i>Eucalyptus tereticornis</i> . <i>Molecular Biology Reports</i> , 2016, 43, 1129-1146.	1.0	11
4735	Meta-analysis of gene expression profiles identifies differential biomarkers for hepatocellular carcinoma and cholangiocarcinoma. <i>Tumor Biology</i> , 2016, 37, 12755-12766.	0.8	15
4736	Genome-Wide Discovery of Tissue-Specific Genes in Maize. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1204-1214.	1.0	3
4737	Quantitative Analysis of Evolvability using Vertex Centralities in Phenotype Network. , 2016, , .		3
4739	Immune signature of urothelial cancer associated with grade, recurrence, and invasion. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2016, 34, 418.e17-418.e26.	0.8	5
4740	Systems Biology Approaches to Improve Drought Stress Tolerance in Plants: State of the Art and Future Challenges. , 2016, , 433-471.		1
4741	Variability and exposure classification of urinary phenol and paraben metabolite concentrations in reproductive-aged women. <i>Environmental Research</i> , 2016, 151, 513-520.	3.7	44
4742	Thiol-Disulfide Exchange in Gram-Positive Firmicutes. <i>Trends in Microbiology</i> , 2016, 24, 902-915.	3.5	33
4743	Lithium-responsive genes and gene networks in bipolar disorder patient-derived lymphoblastoid cell lines. <i>Pharmacogenomics Journal</i> , 2016, 16, 446-453.	0.9	40
4744	Laminarin favorably modulates gut microbiota in mice fed a high-fat diet. <i>Food and Function</i> , 2016, 7, 4193-4201.	2.1	74
4745	Protein Interaction Network of Human Protein Kinase D2 Revealed by Chemical Cross-Linking/Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 3686-3699.	1.8	14



#	ARTICLE	IF	CITATIONS
4746	Human Sirtuin 2 Localization, Transient Interactions, and Impact on the Proteome Point to Its Role in Intracellular Trafficking. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3107-3125.	2.5	22
4747	<scp>RNA</scp>â€sequencing profiles hippocampal gene expression in a validated model of cancerâ€induced depression. <i>Genes, Brain and Behavior</i> , 2016, 15, 711-721.	1.1	10
4748	Micronome revealed miR-19a/b as key regulator of SOCS3 during cancer related inflammation of oral squamous cell carcinoma. <i>Gene</i> , 2016, 594, 30-40.	1.0	29
4749	Ecological perspectives of hydrogen fermentation by microbial consortia: What we have learned and the way forward. <i>International Journal of Hydrogen Energy</i> , 2016, 41, 17297-17308.	3.8	24
4750	Profiling Carbonylated Proteins in Heart and Skeletal Muscle Mitochondria from Trained and Untrained Mice. <i>Journal of Proteome Research</i> , 2016, 15, 3666-3678.	1.8	11
4751	Fungal community composition in soils subjected to longâ€term chemical fertilization is most influenced by the type of organic matter. <i>Environmental Microbiology</i> , 2016, 18, 5137-5150.	1.8	209
4752	Contrasting Ecological Processes and Functional Compositions Between Intestinal Bacterial Community in Healthy and Diseased Shrimp. <i>Microbial Ecology</i> , 2016, 72, 975-985.	1.4	142
4753	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. <i>BioSystems</i> , 2016, 150, 78-86.	0.9	11
4754	Gene Expression Architecture of Mouse Dorsal and Tail Skin Reveals Functional Differences in Inflammation and Cancer. <i>Cell Reports</i> , 2016, 16, 1153-1165.	2.9	20
4755	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. <i>Science of the Total Environment</i> , 2016, 572, 697-712.	3.9	213
4756	Gene signatures associated with adaptive humoral immunity following seasonal influenza A/H1N1 vaccination. <i>Genes and Immunity</i> , 2016, 17, 371-379.	2.2	26
4757	Allosteric mechanism of cyclopropylindolobenzazepine inhibitors for HCV NS5B RdRp via dynamic correlation network analysis. <i>Molecular BioSystems</i> , 2016, 12, 3280-3293.	2.9	18
4758	Expression profiling identifies Sertoli and Leydig cell genes as Fsh targets in adult zebrafish testis. <i>Molecular and Cellular Endocrinology</i> , 2016, 437, 237-251.	1.6	58
4759	Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways. <i>Bioinformatics</i> , 2016, 32, i128-i136.	1.8	11
4760	Regulatory Divergence among Beta-Keratin Genes during Bird Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2769-2780.	3.5	11
4761	Recurrent neural network based hybrid model for reconstructing gene regulatory network. <i>Computational Biology and Chemistry</i> , 2016, 64, 322-334.	1.1	43
4762	Uncovering Earthâ€™s virome. <i>Nature</i> , 2016, 536, 425-430.	13.7	880
4763	Detecting signals of detrimental prescribing cascades from social media. <i>Artificial Intelligence in Medicine</i> , 2016, 71, 43-56.	3.8	12

#	ARTICLE	IF	CITATIONS
4764	Systems Analysis of the Complement-Induced Priming Phase of Liver Regeneration. <i>Journal of Immunology</i> , 2016, 197, 2500-2508.	0.4	22
4765	MathIOmica: An Integrative Platform for Dynamic Omics. <i>Scientific Reports</i> , 2016, 6, 37237.	1.6	35
4766	Candidate methylated genes in osteoarthritis explored by bioinformatics analysis. <i>Knee</i> , 2016, 23, 1035-1043.	0.8	5
4767	pH drop impacts differentially skin and gut microbiota of the Amazonian fish tambaqui ( <i>Colossoma</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	131
4768	<scp>CLPP</scp> coordinates mitoribosomal assembly through the regulation of <scp>ERAL</scp> 1 levels. <i>EMBO Journal</i> , 2016, 35, 2566-2583.	3.5	123
4769	Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. <i>Scientific Reports</i> , 2016, 6, 32655.	1.6	46
4770	Markers for toxicity to HepG2 exposed to cadmium sulphide quantum dots; damage to mitochondria. <i>Toxicology</i> , 2016, 374, 18-28.	2.0	47
4771	Lineage-specific roles of the cytoplasmic polyadenylation factor CPEB4 in the regulation of melanoma drivers. <i>Nature Communications</i> , 2016, 7, 13418.	5.8	46
4772	Acetylome analysis reveals the involvement of lysine acetylation in diverse biological processes in <i>Phytophthora sojae</i> . <i>Scientific Reports</i> , 2016, 6, 29897.	1.6	59
4773	De novo transcriptome sequencing in <i>Monsonia burkeana</i> revealed putative genes for key metabolic pathways involved in tea quality and medicinal value. <i>3 Biotech</i> , 2016, 6, 250.	1.1	3
4774	Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues. <i>Molecular Cell</i> , 2016, 64, 982-992.	4.5	405
4775	Reprogramming mouse fibroblasts into engraftable myeloerythroid and lymphoid progenitors. <i>Nature Communications</i> , 2016, 7, 13396.	5.8	22
4776	Altered intestinal microbiotaâ€œhost mitochondria crosstalk in new onset Crohnâ€™s disease. <i>Nature Communications</i> , 2016, 7, 13419.	5.8	326
4777	Systems-Pharmacology Dissection of Traditional Chinese Medicine Compound Saffron Formula Reveals Multi-scale Treatment Strategy for Cardiovascular Diseases. <i>Scientific Reports</i> , 2016, 6, 19809.	1.6	56
4778	Genomic identification of WRKY transcription factors in carrot ( <i>Daucus carota</i> ) and analysis of evolution and homologous groups for plants. <i>Scientific Reports</i> , 2016, 6, 23101.	1.6	68
4779	Integrated microRNA and messenger RNA analysis in aortic stenosis. <i>Scientific Reports</i> , 2016, 6, 36904.	1.6	25
4780	Molecular basis for the broad substrate selectivity of a peptide prenyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14037-14042.	3.3	45
4781	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016, 45, 1148-1161.	6.6	174

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4782	Cut microbiota composition and <i>Clostridium difficile</i> infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , 2016, 6, 25945.	1.6	207
4783	Cellular Assays for Ferredoxins: A Strategy for Understanding Electron Flow through Protein Carriers That Link Metabolic Pathways. <i>Biochemistry</i> , 2016, 55, 7047-7064.	1.2	44
4784	The Qatar genome: a population-specific tool for precision medicine in the Middle East. <i>Human Genome Variation</i> , 2016, 3, 16016.	0.4	103
4785	Hsa-miR-137, hsa-miR-520e and hsa-miR-590-3p perform crucial roles in Lynch syndrome. <i>Oncology Letters</i> , 2016, 12, 2011-2017.	0.8	11
4786	Coordinate Regulation of Metabolite Glycosylation and Stress Hormone Biosynthesis by TT8 in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 171, 2499-2515.	2.3	45
4787	Transcriptional Repression of IFN Regulatory Factor 7 by MYC Is Critical for Type I IFN Production in Human Plasmacytoid Dendritic Cells. <i>Journal of Immunology</i> , 2016, 197, 3348-3359.	0.4	37
4788	Systematic network assessment of the carcinogenic activities of cadmium. <i>Toxicology and Applied Pharmacology</i> , 2016, 310, 150-158.	1.3	32
4789	Pro-fibrotic effects of PFKFB4-mediated glycolytic reprogramming in fibrous dysplasia. <i>Biomaterials</i> , 2016, 107, 61-73.	5.7	8
4790	Correlation-based iterative clustering methods for time course data: The identification of temporal gene response modules for influenza infection in humans. <i>Infectious Disease Modelling</i> , 2016, 1, 28-39.	1.2	12
4791	Transcriptional Regulation of <i>Arabidopsis</i> Polycomb Repressive Complex 2 Coordinates Cell-Type Proliferation and Differentiation. <i>Plant Cell</i> , 2016, 28, 2616-2631.	3.1	78
4792	<i>In silico</i> prediction of chemical mechanism of action via an improved network-based inference method. <i>British Journal of Pharmacology</i> , 2016, 173, 3372-3385.	2.7	73
4793	Consistently altered expression of gene sets in postmortem brains of individuals with major psychiatric disorders. <i>Translational Psychiatry</i> , 2016, 6, e890-e890.	2.4	63
4794	Identification of transcription hubs that control lipid metabolism and carbon concentrating mechanism in model microalgae <i>Chlamydomonas reinhardtii</i> using regulatory networks: Regulatory networks hubs in <i>C. reinhardtii</i> that control lipid and carbon concentrating metabolic pathways. , 2016, , ,		1
4795	Exosome-derived microRNAs contribute to prostate cancer chemoresistance. <i>International Journal of Oncology</i> , 2016, 49, 838-846.	1.4	74
4796	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. <i>Nature Medicine</i> , 2016, 22, 1187-1191.	15.2	844
4797	InteractoMIX: a suite of computational tools to exploit interactomes in biological and clinical research. <i>Biochemical Society Transactions</i> , 2016, 44, 917-924.	1.6	3
4798	Novel Aquaporin Regulatory Mechanisms Revealed by Interactomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3473-3487.	2.5	80
4799	Cross-species Conservation of context-specific networks. <i>BMC Systems Biology</i> , 2016, 10, 76.	3.0	4

#	ARTICLE	IF	CITATIONS
4800	Bayesian state space models for dynamic genetic network construction across multiple tissues. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 273-290.	0.2	4
4801	The Role of BDNF in Age-Dependent Changes of Excitatory and Inhibitory Synaptic Markers in the Human Prefrontal Cortex. <i>Neuropsychopharmacology</i> , 2016, 41, 3080-3091.	2.8	74
4802	TNIP2 is a Hub Protein in the NF- $\kappa$ B Network with Both Protein and RNA Mediated Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3435-3449.	2.5	27
4803	A user-centred approach to information visualisation in nano-health. <i>International Journal of Bioinformatics Research and Applications</i> , 2016, 12, 95.	0.1	4
4804	Inference of hierarchical regulatory network of TCF7L2 binding sites in MCF7 cell line. <i>International Journal of Computational Biology and Drug Design</i> , 2016, 9, 25.	0.3	2
4805	Visual Analysis of Biomolecular Cavities: State of the Art. <i>Computer Graphics Forum</i> , 2016, 35, 527-551.	1.8	46
4806	An integrative approach predicted co-expression sub-networks regulating properties of stem cells and differentiation. <i>Computational Biology and Chemistry</i> , 2016, 64, 250-262.	1.1	16
4807	Bacterial diversity across a highly stratified ecosystem: A salt-wedge Mediterranean estuary. <i>Systematic and Applied Microbiology</i> , 2016, 39, 398-408.	1.2	17
4808	Co-expressed miRNAs in gastric adenocarcinoma. <i>Genomics</i> , 2016, 108, 93-101.	1.3	40
4809	<i>In vitro</i> maturation alters gene expression in bovine oocytes. <i>Zygote</i> , 2016, 24, 624-633.	0.5	20
4810	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <i>Science Translational Medicine</i> , 2016, 8, 343ra82.	5.8	1,012
4811	Comparing Drug Images and Repurposing Drugs with BioGPS and FLAPdock: The Thymidylate Synthase Case. <i>ChemMedChem</i> , 2016, 11, 1653-1666.	1.6	21
4812	Metabolomics profiling of the free and total oxidised lipids in urine by LC-MS/MS: application in patients with rheumatoid arthritis. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 6307-6319.	1.9	28
4813	Role of fibronectin in the process of human intestinal cell disruption during <i>E. histolytica</i> infection. <i>Comparative Clinical Pathology</i> , 2016, 25, 1077-1080.	0.3	0
4814	Normal pregnancy-induced amino acid metabolic stress in a longitudinal cohort of pregnant women: novel insights generated from UPLC-QTOFMS-based urine metabolomic study. <i>Metabolomics</i> , 2016, 12, 1.	1.4	10
4815	Temperature controls on the basal emission rate of isoprene in a tropical tree <i>Ficus septica</i> : exploring molecular regulatory mechanisms. <i>Plant, Cell and Environment</i> , 2016, 39, 2260-2275.	2.8	14
4816	Bioinformatics Prediction and Experimental Validation of MicroRNAs Involved in Cross-Kingdom Interaction. <i>Journal of Computational Biology</i> , 2016, 23, 976-989.	0.8	34
4817	Altered expression of the bZIP transcription factor DRINK ME affects growth and reproductive development in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 437-451.	2.8	40

#	ARTICLE	IF	CITATIONS
4818	Combined Metabolomics and Transcriptomics Approaches to Assess the IL-6 Blockade as a Therapeutic of ALS: Deleterious Alteration of Lipid Metabolism. <i>Neurotherapeutics</i> , 2016, 13, 905-917.	2.1	46
4819	Identification of potential therapeutic targets for lung cancer by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 13, 1975-1982.	1.1	15
4820	Identification of genes and signaling pathways associated with squamous cell carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 1382-1390.	0.8	13
4821	Knockdown of EWSR1/FLI1 expression alters the transcriptome of Ewing sarcoma cells in vitro. <i>Journal of Bone Oncology</i> , 2016, 5, 153-158.	1.0	7
4822	Quantitative proteomics identifies myoferlin as a novel regulator of A Disintegrin and Metalloproteinase 12 in HeLa cells. <i>Journal of Proteomics</i> , 2016, 148, 94-104.	1.2	16
4823	Developmental Transcriptomics of the Hawaiian Anchialine Shrimp <i>Halocaridina rubra</i> Holthuis, 1963 (Crustacea: Atyidae). <i>Integrative and Comparative Biology</i> , 2016, 56, 1170-1182.	0.9	10
4824	Life in leaf litter: novel insights into community dynamics of bacteria and fungi during litter decomposition. <i>Molecular Ecology</i> , 2016, 25, 4059-4074.	2.0	297
4825	Effect of Heme Oxygenase-1 Deficiency on Glomerular Proteomics. <i>American Journal of Nephrology</i> , 2016, 43, 441-450.	1.4	5
4826	Structural mapping of Kelch13 mutations associated with artemisinin resistance in malaria. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 51-56.	1.2	17
4827	Warming and Acidification Effects on Planktonic Heterotrophic Pico- and Nanoflagellates in a Mesocosm Experiment. <i>Protist</i> , 2016, 167, 389-410.	0.6	39
4828	VisualGX: interactive graph visualization within Galaxy. <i>Bioinformatics</i> , 2016, 32, 3525-3527.	1.8	1
4829	Editor's Highlight: Perfluorooctane Sulfonate-Choline Ion Pair Formation: A Potential Mechanism Modulating Hepatic Steatosis and Oxidative Stress in Mice. <i>Toxicological Sciences</i> , 2016, 153, 186-197.	1.4	24
4830	Inferring active regulatory networks from gene expression data using a combination of prior knowledge and enrichment analysis. <i>BMC Bioinformatics</i> , 2016, 17, 181.	1.2	30
4831	Robust Inference of Identity by Descent from Exome-Sequencing Data. <i>American Journal of Human Genetics</i> , 2016, 99, 1106-1116.	2.6	8
4832	Thermophilic archaea activate butane via alkyl-coenzyme M formation. <i>Nature</i> , 2016, 539, 396-401.	13.7	279
4833	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. <i>Nature Microbiology</i> , 2016, 1, 16177.	5.9	194
4834	Contrasting Linguistic and Genetic Origins of the Asian Source Populations of Malagasy. <i>Scientific Reports</i> , 2016, 6, 26066.	1.6	48
4835	Network Analysis Implicates Alpha-Synuclein (Snca) in the Regulation of Ovariectomy-Induced Bone Loss. <i>Scientific Reports</i> , 2016, 6, 29475.	1.6	17

#	ARTICLE	IF	CITATIONS
4836	The ubiquitin ligase TRIM27 functions as a host restriction factor antagonized by Mycobacterium tuberculosis PtpA during mycobacterial infection. <i>Scientific Reports</i> , 2016, 6, 34827.	1.6	46
4837	Effects of organic loading rate on hydrogen and volatile fatty acid production and microbial community during acidogenic hydrogenesis in a continuous stirred tank reactor using molasses wastewater. <i>Journal of Applied Microbiology</i> , 2016, 121, 1627-1636.	1.4	26
4838	Gene Expression Analysis Through Network Biology: Bioinformatics Approaches. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 15-32.	0.6	2
4839	Rapid Evaporative Ionisation Mass Spectrometry (REIMS) Provides Accurate Direct from Culture Species Identification within the Genus <i>Candida</i> . <i>Scientific Reports</i> , 2016, 6, 36788.	1.6	48
4840	Systems pharmacology exploration of botanic drug pairs reveals the mechanism for treating different diseases. <i>Scientific Reports</i> , 2016, 6, 36985.	1.6	61
4841	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016, 9, rs6.	1.6	119
4842	CD8 + T Cells from Human Neonates Are Biased toward an Innate Immune Response. <i>Cell Reports</i> , 2016, 17, 2151-2160.	2.9	64
4843	Transcriptome sequencing reveals e-cigarette vapor and mainstream-smoke from tobacco cigarettes activate different gene expression profiles in human bronchial epithelial cells. <i>Scientific Reports</i> , 2016, 6, 23984.	1.6	72
4844	Impaired Gut-Liver-Brain Axis in Patients with Cirrhosis. <i>Scientific Reports</i> , 2016, 6, 26800.	1.6	163
4845	Altered protein phosphorylation as a resource for potential AD biomarkers. <i>Scientific Reports</i> , 2016, 6, 30319.	1.6	31
4846	Meta-analysis of gene expression studies in endometrial cancer identifies gene expression profiles associated with aggressive disease and patient outcome. <i>Scientific Reports</i> , 2016, 6, 36677.	1.6	48
4847	Genetic determination of the enhanced drought resistance of rice maintainer HuHan2B by pedigree breeding. <i>Scientific Reports</i> , 2016, 6, 37302.	1.6	8
4848	Genome wide transcriptome profiling of <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> conidial germination reveals new insights into infection-related genes. <i>Scientific Reports</i> , 2016, 6, 37353.	1.6	45
4849	<i>Pfhrp2</i> -deleted <i>Plasmodium falciparum</i> parasites in the Democratic Republic of Congo: A national cross-sectional survey. <i>Journal of Infectious Diseases</i> , 2017, 216, jiw538.	1.9	100
4850	Partial exhaustion of CD8 T cells and clinical response to teplizumab in new-onset type 1 diabetes. <i>Science Immunology</i> , 2016, 1, .	5.6	169
4851	Mergeomics: a web server for identifying pathological pathways, networks, and key regulators via multidimensional data integration. <i>BMC Genomics</i> , 2016, 17, 722.	1.2	59
4852	In silico identification of essential proteins in <i>Corynebacterium pseudotuberculosis</i> based on protein-protein interaction networks. <i>BMC Systems Biology</i> , 2016, 10, 103.	3.0	24
4853	Identification of potential therapeutic targets for colorectal cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 12, 5092-5098.	0.8	23



#	ARTICLE	IF	CITATIONS
4854	Role of DNA Repair Factor Xeroderma Pigmentosum Protein Group C in Response to Replication Stress As Revealed by DNA Fragile Site Affinity Chromatography and Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 4505-4517.	1.8	3
4855	Identification of transcription factors (TFs) and targets involved in the cholangiocarcinoma (CCA) by integrated analysis. <i>Cancer Gene Therapy</i> , 2016, 23, 439-445.	2.2	15
4856	An interactive web-based application for Comprehensive Analysis of RNAi-screen Data. <i>Nature Communications</i> , 2016, 7, 10578.	5.8	13
4857	Evolution of the microbial community of the biofilm in a methane-based membrane biofilm reactor reducing multiple electron acceptors. <i>Environmental Science and Pollution Research</i> , 2016, 23, 9540-9548.	2.7	38
4858	A comprehensive gene expression analysis at sequential stages of in vitro cardiac differentiation from isolated MESP1-expressing-mesoderm progenitors. <i>Scientific Reports</i> , 2016, 6, 19386.	1.6	53
4859	Genome-wide identification and characterization of long intergenic noncoding RNAs and their potential association with larval development in the Pacific oyster. <i>Scientific Reports</i> , 2016, 6, 20796.	1.6	42
4860	Metabolic Biomarkers and Neurodegeneration: A Pathway Enrichment Analysis of Alzheimer's Disease, Parkinson's Disease, and Amyotrophic Lateral Sclerosis. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 645-661.	1.0	122
4861	Roles of Distal and Genic Methylation in the Development of Prostate Tumorigenesis Revealed by Genome-wide DNA Methylation Analysis. <i>Scientific Reports</i> , 2016, 6, 22051.	1.6	19
4862	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw071.	3.2	34
4863	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in <i>Acinetobacter baumannii</i> strain AB5075. <i>Nature Communications</i> , 2016, 7, 13414.	5.8	81
4864	High hydrostatic pressure adaptive strategies in an obligate piezophile <i>Pyrococcus yayanosii</i> . <i>Scientific Reports</i> , 2016, 6, 27289.	1.6	53
4865	Genome-wide differential expression of genes and small RNAs in testis of two different porcine breeds and at two different ages. <i>Scientific Reports</i> , 2016, 6, 26852.	1.6	30
4866	Targeting PSG1 to enhance chemotherapeutic efficacy: new application for anti-coagulant the dicumarol. <i>Clinical Science</i> , 2016, 130, 2267-2276.	1.8	3
4867	Genome-wide profiles of methylation, microRNAs, and gene expression in chemoresistant breast cancer. <i>Scientific Reports</i> , 2016, 6, 24706.	1.6	40
4868	SWOT Analysis and Complex Network Analysis to Enhance Governance in Universities by Collaboration between Academic and Administrative Faculty. , 2016, , .		7
4869	AML suppresses hematopoiesis by releasing exosomes that contain microRNAs targeting c-MYB. <i>Science Signaling</i> , 2016, 9, ra88.	1.6	132
4870	Transcriptome- and proteome-oriented identification of dysregulated eIF4G, STAT3, and Hippo pathways altered by PIK3CA H1047R in HER2/ER-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2016, 160, 457-474.	1.1	13
4871	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016, 1, 16152.	5.9	56



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4872	RNA-sequencing Reveals Global Transcriptomic Changes in <i>Nicotiana tabacum</i> Responding to Topping and Treatment of Axillary-shoot Control Chemicals. <i>Scientific Reports</i> , 2016, 5, 18148.	1.6	29
4873	Comparative transcriptome profiling of longissimus muscle tissues from Qianhua Mutton Merino and Small Tail Han sheep. <i>Scientific Reports</i> , 2016, 6, 33586.	1.6	39
4874	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	3.2	207
4875	Model of the delayed translation of cyclin B maternal mRNA after sea urchin fertilization. <i>Molecular Reproduction and Development</i> , 2016, 83, 1070-1082.	1.0	4
4876	UNR/CSDE1 Drives a Post-transcriptional Program to Promote Melanoma Invasion and Metastasis. <i>Cancer Cell</i> , 2016, 30, 694-707.	7.7	131
4877	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. <i>Cell</i> , 2016, 167, 985-1000.e21.	13.5	259
4878	MicroRNA profiling of cisplatin-resistant oral squamous cell carcinoma cell lines enriched with cancer-stem-cell-like and epithelial-mesenchymal transition-type features. <i>Scientific Reports</i> , 2016, 6, 23932.	1.6	51
4879	Comparative genomic analysis of novel <i>Acinetobacter</i> symbionts: A combined systems biology and genomics approach. <i>Scientific Reports</i> , 2016, 6, 29043.	1.6	33
4880	The structural origin of metabolic quantitative diversity. <i>Scientific Reports</i> , 2016, 6, 31463.	1.6	18
4881	Co-acclimation of bacterial communities under stresses of hydrocarbons with different structures. <i>Scientific Reports</i> , 2016, 6, 34588.	1.6	44
4882	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. <i>Scientific Reports</i> , 2016, 6, 36111.	1.6	28
4883	A graphical model approach visualizes regulatory relationships between genome-wide transcription factor binding profiles. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw102.	3.2	1
4884	AMIGO2, a toolbox for dynamic modeling, optimization and control in systems biology. <i>Bioinformatics</i> , 2016, 32, 3357-3359.	1.8	124
4885	Bimolecular complementation affinity purification (BiCAP) reveals dimer-specific protein interactions for ERBB2 dimers. <i>Science Signaling</i> , 2016, 9, ra69.	1.6	51
4886	Enhanced T cell responses to IL-6 in type 1 diabetes are associated with early clinical disease and increased IL-6 receptor expression. <i>Science Translational Medicine</i> , 2016, 8, 356ra119.	5.8	82
4887	Identification of key player genes in gene regulatory networks. <i>BMC Systems Biology</i> , 2016, 10, 88.	3.0	32
4888	Networking Omic Data to Envisage Systems Biological Regulation. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 121-141.	0.6	0
4889	Applications of Systems Biology to Improve Pig Health. , 2016, , 33-59.		0

#	ARTICLE	IF	CITATIONS
4890	Systems Pharmacology Dissection of the Integrated Treatment for Cardiovascular and Gastrointestinal Disorders by Traditional Chinese Medicine. <i>Scientific Reports</i> , 2016, 6, 32400.	1.6	48
4891	Identification of lncRNA functions in lung cancer based on associated protein-protein interaction modules. <i>Scientific Reports</i> , 2016, 6, 35939.	1.6	18
4892	Evolution of Enzyme Superfamilies: Comprehensive Exploration of Sequence-Function Relationships. <i>Biochemistry</i> , 2016, 55, 6375-6388.	1.2	56
4893	Human Prostate Cancer Hallmarks Map. <i>Scientific Reports</i> , 2016, 6, 30691.	1.6	24
4894	Integrative omics connects N-glycoproteome-wide alterations with pathways and regulatory events in induced pluripotent stem cells. <i>Scientific Reports</i> , 2016, 6, 36109.	1.6	2
4895	SSA-ME Detection of cancer driver genes using mutual exclusivity by small subnetwork analysis. <i>Scientific Reports</i> , 2016, 6, 36257.	1.6	12
4896	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw090.	3.2	17
4897	Depicting Gene Co-expression Networks Underlying eQTLs. , 2016, , 1-31.		0
4898	Applications of Systems Genetics and Biology for Obesity Using Pig Models. , 2016, , 25-42.		7
4899	BATMAN-TCM: a Bioinformatics Analysis Tool for Molecular mechANism of Traditional Chinese Medicine. <i>Scientific Reports</i> , 2016, 6, 21146.	1.6	530
4900	To Unveil the Molecular Mechanisms of Qi and Blood through Systems Biology-Based Investigation into Si-Jun-Zi-Tang and Si-Wu-Tang formulae. <i>Scientific Reports</i> , 2016, 6, 34328.	1.6	24
4901	Biomedical network regulated by <i>acanthopanax cortex</i> (Wu-Jia-Pi) for ossification. , 2016, , .		0
4902	petal: Co-expression network modelling in R. <i>BMC Systems Biology</i> , 2016, 10, 51.	3.0	35
4903	Direct reprogramming of fibroblasts into renal tubular epithelial cells by defined transcription factors. <i>Nature Cell Biology</i> , 2016, 18, 1269-1280.	4.6	113
4904	Integrative analysis of cancer genes in a functional interactome. <i>Scientific Reports</i> , 2016, 6, 29228.	1.6	6
4905	Sex differences in colonization of gut microbiota from a man with short-term vegetarian and inulin-supplemented diet in germ-free mice. <i>Scientific Reports</i> , 2016, 6, 36137.	1.6	52
4906	Differential pathway network analysis used to identify key pathways associated with pediatric pneumonia. <i>Microbial Pathogenesis</i> , 2016, 101, 50-55.	1.3	3
4907	Giraffe genome sequence reveals clues to its unique morphology and physiology. <i>Nature Communications</i> , 2016, 7, 11519.	5.8	47

#	ARTICLE	IF	CITATIONS
4908	Altered expression of mRNA profiles in blood of early-onset schizophrenia. <i>Scientific Reports</i> , 2016, 6, 16767.	1.6	24
4909	Microbial community profiling shows dysbiosis in the lesional skin of Vitiligo subjects. <i>Scientific Reports</i> , 2016, 6, 18761.	1.6	122
4910	Quantitative Analysis of Global Proteome and Lysine Acetylome Reveal the Differential Impacts of VPA and SAHA on HL60 Cells. <i>Scientific Reports</i> , 2016, 6, 19926.	1.6	34
4911	Comprehensive analysis of the polygalacturonase and pectin methylesterase genes in <i>Brassica rapa</i> shed light on their different evolutionary patterns. <i>Scientific Reports</i> , 2016, 6, 25107.	1.6	34
4912	Summer holidays as break-point in shaping a tannery sludge microbial community around a stable core microbiota. <i>Scientific Reports</i> , 2016, 6, 30376.	1.6	9
4913	A path-based measurement for human miRNA functional similarities using miRNA-disease associations. <i>Scientific Reports</i> , 2016, 6, 32533.	1.6	29
4914	Genomic analysis reveals selection in Chinese native black pig. <i>Scientific Reports</i> , 2016, 6, 36354.	1.6	32
4915	Exploring the spatial relatedness network of the global system of international migration. <i>Journal of Maps</i> , 2016, 12, 570-576.	1.0	3
4916	Unraveling the molecular basis of oxidative stress management in a drought tolerant rice genotype Nagina 22. <i>BMC Genomics</i> , 2016, 17, 774.	1.2	25
4917	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	3.6	51
4918	Enrichment of the lung microbiome with oral taxa is associated with lung inflammation of a Th17 phenotype. <i>Nature Microbiology</i> , 2016, 1, 16031.	5.9	436
4919	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. <i>Nature Microbiology</i> , 2016, 1, 16005.	5.9	384
4920	Human genome-wide RNAi screen reveals host factors required for enterovirus 71 replication. <i>Nature Communications</i> , 2016, 7, 13150.	5.8	47
4921	Network analysis identifies Rv0324 and Rv0880 as regulators of bedaquiline tolerance in <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2016, 1, 16078.	5.9	71
4922	Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate. <i>Scientific Reports</i> , 2016, 6, 21871.	1.6	149
4923	Genome-wide Identification and Structural, Functional and Evolutionary Analysis of WRKY Components of Mulberry. <i>Scientific Reports</i> , 2016, 6, 30794.	1.6	39
4924	Identification of Potential Therapeutics to Conquer Drug Resistance in <i>Salmonella typhimurium</i> : Drug Repurposing Strategy. <i>BioDrugs</i> , 2016, 30, 593-605.	2.2	17
4925	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016, 7, 11362.	5.8	214

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4926	Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. <i>Scientific Reports</i> , 2016, 6, 21635.	1.6	25
4927	Proteome-wide analysis of lysine acetylation in the plant pathogen <i>Botrytis cinerea</i> . <i>Scientific Reports</i> , 2016, 6, 29313.	1.6	77
4928	Artificial Analogues of Circulating Box C/D RNAs Induce Strong Innate Immune Response and MicroRNA Activation in Human Adenocarcinoma Cells. <i>Advances in Experimental Medicine and Biology</i> , 2016, 924, 121-125.	0.8	15
4929	In silico prediction of specific pathways that regulate mesangial cell proliferation in IgA nephropathy. <i>Medical Hypotheses</i> , 2016, 97, 38-45.	0.8	5
4930	Indicator species and co-occurrence in communities of arbuscular mycorrhizal fungi at the European scale. <i>Soil Biology and Biochemistry</i> , 2016, 103, 464-470.	4.2	43
4931	The simple neuroendocrine-immune regulatory network in oyster <i>Crassostrea gigas</i> mediates complex functions. <i>Scientific Reports</i> , 2016, 6, 26396.	1.6	52
4932	Effects of captivity and artificial breeding on microbiota in feces of the red-crowned crane ( <i>Grus</i> ) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 5	1.6	63
4933	Data integration for clinical decision support. , 2016, , .		1
4934	Identification potential biomarkers in pulmonary tuberculosis and latent infection based on bioinformatics analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 500.	1.3	13
4935	Transcriptional profile of SH-SY5Y human neuroblastoma cells transfected by <i>Toxoplasma</i> rhoptry protein 16. <i>Molecular Medicine Reports</i> , 2016, 14, 4099-4108.	1.1	5
4936	Network Analysis and Applications in Pediatric Research. <i>Translational Bioinformatics</i> , 2016, , 251-274.	0.0	0
4937	Multiscale design of coarse-grained elastic network-based potentials for the $\mu$ opioid receptor. <i>Journal of Molecular Modeling</i> , 2016, 22, 227.	0.8	6
4938	Identification of candidate biomarkers and analysis of prognostic values in ovarian cancer by integrated bioinformatics analysis. <i>Medical Oncology</i> , 2016, 33, 130.	1.2	75
4939	Genome-wide analysis of DNA methylation in obese, lean and miniature pig breeds. <i>Scientific Reports</i> , 2016, 6, 30160.	1.6	29
4940	Retinal expression of small non-coding RNAs in a murine model of proliferative retinopathy. <i>Scientific Reports</i> , 2016, 6, 33947.	1.6	29
4941	Integrating <i>Candida albicans</i> metabolism with biofilm heterogeneity by transcriptome mapping. <i>Scientific Reports</i> , 2016, 6, 35436.	1.6	39
4942	Identification of Specific Long Non-Coding RNA Expression: Profile and Analysis of Association with Clinicopathologic Characteristics and <i>BRAF</i> Mutation in Papillary Thyroid Cancer. <i>Thyroid</i> , 2016, 26, 1719-1732.	2.4	24
4943	Long-term potentiation modulates synaptic phosphorylation networks and reshapes the structure of the postsynaptic interactome. <i>Science Signaling</i> , 2016, 9, rs8.	1.6	96

#	ARTICLE	IF	CITATIONS
4944	Cell wall dynamics during apple development and storage involves hemicellulose modifications and related expressed genes. <i>BMC Plant Biology</i> , 2016, 16, 201.	1.6	83
4946	Environmental Tobacco Smoke Alters Metabolic Systems in Adult Rats. <i>Chemical Research in Toxicology</i> , 2016, 29, 1818-1827.	1.7	12
4947	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. <i>Npj Genomic Medicine</i> , 2016, 1, .	1.7	19
4948	Comprehensive profiling of lysine acetylproteome analysis reveals diverse functions of lysine acetylation in common wheat. <i>Scientific Reports</i> , 2016, 6, 21069.	1.6	87
4949	Matrix factorization reveals aging-specific co-expression gene modules in the fat and muscle tissues in nonhuman primates. <i>Scientific Reports</i> , 2016, 6, 34335.	1.6	3
4950	Multi-omics Evidence for Inheritance of Energy Pathways in Red Blood Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3614-3623.	2.5	18
4951	Flux control through protein phosphorylation in yeast. <i>FEMS Yeast Research</i> , 2016, 16, fow096.	1.1	29
4952	Transcriptomic responses of a simplified soil microcosm to a plant pathogen and its biocontrol agent reveal a complex reaction to harsh habitat. <i>BMC Genomics</i> , 2016, 17, 838.	1.2	13
4953	Big Data and Cancer Research. , 2016, , 259-276.		1
4954	Characterization of Protein Lysine Propionylation in <i>Escherichia coli</i> : Global Profiling, Dynamic Change, and Enzymatic Regulation. <i>Journal of Proteome Research</i> , 2016, 15, 4696-4708.	1.8	50
4955	Identification of novel genes and pathways in carotid atheroma using integrated bioinformatic methods. <i>Scientific Reports</i> , 2016, 6, 18764.	1.6	16
4956	Deciphering the Potential Pharmaceutical Mechanism of Chinese Traditional Medicine (Gui-Zhi-Shao-Yao-Zhi-Mu) on Rheumatoid Arthritis. <i>Scientific Reports</i> , 2016, 6, 22602.	1.6	31
4957	Polycomb repressive complex 1 controls uterine decidualization. <i>Scientific Reports</i> , 2016, 6, 26061.	1.6	18
4958	RNA-seq analysis of the hypothalamic transcriptome reveals the networks regulating physiopathological progress in the diabetic GK rat. <i>Scientific Reports</i> , 2016, 6, 34138.	1.6	17
4959	Analysis of microRNA and Gene Expression Profiles in Multiple Sclerosis: Integrating Interaction Data to Uncover Regulatory Mechanisms. <i>Scientific Reports</i> , 2016, 6, 34512.	1.6	63
4960	A systems-oriented analysis of the grapevine R2R3-MYB transcription factor family uncovers new insights into the regulation of stilbene accumulation. <i>DNA Research</i> , 2016, 23, 451-466.	1.5	141
4961	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	6.0	157
4962	KLHL21, a novel gene that contributes to the progression of hepatocellular carcinoma. <i>BMC Cancer</i> , 2016, 16, 815.	1.1	44

#	ARTICLE	IF	CITATIONS
4963	Informatics for Metabolomics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 939, 91-115.	0.8	28
4964	A Novel Method for Alignment-free DNA Sequence Similarity Analysis Based on the Characterization of Complex Networks. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S40474.	0.6	10
4965	BTR: training asynchronous Boolean models using single-cell expression data. <i>BMC Bioinformatics</i> , 2016, 17, 355.	1.2	63
4966	Genomic analyses of tropical beef cattle fertility based on genotyping pools of Brahman cows with unknown pedigree1. <i>Journal of Animal Science</i> , 2016, 94, 4096-4108.	0.2	29
4967	Bioinformatics analysis of gene expression profiles of dermatomyositis. <i>Molecular Medicine Reports</i> , 2016, 14, 3785-3790.	1.1	3
4968	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. G3: Genes, Genomes, Genetics, 2016, 6, 3927-3939.	0.8	187
4969	BcCluster: A Bladder Cancer Database at the Molecular Level. <i>Bladder Cancer</i> , 2016, 2, 65-76.	0.2	4
4970	Practical Approaches for Mining Frequent Patterns in Molecular Datasets. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38419.	1.0	2
4971	Comparative Proteomic Analysis of Advanced Ovarian Cancer Tissue to Identify Potential Biomarkers of Responders and Nonresponders to First-Line Chemotherapy of Carboplatin and Paclitaxel. <i>Biomarkers in Cancer</i> , 2016, 8, BIC.S35775.	3.6	20
4972	Synergistic Modification Induced Specific Recognition between Histone and TRIM24 via Fluctuation Correlation Network Analysis. <i>Scientific Reports</i> , 2016, 6, 24587.	1.6	15
4973	Graph theoretical biomarkers for schizophrenic Brain Functional Networks. , 2016, , .		3
4974	High frequency of +1 programmed ribosomal frameshifting in <i>Euplotes octocarinatus</i> . <i>Scientific Reports</i> , 2016, 6, 21139.	1.6	48
4975	Discriminative gene co-expression network analysis uncovers novel modules involved in the formation of phosphate deficiency-induced root hairs in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2016, 6, 26820.	1.6	21
4976	Low abundance of Archaeorhizomycetes among fungi in soil metatranscriptomes. <i>Scientific Reports</i> , 2016, 6, 38455.	1.6	32
4977	Rhizoma <i>Dioscoreae</i> extract protects against alveolar bone loss by regulating the cell cycle: A predictive study based on the protein-protein interaction network. <i>Molecular Medicine Reports</i> , 2016, 13, 5342-5348.	1.1	1
4978	Genome-wide Analysis of WD40 Protein Family in Human. <i>Scientific Reports</i> , 2016, 6, 39262.	1.6	43
4979	pATsi: Paralogs and Singleton Genes from <i>Arabidopsis thaliana</i> . <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S32536.	0.6	15
4980	Identifying Cell Type-Specific Transcription Factors by Integrating ChIP-seq and eQTL Data-Application to Monocyte Gene Regulation. <i>Gene Regulation and Systems Biology</i> , 2016, 10, GRSB.S40768.	2.3	4

#	ARTICLE	IF	CITATIONS
4981	Systematic analysis of the molecular mechanism underlying atherosclerosis using a text mining approach. <i>Human Genomics</i> , 2016, 10, 14.	1.4	12
4982	Factors associated with needle sharing among people who inject drugs in Yunnan, China: a combined network and regression analysis. <i>Infectious Diseases of Poverty</i> , 2016, 5, 73.	1.5	4
4983	Computational analysis reveals microRNA-mRNA regulatory network in esophageal squamous cell carcinoma. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2016, 36, 834-838.	1.0	0
4984	PTIR: Predicted Tomato Interactome Resource. <i>Scientific Reports</i> , 2016, 6, 25047.	1.6	32
4985	MORO: a Cytoscape app for relationship analysis between modularity and robustness in large-scale biological networks. <i>BMC Systems Biology</i> , 2016, 10, 122.	3.0	8
4986	Allele-specific expression in the human heart and its application to postoperative atrial fibrillation and myocardial ischemia. <i>Genome Medicine</i> , 2016, 8, 127.	3.6	6
4987	Improper hydration induces global gene expression changes associated with renal development in infant mice. <i>Genes and Nutrition</i> , 2016, 11, 28.	1.2	2
4988	An integrative genomics approach for identifying novel functional consequences of PBRM1 truncated mutations in clear cell renal cell carcinoma (ccRCC). <i>BMC Genomics</i> , 2016, 17, 515.	1.2	24
4989	XMRF: an R package to fit Markov Networks to high-throughput genetics data. <i>BMC Systems Biology</i> , 2016, 10, 69.	3.0	15
4990	Integrative transcriptome network analysis of iPSC-derived neurons from schizophrenia and schizoaffective disorder patients with 22q11.2 deletion. <i>BMC Systems Biology</i> , 2016, 10, 105.	3.0	93
4991	Integrated analysis of omics data using microRNA-target mRNA network and PPI network reveals regulation of <i>Gnai1</i> function in the spinal cord of <i>Ews/Ewsr1</i> KO mice. <i>BMC Medical Genomics</i> , 2016, 9, 33.	0.7	4
4992	Identification of microRNAs regulating <i>Escherichia coli</i> F18 infection in Meishan weaned piglets. <i>Biology Direct</i> , 2016, 11, 59.	1.9	15
4993	Identification of protein complexes from multi-relationship protein interaction networks. <i>Human Genomics</i> , 2016, 10, 17.	1.4	14
4994	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw081.	1.4	22
4995	Prophages of the genus <i>Bacteriophage</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	1.8	66
4996	Population genetic evidence for cold adaptation in European <i>Drosophila melanogaster</i> populations. <i>Molecular Ecology</i> , 2016, 25, 1175-1191.	2.0	25
4997	Marine Microbial Systems Ecology: Microbial Networks in the Sea. , 2016, , 335-344.		2
4998	Global transcriptome analysis for identification of interactions between coding and noncoding RNAs during human erythroid differentiation. <i>Frontiers of Medicine</i> , 2016, 10, 297-310.	1.5	33



#	ARTICLE	IF	CITATIONS
4999	Network analysis of genes and their association with diseases. <i>Gene</i> , 2016, 590, 68-78.	1.0	31
5000	CyTRANSFINDER: a Cytoscape 3.3 plugin for three-component (TF, gene, miRNA) signal transduction pathway construction. <i>BMC Bioinformatics</i> , 2016, 17, 157.	1.2	14
5001	Transcriptome analysis of secondary cell wall development in <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2016, 17, 23.	1.2	22
5002	Comparative transcriptomics and comprehensive marker resource development in mulberry. <i>BMC Genomics</i> , 2016, 17, 98.	1.2	18
5003	Bayesian module identification from multiple noisy networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2016, 2016, 5.	1.4	5
5004	Presence of pathogenic <i>Escherichia coli</i> is correlated with bacterial community diversity and composition on pre-harvest cattle hides. <i>Microbiome</i> , 2016, 4, 9.	4.9	25
5005	Differential co-expression analysis of venous thromboembolism based on gene expression profile data. <i>Experimental and Therapeutic Medicine</i> , 2016, 11, 2193-2200.	0.8	3
5006	A Network Biology Approach to Decipher Stress Response in Bacteria Using <i>Escherichia coli</i> As a Model. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 310-324.	1.0	19
5007	Identification of genes associated with renal cell carcinoma using gene expression profiling analysis. <i>Oncology Letters</i> , 2016, 12, 73-78.	0.8	18
5008	Correlations between the composition of modular fungal communities and litter decomposition-associated ecosystem functions. <i>Fungal Ecology</i> , 2016, 22, 106-114.	0.7	46
5009	Network and biosignature analysis for the integration of transcriptomic and metabolomic data to characterize leaf senescence process in sunflower. <i>BMC Bioinformatics</i> , 2016, 17, 174.	1.2	45
5010	Interaction network of tobacco etch potyvirus Nla protein with the host proteome during infection. <i>BMC Genomics</i> , 2016, 17, 87.	1.2	57
5011	Urinary proteomics and metabolomics studies to monitor bladder health and urological diseases. <i>BMC Urology</i> , 2016, 16, 11.	0.6	32
5012	Efficient and biologically relevant consensus strategy for Parkinson's disease gene prioritization. <i>BMC Medical Genomics</i> , 2016, 9, 12.	0.7	29
5013	Global investigation of composition and interaction networks in gut microbiomes of individuals belonging to diverse geographies and age-groups. <i>Gut Pathogens</i> , 2016, 8, 17.	1.6	38
5014	<i>N</i> -Myristoyltransferase Inhibition Induces ER-Stress, Cell Cycle Arrest, and Apoptosis in Cancer Cells. <i>ACS Chemical Biology</i> , 2016, 11, 2165-2176.	1.6	60
5015	Integrated genome browser: visual analytics platform for genomics. <i>Bioinformatics</i> , 2016, 32, 2089-2095.	1.8	347
5016	Transcription, Signaling Receptor Activity, Oxidative Phosphorylation, and Fatty Acid Metabolism Mediate the Presence of Closely Related Species in Distinct Intertidal and Cold-Seep Habitats. <i>Genome Biology and Evolution</i> , 2016, 8, 51-69.	1.1	13

#	ARTICLE	IF	CITATIONS
5017	APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. <i>Nucleic Acids Research</i> , 2016, 44, W529-W535.	6.5	112
5018	Multiplexed Isobaric Tagging Protocols for Quantitative Mass Spectrometry Approaches to Auditory Research. <i>Methods in Molecular Biology</i> , 2016, 1427, 109-133.	0.4	1
5019	PTP1B controls non-mitochondrial oxygen consumption by regulating RNF213 to promote tumour survival during hypoxia. <i>Nature Cell Biology</i> , 2016, 18, 803-813.	4.6	95
5020	Identification of Candidate Cyclin-dependent kinase 1 (Cdk1) Substrates in Mitosis by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2448-2461.	2.5	54
5021	Transcriptome Display During Testicular Differentiation of Channel Catfish ( <i>Ictalurus punctatus</i> ) as Revealed by RNA-Seq Analysis. <i>Biology of Reproduction</i> , 2016, 95, 19-19.	1.2	35
5022	Systematic Functional Annotation and Visualization of Biological Networks. <i>Cell Systems</i> , 2016, 2, 412-421.	2.9	142
5023	Expression profile analysis based on DNA microarray for patients undergoing off-pump coronary artery bypass surgery. <i>Experimental and Therapeutic Medicine</i> , 2016, 11, 864-872.	0.8	6
5024	Regular expressions of MS/MS spectra for partial annotation of metabolite features. <i>Metabolomics</i> , 2016, 12, 1.	1.4	6
5025	ProXL (Protein Cross-Linking Database): A Platform for Analysis, Visualization, and Sharing of Protein Cross-Linking Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016, 15, 2863-2870.	1.8	51
5026	Association of functional genetic variants of CTLA4 with reduced serum CTLA4 protein levels and increased risk of idiopathic recurrent miscarriages. <i>Fertility and Sterility</i> , 2016, 106, 1115-1123.e6.	0.5	20
5027	Protein-Protein Interactions Suggest Novel Activities of Human Cytomegalovirus Tegument Protein pUL103. <i>Journal of Virology</i> , 2016, 90, 7798-7810.	1.5	21
5028	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740.	9.0	6,181
5029	Transcriptional signatures of influenza A/H1N1-specific IgG memory-like B cell response in older individuals. <i>Vaccine</i> , 2016, 34, 3993-4002.	1.7	39
5030	A PPAR $\beta$ -Bnip3 Axis Couples Adipose Mitochondrial Fusion-Fission Balance to Systemic Insulin Sensitivity. <i>Diabetes</i> , 2016, 65, 2591-2605.	0.3	45
5031	Combined Transcriptomic and Proteomic Approach to Identify Toxicity Pathways in Early Life Stages of Japanese Medaka ( <i>Oryzias latipes</i> ) Exposed to 1,2,5,6-Tetrabromocyclooctane (TBCO). <i>Environmental Science &amp; Technology</i> , 2016, 50, 7781-7790.	4.6	48
5032	Yeast two-hybrid screening identified WDR77 as a novel interacting partner of TSC22D2. <i>Tumor Biology</i> , 2016, 37, 12503-12512.	0.8	30
5033	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 34-44.	0.4	22
5034	Daphnia parasite dynamics across multiple <i>Caullerya</i> epidemics indicate selection against common parasite genotypes. <i>Zoology</i> , 2016, 119, 314-321.	0.6	11

#	ARTICLE	IF	CITATIONS
5035	Identification of microRNA-mRNA interactions in atrial fibrillation using microarray expression profiles and bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 13, 4535-4540.	1.1	12
5036	Identifying functional cancer-specific miRNA-mRNA interactions in testicular germ cell tumor. <i>Journal of Theoretical Biology</i> , 2016, 404, 82-96.	0.8	7
5037	A Collaborative Approach for Scoping Ecosystem Services with Stakeholders: The Case of Arrábida Natural Park. <i>Environmental Management</i> , 2016, 58, 323-342.	1.2	36
5038	A Graph Based Framework to Model Virus Integration Sites. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 69-77.	1.9	5
5039	Epithelial Regeneration After Gastric Ulceration Causes Prolonged Cell-Type Alterations. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016, 2, 625-647.	2.3	41
5040	Computational identification and systematic classification of novel GRAS genes in <i>Isatis indigotica</i> . <i>Chinese Journal of Natural Medicines</i> , 2016, 14, 161-176.	0.7	9
5041	A ribosome-related signature in peripheral blood CLL B cells is linked to reduced survival following treatment. <i>Cell Death and Disease</i> , 2016, 7, e2249-e2249.	2.7	24
5042	Key genes and pathways predicted in papillary thyroid carcinoma based on bioinformatics analysis. <i>Journal of Endocrinological Investigation</i> , 2016, 39, 1285-1293.	1.8	17
5043	Assimilation of microbial and plant carbon by active prokaryotic and fungal populations in glacial forefields. <i>Soil Biology and Biochemistry</i> , 2016, 98, 30-41.	4.2	55
5044	Interactome of the hepatitis C virus: Literature mining with ANDSystem. <i>Virus Research</i> , 2016, 218, 40-48.	1.1	25
5045	Comparison of microbial communities of activated sludge and membrane biofilm in 10 full-scale membrane bioreactors. <i>Water Research</i> , 2016, 101, 214-225.	5.3	106
5046	Identification of novel direct targets of <i>Drosophila Sine oculis</i> and <i>Eyes absent</i> by integration of genome-wide data sets. <i>Developmental Biology</i> , 2016, 415, 157-167.	0.9	9
5047	Identification of novel gene and pathway targets for human epilepsy treatment. <i>Biological Research</i> , 2016, 49, 3.	1.5	10
5048	A novel systems pharmacology platform to dissect action mechanisms of traditional Chinese medicines for bovine viral diarrhea disease. <i>European Journal of Pharmaceutical Sciences</i> , 2016, 94, 33-45.	1.9	51
5049	Proteometabolomic analysis of transgenic tomato overexpressing oxalate decarboxylase uncovers novel proteins potentially involved in defense mechanism against <i>Sclerotinia</i> . <i>Journal of Proteomics</i> , 2016, 143, 242-253.	1.2	24
5050	An integrative data mining approach to identifying adverse outcome pathway signatures. <i>Toxicology</i> , 2016, 350-352, 49-61.	2.0	47
5051	The Hyper-Modular Associative Mind: A Computational Analysis of Associative Responses of Persons with Asperger Syndrome. <i>Language and Speech</i> , 2016, 59, 297-317.	0.6	34
5052	A Network Analysis of Leadership Theory. <i>Journal of Management</i> , 2016, 42, 1374-1403.	6.3	110

#	ARTICLE	IF	CITATIONS
5053	Multi-breed and multi-trait co-association analysis of meat tenderness and other meat quality traits in three French beef cattle breeds. <i>Genetics Selection Evolution</i> , 2016, 48, 37.	1.2	50
5054	Diffany: an ontology-driven framework to infer, visualise and analyse differential molecular networks. <i>BMC Bioinformatics</i> , 2016, 17, 18.	1.2	30
5055	CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETworks. <i>BMC Bioinformatics</i> , 2016, 17, 64.	1.2	13
5056	Combined small RNA and degradome sequencing to identify miRNAs and their targets in response to drought in foxtail millet. <i>BMC Genetics</i> , 2016, 17, 57.	2.7	56
5057	IL-10 and integrin signaling pathways are associated with head and neck cancer progression. <i>BMC Genomics</i> , 2016, 17, 38.	1.2	43
5058	Cascade: an RNA-seq visualization tool for cancer genomics. <i>BMC Genomics</i> , 2016, 17, 75.	1.2	2
5059	Identification and expression analysis of genes related to calyx persistence in Korla fragrant pear. <i>BMC Genomics</i> , 2016, 17, 132.	1.2	31
5060	Deciphering the transcriptional regulation and spatiotemporal distribution of immunity response in barley to <i>Pyrenophora graminea</i> fungal invasion. <i>BMC Genomics</i> , 2016, 17, 256.	1.2	11
5061	Methamphetamine abuse affects gene expression in brain-derived microglia of SIV-infected macaques to enhance inflammation and promote virus targets. <i>BMC Immunology</i> , 2016, 17, 7.	0.9	53
5062	Liver and blood cytokine microenvironment in HCV patients is associated to liver fibrosis score: a proinflammatory cytokine ensemble orchestrated by TNF and tuned by IL-10. <i>BMC Microbiology</i> , 2016, 16, 3.	1.3	33
5063	Abscisic acid transcriptomic signaling varies with grapevine organ. <i>BMC Plant Biology</i> , 2016, 16, 72.	1.6	45
5064	Integrative meta-analysis identifies microRNA-regulated networks in infantile hemangioma. <i>BMC Medical Genetics</i> , 2016, 17, 4.	2.1	18
5065	Key role of lipid management in nitrogen and aroma metabolism in an evolved wine yeast strain. <i>Microbial Cell Factories</i> , 2016, 15, 32.	1.9	33
5066	Building a glaucoma interaction network using a text mining approach. <i>BioData Mining</i> , 2016, 9, 17.	2.2	4
5067	Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016, 4, 2.	4.9	118
5068	Candidate genes and pathogenesis investigation for sepsis-related acute respiratory distress syndrome based on gene expression profile. <i>Biological Research</i> , 2016, 49, 25.	1.5	20
5069	NaCl stress-induced transcriptomics analysis of <i>Salix linearistipularis</i> (syn. <i>Salix mongolica</i> ). <i>Journal of Biological Research</i> , 2016, 23, 1.	2.2	14
5070	Regulation of Platelet Derived Growth Factor Signaling by Leukocyte Common Antigen-related (LAR) Protein Tyrosine Phosphatase: A Quantitative Phosphoproteomics Study. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1823-1836.	2.5	10

#	ARTICLE	IF	CITATIONS
5071	Electronic Sorting of Immune Cell Subpopulations Based on Highly Plastic Genes. <i>Journal of Immunology</i> , 2016, 197, 665-673.	0.4	13
5072	A Brief Review on the Ecological Network Analysis with Applications in the Emerging Medical Ecology. <i>Springer Protocols</i> , 2016, , 7-39.	0.1	7
5073	Methods for accurate quantification of LTR-retrotransposon copy number using short-read sequence data: a case study in Sorghum. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1871-1883.	1.0	5
5074	SPAG5 as a prognostic biomarker and chemotherapy sensitivity predictor in breast cancer: a retrospective, integrated genomic, transcriptomic, and protein analysis. <i>Lancet Oncology, The</i> , 2016, 17, 1004-1018.	5.1	105
5075	Illuminating structural proteins in viral "dark matter" with metaproteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2436-2441.	3.3	95
5076	The RING 2.0 web server for high quality residue interaction networks. <i>Nucleic Acids Research</i> , 2016, 44, W367-W374.	6.5	369
5077	KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , 2016, 44, W98-W104.	6.5	45
5078	Systematic tracking of coordinated differential network motifs identifies novel disease-related genes by integrating multiple data. <i>Neurocomputing</i> , 2016, 206, 3-12.	3.5	4
5079	Bioinformatic analysis reveals the expression of unique transcriptomic signatures in Zika virus infected human neural stem cells. <i>Cell and Bioscience</i> , 2016, 6, 42.	2.1	51
5080	Large-Scale Functional RNAi Screen in <i>C. elegans</i> Identifies TGF- $\beta$ 2 and Notch Signaling Pathways as Modifiers of <i>CACNA1A</i> . <i>ASN Neuro</i> , 2016, 8, 175909141663702.	1.5	4
5081	Differences in genome-wide gene expression response in peripheral blood mononuclear cells between young and old men upon caloric restriction. <i>Genes and Nutrition</i> , 2016, 11, 13.	1.2	6
5082	G-DOC Plus " an integrative bioinformatics platform for precision medicine. <i>BMC Bioinformatics</i> , 2016, 17, 193.	1.2	39
5083	RNA-Seq analysis uncovers non-coding small RNA system of <i>Mycobacterium neoaurum</i> in the metabolism of sterols to accumulate steroid intermediates. <i>Microbial Cell Factories</i> , 2016, 15, 64.	1.9	19
5084	Ligand cluster-based protein network and ePlatton, a multi-target ligand finder. <i>Journal of Cheminformatics</i> , 2016, 8, 23.	2.8	1
5085	A Rat Model to Study the Effects of Diet-Induced Obesity on Radiation-Induced Mammary Carcinogenesis. <i>Radiation Research</i> , 2016, 185, 505.	0.7	7
5086	Fruit metabolite networks in engineered and non-engineered tomato genotypes reveal fluidity in a hormone and agroecosystem specific manner. <i>Metabolomics</i> , 2016, 12, 103.	1.4	21
5087	A hollow bacterial diversity pattern with elevation in Wolong Nature Reserve, Western Sichuan Plateau. <i>Journal of Soils and Sediments</i> , 2016, 16, 2365-2374.	1.5	20
5088	Novel nitrifiers and comammox in a full-scale hybrid biofilm and activated sludge reactor revealed by metagenomic approach. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8225-8237.	1.7	90

#	ARTICLE	IF	CITATIONS
5089	Clinical impact and network of determinants of tumour necrosis in colorectal cancer. <i>British Journal of Cancer</i> , 2016, 114, 1334-1342.	2.9	55
5090	Comparative analyses of population-scale phenomic data in electronic medical records reveal race-specific disease networks. <i>Bioinformatics</i> , 2016, 32, i101-i110.	1.8	39
5091	Distinct metabolic changes between wheat embryo and endosperm during grain development revealed by 2D <sup>15</sup> N-based integrative proteome analysis. <i>Proteomics</i> , 2016, 16, 1515-1536.	1.3	43
5092	Histone Chaperone SSRP1 is Essential for Wnt Signaling Pathway Activity During Osteoblast Differentiation. <i>Stem Cells</i> , 2016, 34, 1369-1376.	1.4	32
5093	Insights into the Ecology and Evolution of Polyploid Plants through Network Analysis. <i>Molecular Ecology</i> , 2016, 25, 2644-2660.	2.0	35
5094	Phenotyping hepatocellular metabolism using uniformly labeled carbon-13 molecular probes and LC-HRMS stable isotope tracing. <i>Analytical Biochemistry</i> , 2016, 508, 129-137.	1.1	8
5095	Regulation of Gene Expression in <i>Shewanella oneidensis</i> MR-1 during Electron Acceptor Limitation and Bacterial Nanowire Formation. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5428-5443.	1.4	59
5096	Peptide affinity analysis of proteins that bind to an unstructured NH <sub>2</sub> -terminal region of the osmoprotective transcription factor NFAT5. <i>Physiological Genomics</i> , 2016, 48, 290-305.	1.0	8
5097	Genome-wide transcriptome analysis of female-sterile rice ovule shed light on its abortive mechanism. <i>Planta</i> , 2016, 244, 1011-1028.	1.6	18
5098	The Exonuclease Trex2 Shapes Psoriatic Phenotype. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2345-2355.	0.3	15
5099	A novel approach to detect resistance mechanisms reveals FGR as a factor mediating HDAC inhibitor SAHA resistance in B cell lymphoma. <i>Molecular Oncology</i> , 2016, 10, 1232-1244.	2.1	13
5100	LAR protein tyrosine phosphatase regulates focal adhesions via CDK1. <i>Journal of Cell Science</i> , 2016, 129, 2962-71.	1.2	52
5101	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	3.9	159
5102	Identification of candidate causal genes and their associated pathogenic mechanisms underlying teratozoospermia based on the spermatozoa transcript profiles. <i>Andrologia</i> , 2016, 48, 576-583.	1.0	10
5103	Directed random walks and constraint programming reveal active pathways in hepatocyte growth factor signaling. <i>FEBS Journal</i> , 2016, 283, 350-360.	2.2	5
5104	Acoustic sequences in non-human animals: a tutorial review and prospectus. <i>Biological Reviews</i> , 2016, 91, 13-52.	4.7	213
5105	COWB: A cloud-based framework supporting collaborative knowledge management within biomedical communities. <i>Future Generation Computer Systems</i> , 2016, 54, 399-408.	4.9	9
5106	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. <i>Plant Physiology</i> , 2016, 170, 1549-1565.	2.3	47



#	ARTICLE	IF	CITATIONS
5107	Trans-Omics: How To Reconstruct Biochemical Networks Across Multiple "Omic"™ Layers. Trends in Biotechnology, 2016, 34, 276-290.	4.9	221
5108	Assembly of the <i>Caenorhabditis elegans</i> gut microbiota from diverse soil microbial environments. ISME Journal, 2016, 10, 1998-2009.	4.4	296
5109	Understanding the functional impact of copy number alterations in breast cancer using a network modeling approach. Molecular BioSystems, 2016, 12, 963-972.	2.9	25
5110	NRP1 is targeted by miR-130a and miR-130b, and is associated with multidrug resistance in epithelial ovarian cancer based on integrated gene network analysis. Molecular Medicine Reports, 2016, 13, 188-196.	1.1	27
5111	Non-canonical pathway network modelling and ubiquitination site prediction through homology modelling of NF- $\kappa$ B. Gene, 2016, 581, 48-56.	1.0	14
5112	CanisOme " The protein signatures of Canis lupus familiaris diseases. Journal of Proteomics, 2016, 136, 193-201.	1.2	12
5113	DESM: portal for microbial knowledge exploration systems. Nucleic Acids Research, 2016, 44, D624-D633.	6.5	12
5114	Potential involvement of the interleukin-18 pathway in schizophrenia. Journal of Psychiatric Research, 2016, 74, 10-16.	1.5	15
5115	Retention, Molecular Evolution, and Expression Divergence of the Auxin/Indole Acetic Acid and Auxin Response Factor Gene Families in <i>Brassica Rapa</i> Shed Light on Their Evolution Patterns in Plants. Genome Biology and Evolution, 2016, 8, 302-316.	1.1	35
5116	Molecular systems evaluation of oligomerogenic APPE693Q and fibrillogenic APPKM670/671NL/PSEN1 <sup>1</sup> exon9 mouse models identifies shared features with human Alzheimer's brain molecular pathology. Molecular Psychiatry, 2016, 21, 1099-1111.	4.1	18
5117	Combined Large-Scale Phenotyping and Transcriptomics in Maize Reveals a Robust Growth Regulatory Network. Plant Physiology, 2016, 170, 1848-1867.	2.3	49
5118	Elevated nutrients change bacterial community composition and connectivity: high throughput sequencing of young marine biofilms. Biofouling, 2016, 32, 57-69.	0.8	87
5119	Use of the BioGRID Database for Analysis of Yeast Protein and Genetic Interactions. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088880.	0.2	23
5120	Novel insights into human respiratory syncytial virus-host factor interactions through integrated proteomics and transcriptomics analysis. Expert Review of Anti-Infective Therapy, 2016, 14, 285-297.	2.0	24
5121	Repositioning of drugs using open-access data portal DTome: A test case with probenecid (Review). International Journal of Molecular Medicine, 2016, 37, 3-10.	1.8	11
5122	Neonatal mitochondrial abnormalities due to PINK1 deficiency: Proteomics reveals early changes relevant to Parkinson's disease. Data in Brief, 2016, 6, 428-432.	0.5	8
5123	Construction and analysis of a genome-scale metabolic network for <i>Bacillus licheniformis</i> WX-02. Research in Microbiology, 2016, 167, 282-289.	1.0	8
5124	Cross-species proteomics in analysis of mammalian sperm proteins. Journal of Proteomics, 2016, 135, 38-50.	1.2	31



#	ARTICLE	IF	CITATIONS
5125	The ubiquitin ligase Ubr4 controls stability of podocin/MEC-2 supercomplexes. <i>Human Molecular Genetics</i> , 2016, 25, 1328-1344.	1.4	45
5126	Ozone Exposure Increases Circulating Stress Hormones and Lipid Metabolites in Humans. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 1382-1391.	2.5	159
5127	Potential sources of microbial colonizers in an initial soil ecosystem after retreat of an alpine glacier. <i>ISME Journal</i> , 2016, 10, 1625-1641.	4.4	99
5128	MicroRNA expression profiles in response to drought stress in <i>Sorghum bicolor</i> . <i>Gene Expression Patterns</i> , 2016, 20, 88-98.	0.3	66
5129	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	9.0	44
5130	Systematic identification and annotation of human methylation marks based on bisulfite sequencing methylomes reveals distinct roles of cell type-specific hypomethylation in the regulation of cell identity genes. <i>Nucleic Acids Research</i> , 2016, 44, 75-94.	6.5	83
5131	Systems Approaches to Understanding Aging. , 2016, , 241-261.		1
5132	Synergy evaluation by a pathway-pathway interaction network: a new way to predict drug combination. <i>Molecular BioSystems</i> , 2016, 12, 614-623.	2.9	54
5133	Microarray analysis of di-n-butyl phthalate and 17 $\beta$ -ethinyl-oestradiol responses in three-spined stickleback testes reveals novel candidate genes for endocrine disruption. <i>Ecotoxicology and Environmental Safety</i> , 2016, 124, 96-104.	2.9	10
5134	Integrated Genomic and Network-Based Analyses of Complex Diseases and Human Disease Network. <i>Journal of Genetics and Genomics</i> , 2016, 43, 349-367.	1.7	21
5135	Regulatory T Cells Orchestrate Similar Immune Evasion of Fetuses and Tumors in Mice. <i>Journal of Immunology</i> , 2016, 196, 678-690.	0.4	14
5136	A systems pharmacology approach to decipher the mechanism of danggui-shaoyao-san decoction for the treatment of neurodegenerative diseases. <i>Journal of Ethnopharmacology</i> , 2016, 178, 66-81.	2.0	52
5137	Polygenic associations of neurodevelopmental genes in suicide attempt. <i>Molecular Psychiatry</i> , 2016, 21, 1381-1390.	4.1	84
5138	Visualization of Host-Poliovirus Interaction Topologies Using Protein Interaction Reporter Technology. <i>Journal of Virology</i> , 2016, 90, 1973-1987.	1.5	38
5139	Antiviral innate immunity through the lens of systems biology. <i>Virus Research</i> , 2016, 218, 10-17.	1.1	10
5140	metaModules identifies key functional subnetworks in microbiome-related disease. <i>Bioinformatics</i> , 2016, 32, 1678-1685.	1.8	21
5141	Aberrant expression of long noncoding RNAs in cumulus cells isolated from PCOS patients. <i>Journal of Assisted Reproduction and Genetics</i> , 2016, 33, 111-121.	1.2	61
5142	Cancer RNA-Seq Nexus: a database of phenotype-specific transcriptome profiling in cancer cells. <i>Nucleic Acids Research</i> , 2016, 44, D944-D951.	6.5	111

#	ARTICLE	IF	CITATIONS
5143	Exploring Transcription Factors-microRNAs Co-regulation Networks in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2016, 42, 1037-1045.	2.3	49
5144	Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. <i>Plant Physiology</i> , 2016, 170, 136-146.	2.3	62
5145	Comparative transcriptome analysis of atrial septal defect identifies dysregulated genes during heart septum morphogenesis. <i>Gene</i> , 2016, 575, 303-312.	1.0	19
5146	A novel framework for inferring condition-specific TF and miRNA co-regulation of protein-protein interactions. <i>Gene</i> , 2016, 577, 55-64.	1.0	8
5147	Systems Approaches towards Molecular Profiling of Human Immunity. <i>Trends in Immunology</i> , 2016, 37, 53-67.	2.9	22
5148	Temporal lobe in human aging: A quantitative protein profiling study of samples from Chinese Human Brain Bank. <i>Experimental Gerontology</i> , 2016, 73, 31-41.	1.2	22
5149	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	3.2	28
5150	Integrative Analyses of Colorectal Cancer Show Immunoscore Is a Stronger Predictor of Patient Survival Than Microsatellite Instability. <i>Immunity</i> , 2016, 44, 698-711.	6.6	814
5151	Integrated analysis of long non-coding RNA competing interactions reveals the potential role in progression of human gastric cancer. <i>International Journal of Oncology</i> , 2016, 48, 1965-1976.	1.4	110
5152	A matter of quantity: Common features in the drought response of transgenic plants overexpressing HD-Zip I transcription factors. <i>Plant Science</i> , 2016, 251, 139-154.	1.7	28
5153	Phosphoproteome analysis of <i>B. cinerea</i> in response to different plant-based elicitors. <i>Journal of Proteomics</i> , 2016, 139, 84-94.	1.2	26
5154	Improving Functional Annotation in the DRE-TIM Metallolyase Superfamily through Identification of Active Site Fingerprints. <i>Biochemistry</i> , 2016, 55, 1863-1872.	1.2	9
5155	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
5156	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. <i>Computational Biology and Chemistry</i> , 2016, 62, 60-69.	1.1	36
5157	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D620-D623.	6.5	69
5158	Immunoprecipitation and mass spectrometry defines an extensive RBM45 protein-protein interaction network. <i>Brain Research</i> , 2016, 1647, 79-93.	1.1	43
5159	Expression quantitative trait analysis reveals fine germline transcript regulation in mouse lung tumors. <i>Cancer Letters</i> , 2016, 375, 221-230.	3.2	2
5160	Hyperlipidemia, Disease Associations, and Top 10 Potential Drug Targets: A Network View. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 152-168.	1.0	16

#	ARTICLE	IF	CITATIONS
5161	Comprehensive Genomic Analysis and Expression Profiling of the NOX Gene Families under Abiotic Stresses and Hormones in Plants. <i>Genome Biology and Evolution</i> , 2016, 8, 791-810.	1.1	41
5162	<i>In silico</i> tools and transcriptomics analyses in the mutagenicity assessment of cosmetic ingredients: a proof-of-principle on how to add weight to the evidence. <i>Mutagenesis</i> , 2016, 31, 453-461.	1.0	9
5163	Transcriptional regulatory networks in <i>Arabidopsis thaliana</i> during single and combined stresses. <i>Nucleic Acids Research</i> , 2016, 44, 3147-3164.	6.5	62
5164	Genomic, Lipidomic and Metabolomic Analysis of Cyclooxygenase-null Cells: Eicosanoid Storm, Cross Talk, and Compensation by COX-1. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 81-93.	3.0	13
5165	Magnetic resonance analysis of malignant transformation in recurrent glioma. <i>Neuro-Oncology</i> , 2016, 18, 1169-1179.	0.6	28
5166	Thermodynamic measures of cancer: Gibbs free energy and entropy of protein-protein interactions. <i>Journal of Biological Physics</i> , 2016, 42, 339-350.	0.7	42
5167	Transcriptome and metabolite profiling reveals that prolonged drought modulates the phenylpropanoid and terpenoid pathway in white grapes ( <i>Vitis vinifera</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 67.	1.6	269
5168	A computational model of cardiac fibroblast signaling predicts context-dependent drivers of myofibroblast differentiation. <i>Journal of Molecular and Cellular Cardiology</i> , 2016, 94, 72-81.	0.9	79
5169	The analysis of Gene Regulatory Networks in plant evo-devo. <i>Journal of Experimental Botany</i> , 2016, 67, 2549-2563.	2.4	11
5170	<i>Arabidopsis</i> <i>GERANYLGERANYL DIPHOSPHATE SYNTHASE 11</i> is a hub isozyme required for the production of most photosynthesis-related isoprenoids. <i>New Phytologist</i> , 2016, 209, 252-264.	3.5	131
5171	Application of Market Basket Analysis for the Visualization of Transaction Data Based on Human Lifestyle and Spectroscopic Measurements. <i>Analytical Chemistry</i> , 2016, 88, 2714-2719.	3.2	28
5172	Suboptimal culture conditions induce more deviations in gene expression in male than female bovine blastocysts. <i>BMC Genomics</i> , 2016, 17, 72.	1.2	58
5173	Circulating microRNAs as biomarkers in patients with allergic rhinitis and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1423-1432.	1.5	176
5174	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. <i>ISME Journal</i> , 2016, 10, 1823-1835.	4.4	126
5175	Gene co-expression analyses: an overview from microarray collections in <i>Arabidopsis thaliana</i> . <i>Briefings in Bioinformatics</i> , 2017, 18, bbw002.	3.2	7
5176	TGF- $\beta$ 1 prevents rat retinal insult induced by amyloid- $\beta$ (1-42) oligomers. <i>European Journal of Pharmacology</i> , 2016, 787, 72-77.	1.7	39
5177	GAME9 regulates the biosynthesis of steroidal alkaloids and upstream isoprenoids in the plant mevalonate pathway. <i>Nature Communications</i> , 2016, 7, 10654.	5.8	239
5178	Stress granules and RNA processing bodies are novel autoantibody targets in systemic sclerosis. <i>Arthritis Research and Therapy</i> , 2016, 18, 27.	1.6	16

#	ARTICLE	IF	CITATIONS
5179	Dynamics of Hippocampal Protein Expression During Long-term Spatial Memory Formation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 523-541.	2.5	19
5180	Fibronectin-Containing Extracellular Vesicles Protect Melanocytes against Ultraviolet Radiation-Induced Cytotoxicity. <i>Journal of Investigative Dermatology</i> , 2016, 136, 957-966.	0.3	32
5181	MiRNA-145 Regulates the Development of Congenital Heart Disease Through Targeting FXN. <i>Pediatric Cardiology</i> , 2016, 37, 629-636.	0.6	31
5182	Transcriptomic changes associated with DKK4 overexpression in pancreatic cancer cells detected by RNA-Seq. <i>Tumor Biology</i> , 2016, 37, 10827-10838.	0.8	15
5183	Identification of upstream regulators for synovial expression signature genes in osteoarthritis. <i>Joint Bone Spine</i> , 2016, 83, 545-551.	0.8	19
5184	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016, 15, 339-359.	1.8	26
5185	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	9.0	209
5186	MicroRNA transcriptome profiling of mice brains infected with Japanese encephalitis virus by RNA sequencing. <i>Infection, Genetics and Evolution</i> , 2016, 39, 249-257.	1.0	7
5187	The Human Physiome: how standards, software and innovative service infrastructures are providing the building blocks to make it achievable. <i>Interface Focus</i> , 2016, 6, 20150103.	1.5	30
5188	Genome-wide association and high-resolution phenotyping link <i>Oryza sativa</i> panicle traits to numerous trait-specific QTL clusters. <i>Nature Communications</i> , 2016, 7, 10527.	5.8	165
5189	Viral metagenomics: are we missing the giants?. <i>Current Opinion in Microbiology</i> , 2016, 31, 34-43.	2.3	26
5190	A novel PR10 promoter from <i>Erianthus arundinaceus</i> directs high constitutive transgene expression and is enhanced upon wounding in heterologous plant systems. <i>Molecular Biology Reports</i> , 2016, 43, 17-30.	1.0	13
5191	LmSmdB: an integrated database for metabolic and gene regulatory network in <i>Leishmania major</i> and <i>Schistosoma mansoni</i> . <i>Genomics Data</i> , 2016, 7, 115-118.	1.3	10
5192	Proteomic Analysis of Dynein-Interacting Proteins in Amyotrophic Lateral Sclerosis Synaptosomes Reveals Alterations in the RNA-Binding Protein Staufen1. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 506-522.	2.5	27
5193	Soil bacterial communities associated with natural and commercial <i>Cyclopia</i> spp.. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw016.	1.3	29
5194	Microbial diversity in European alpine permafrost and active layers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw018.	1.3	266
5195	Do Genetic Factors Modify the Relationship Between Obesity and Hypertriglyceridemia?. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 162-171.	5.1	7
5196	Using the Gene Ontology to Annotate Key Players in Parkinson's Disease. <i>Neuroinformatics</i> , 2016, 14, 297-304.	1.5	20

#	ARTICLE	IF	CITATIONS
5197	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
5198	Multilevel functional genomics data integration as a tool for understanding physiology: a network biology perspective. <i>Journal of Applied Physiology</i> , 2016, 120, 297-309.	1.2	10
5199	Drug discovery of neurodegenerative disease through network pharmacology approach in herbs. <i>Biomedicine and Pharmacotherapy</i> , 2016, 78, 272-279.	2.5	18
5200	Exploring and Understanding the Biochemical Diversity of the Human Microbiota. <i>Cell Chemical Biology</i> , 2016, 23, 18-30.	2.5	115
5201	Microbial, host and xenobiotic diversity in the cystic fibrosis sputum metabolome. <i>ISME Journal</i> , 2016, 10, 1483-1498.	4.4	88
5202	How are they different? A quantitative domain comparison of information visualization and data visualization (2000â€“2014). <i>Scientometrics</i> , 2016, 107, 123-165.	1.6	37
5203	Investigating the structural impact of S311C mutation in DRD2 receptor by molecular dynamics & docking studies. <i>Biochimie</i> , 2016, 123, 52-64.	1.3	10
5204	Proteomic data reveals a physiological basis for costs and benefits associated with thermal acclimation. <i>Journal of Experimental Biology</i> , 2016, 219, 969-76.	0.8	35
5205	Organization principles of biological networks: An explorative study. <i>BioSystems</i> , 2016, 141, 31-39.	0.9	9
5206	Serum Metabolite Profiles Are Altered by Erlotinib Treatment and the Integrin $\alpha 1$ -Null Genotype but Not by Post-Traumatic Osteoarthritis. <i>Journal of Proteome Research</i> , 2016, 15, 815-825.	1.8	7
5207	The tumor microenvironment and Immunoscore are critical determinants of dissemination to distant metastasis. <i>Science Translational Medicine</i> , 2016, 8, 327ra26.	5.8	360
5208	Systematic Prioritization of Druggable Mutations in $\sim 45000$ Genomes Across 16 Cancer Types Using a Structural Genomics-based Approach. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 642-656.	2.5	43
5209	Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. <i>Cell Reports</i> , 2016, 14, 2142-2153.	2.9	231
5210	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016, 11, 1362-1371.	1.6	15
5211	Genetics of Lipid Disorders. , 2016, , 159-193.		0
5212	Bisphenols: More unnecessary surprises. <i>Endocrine Disruptors (Austin, Tex )</i> , 2016, 4, e1131032.	1.1	6
5213	Comprehensive Proteomic and Metabolomic Signatures of Nontypeable <i>Haemophilus influenzae</i> -Induced Acute Otitis Media Reveal Bacterial Aerobic Respiration in an Immunosuppressed Environment. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1117-1138.	2.5	18
5214	Generation of an algorithm based on minimal gene sets to clinically subtype triple negative breast cancer patients. <i>BMC Cancer</i> , 2016, 16, 143.	1.1	55

#	ARTICLE	IF	CITATIONS
5215	A robust platform for chemical genomics in bacterial systems. <i>Molecular Biology of the Cell</i> , 2016, 27, 1015-1025.	0.9	57
5216	Biomethane production and microbial community response according to influent concentration of molasses wastewater in a UASB reactor. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 4675-4683.	1.7	11
5217	Genome-wide analysis, expression dynamics and varietal comparison of NAC gene family at various developmental stages in <i>Morus notabilis</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 1305-1317.	1.0	16
5218	TMT-based quantitative proteomics analyses reveal novel defense mechanisms of <i>Brassica napus</i> against the devastating necrotrophic pathogen <i>Sclerotinia sclerotiorum</i> . <i>Journal of Proteomics</i> , 2016, 143, 265-277.	1.2	27
5219	Prediction of human protein-protein interaction by a domain-based approach. <i>Journal of Theoretical Biology</i> , 2016, 396, 144-153.	0.8	9
5220	SDTNBI: an integrated network and chemoinformatics tool for systematic prediction of drug-target interactions and drug repositioning. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw012.	3.2	102
5221	Identification of novel inhibitors of DDR1 against idiopathic pulmonary fibrosis by integrative transcriptome meta-analysis, computational and experimental screening. <i>Molecular BioSystems</i> , 2016, 12, 1540-1551.	2.9	22
5222	Global Epitranscriptomics Profiling of RNA Post-Transcriptional Modifications as an Effective Tool for Investigating the Epitranscriptomics of Stress Response. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 932-944.	2.5	23
5223	Distribution and Relationships of Antimicrobial Resistance Determinants among Extended-Spectrum-Cephalosporin-Resistant or Carbapenem-Resistant <i>Escherichia coli</i> Isolates from Rivers and Sewage Treatment Plants in India. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2972-2980.	1.4	87
5224	Proteomic Analysis of the Mammalian Katanin Family of Microtubule-severing Enzymes Defines Katanin p80 subunit B-like 1 (KATNBL1) as a Regulator of Mammalian Katanin Microtubule-severing. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1658-1669.	2.5	42
5225	New molecular evidence of wine yeast-bacteria interaction unraveled by non-targeted exometabolomic profiling. <i>Metabolomics</i> , 2016, 12, 1.	1.4	26
5226	Cerebellar Transcriptome Profiles of ATXN1 Transgenic Mice Reveal SCA1 Disease Progression and Protection Pathways. <i>Neuron</i> , 2016, 89, 1194-1207.	3.8	86
5227	Illuminating drug action by network integration of disease genes: a case study of myocardial infarction. <i>Molecular BioSystems</i> , 2016, 12, 1653-1666.	2.9	21
5228	Study of pathway cross-talk interactions with NF- $\kappa$ B leading to its activation via ubiquitination or phosphorylation: A brief review. <i>Gene</i> , 2016, 584, 97-109.	1.0	101
5229	Sperm tsRNAs contribute to intergenerational inheritance of an acquired metabolic disorder. <i>Science</i> , 2016, 351, 397-400.	6.0	1,042
5230	A whole genome bioinformatic approach to determine potential latent phase specific targets in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2016, 97, 181-192.	0.8	21
5231	The symbiotic life of <i>Symbiodinium</i> in the open ocean within a new species of calcifying ciliate ( <i>Tiarina</i> sp.). <i>ISME Journal</i> , 2016, 10, 1424-1436.	4.4	37
5232	Structural signatures of DRD4 mutants revealed using molecular dynamics simulations: Implications for drug targeting. <i>Journal of Molecular Modeling</i> , 2016, 22, 14.	0.8	6



#	ARTICLE	IF	CITATIONS
5233	Exploration of rice pistil responses during early post-pollination through a combined proteomic and transcriptomic analysis. <i>Journal of Proteomics</i> , 2016, 131, 214-226.	1.2	21
5234	Genomic, Proteomic, and Metabolite Characterization of Gemfibrozil-Degrading Organism <i>Bacillus</i> sp. GeD10. <i>Environmental Science &amp; Technology</i> , 2016, 50, 744-755.	4.6	30
5235	A network analysis of the Chinese medicine Lianhua-Qingwen formula to identify its main effective components. <i>Molecular BioSystems</i> , 2016, 12, 606-613.	2.9	43
5236	Network Analysis of Lung Transcriptomics Reveals a Distinct B-Cell Signature in Emphysema. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 1242-1253.	2.5	99
5237	Dynamic Control of Enhancer Repertoires Drives Lineage and Stage-Specific Transcription during Hematopoiesis. <i>Developmental Cell</i> , 2016, 36, 9-23.	3.1	204
5238	Comparative analyses of the proteins from <i>Mycobacterium tuberculosis</i> and human genomes: Identification of potential tuberculosis drug targets. <i>Gene</i> , 2016, 579, 69-74.	1.0	11
5239	The transcriptional regulator network of human inflammatory macrophages is defined by open chromatin. <i>Cell Research</i> , 2016, 26, 151-170.	5.7	103
5240	Clonal spread and interspecies transmission of clinically relevant ESBL-producing <i>Escherichia coli</i> of ST410—another successful pandemic clone?. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv155.	1.3	120
5241	Amorfrutin C Induces Apoptosis and Inhibits Proliferation in Colon Cancer Cells through Targeting Mitochondria. <i>Journal of Natural Products</i> , 2016, 79, 2-12.	1.5	39
5242	Hepatitis E virus ORF1 encoded non structural protein—host protein interaction network. <i>Virus Research</i> , 2016, 213, 195-204.	1.1	15
5243	Genome-Wide Gene Expression Analysis Identifies the Proto-oncogene Tyrosine-Protein Kinase Src as a Crucial Virulence Determinant of Infectious Laryngotracheitis Virus in Chicken Cells. <i>Journal of Virology</i> , 2016, 90, 9-21.	1.5	10
5244	Prediction of Declining Renal Function and Albuminuria in Patients With Type 2 Diabetes by Metabolomics. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 696-704.	1.8	62
5245	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , 2016, 26, 161-172.	1.8	137
5246	Integrative computational in-depth analysis of dysregulated miRNA-mRNA interactions in drug-resistant pediatric acute lymphoblastic leukemia cells: an attempt to obtain new potential gene-miRNA pathways involved in response to treatment. <i>Tumor Biology</i> , 2016, 37, 7861-7872.	0.8	28
5247	The conserved salt-responsive genes in the roots of <i>Populus</i> — <i>canescens</i> and <i>Arabidopsis thaliana</i> . <i>Environmental and Experimental Botany</i> , 2016, 129, 48-56.	2.0	23
5248	Systematic analysis of key miRNAs and related signaling pathways in colorectal tumorigenesis. <i>Gene</i> , 2016, 578, 177-184.	1.0	34
5249	The elusive endogenous adipogenic PPAR $\beta$ agonists: Lining up the suspects. <i>Progress in Lipid Research</i> , 2016, 61, 149-162.	5.3	32
5250	BioGRID: A Resource for Studying Biological Interactions in Yeast. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top080754.	0.2	50



#	ARTICLE	IF	CITATIONS
5251	MicroRNA profiling of antler stem cells in potentiated and dormant states and their potential roles in antler regeneration. <i>Molecular Genetics and Genomics</i> , 2016, 291, 943-955.	1.0	16
5252	Rare copy number variants and congenital heart defects in the 22q11.2 deletion syndrome. <i>Human Genetics</i> , 2016, 135, 273-285.	1.8	43
5253	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. <i>American Journal of Human Genetics</i> , 2016, 98, 5-21.	2.6	243
5254	New and Improved Techniques for the Study of Pathogenic Fungi. <i>Trends in Microbiology</i> , 2016, 24, 35-50.	3.5	39
5255	Cross-talk between $\alpha 7$ nAChR and NMDAR revealed by protein profiling. <i>Journal of Proteomics</i> , 2016, 131, 113-121.	1.2	15
5256	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. <i>Journal of Proteomics</i> , 2016, 131, 205-213.	1.2	16
5257	Quantitative proteomic analysis of anticancer drug RH1 resistance in liver carcinoma. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 219-232.	1.1	13
5258	Bacterial predation in a marine host-associated microbiome. <i>ISME Journal</i> , 2016, 10, 1540-1544.	4.4	77
5259	An in-silico approach aimed to clarify the role of Y181C and K103N HIV-1 reverse transcriptase mutations versus Indole Aryl Sulphones. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 63, 49-56.	1.3	4
5260	Mapping the effects of drugs on the immune system. <i>Nature Biotechnology</i> , 2016, 34, 47-54.	9.4	78
5261	An integrative analysis of transcriptomic response of ethanol tolerant strains to ethanol in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2016, 12, 464-476.	2.9	21
5262	Identifying miRNA synergistic regulatory networks in heterogeneous human data via network motifs. <i>Molecular BioSystems</i> , 2016, 12, 454-463.	2.9	9
5263	CD36 Is a Matrix Metalloproteinase-9 Substrate That Stimulates Neutrophil Apoptosis and Removal During Cardiac Remodeling. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 14-25.	5.1	78
5264	<i>Trypanosoma cruzi</i> mitochondrial trypanothione peroxidase is located throughout the cell and its pull down provides one step towards the understanding of its mechanism of action. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1-10.	1.1	8
5265	Comprehensive transcriptomic analysis of the process of gonadal sex differentiation in the turbot ( <i>L. microdon</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	47
5266	DIANA-miRGen v3.0: accurate characterization of microRNA promoters and their regulators. <i>Nucleic Acids Research</i> , 2016, 44, D190-D195.	6.5	53
5267	Acute psychological stress induces short-term variable immune response. <i>Brain, Behavior, and Immunity</i> , 2016, 53, 172-182.	2.0	34
5268	Network Analysis and Visualizations of Water Resources Infrastructure in California: Linking Connectivity and Resilience. <i>Journal of Water Resources Planning and Management - ASCE</i> , 2016, 142, .	1.3	26

#	ARTICLE	IF	CITATIONS
5269	Structureâ€™function discrepancy in Clostridium botulinum C3 toxin for its rational prioritization as a subunit vaccine. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1317-1329.	2.0	13
5270	Computational analysis of protein interaction networks for infectious diseases. Briefings in Bioinformatics, 2016, 17, 517-526.	3.2	63
5271	Identification of key genes associated with the effect of estrogen on ovarian cancer using microarray analysis. Archives of Gynecology and Obstetrics, 2016, 293, 421-427.	0.8	8
5272	Review: High-performance computing to detect epistasis in genome scale data sets. Briefings in Bioinformatics, 2016, 17, 368-379.	3.2	39
5273	A Practical Guide for Exploring Opportunities of Repurposing Drugs for CNS Diseases in Systems Biology. Methods in Molecular Biology, 2016, 1303, 531-547.	0.4	6
5274	Genome neighborhood network reveals insights into enediyne biosynthesis and facilitates prediction and prioritization for discovery. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 261-276.	1.4	55
5275	Metagenomic analysis of microbial community in uranium-contaminated soil. Applied Microbiology and Biotechnology, 2016, 100, 299-310.	1.7	83
5276	Integration of quantitative proteomics data and interaction networks: Identification of dysregulated cellular functions during cancer progression. Methods, 2016, 93, 103-109.	1.9	6
5277	Big-data-based edge biomarkers: study on dynamical drug sensitivity and resistance in individuals. Briefings in Bioinformatics, 2016, 17, 576-592.	3.2	57
5278	Diversity of Interstitial Lung Fibroblasts Is Regulated by Platelet-Derived Growth Factor Receptor $\alpha$ Kinase Activity. American Journal of Respiratory Cell and Molecular Biology, 2016, 54, 532-545.	1.4	85
5279	Altered Blood Gene Expression of Tumor-Related Genes (PRKCB, BECN1, and CDKN2A) in Alzheimerâ€™s Disease. Molecular Neurobiology, 2016, 53, 5902-5911.	1.9	15
5280	Characterization of the bacterial communities of casts from Eisenia andrei fed with different substrates. Applied Soil Ecology, 2016, 98, 103-111.	2.1	56
5281	Bacterial diversity indicates dietary overlap among bats of different feeding habits. Microbiological Research, 2016, 182, 99-108.	2.5	42
5282	A Systems Genetics Approach Identifies Gene Regulatory Networks Associated with Fatty Acid Composition in Brassica rapa Seed. Plant Physiology, 2016, 170, 568-585.	2.3	34
5283	Utilization of information from gene networks towards a better understanding of functional similarities between complex traits: a dairy cattle model. Journal of Applied Genetics, 2016, 57, 129-133.	1.0	2
5284	Microbiome shifts and the inhibition of quorum sensing by Black Band Disease cyanobacteria. ISME Journal, 2016, 10, 1204-1216.	4.4	82
5285	Genome-Wide Chromatin Immunoprecipitation in Candida albicans and Other Yeasts. Methods in Molecular Biology, 2016, 1361, 161-184.	0.4	4
5286	Microbial diversity at Mitchell Peninsula, Eastern Antarctica: a potential biodiversity â€™hotspotâ€™. Polar Biology, 2016, 39, 237-249.	0.5	101

#	ARTICLE	IF	CITATIONS
5287	Comparative plasma proteomic studies of pulmonary TiO <sub>2</sub> nanoparticle exposure in rats using liquid chromatography tandem mass spectrometry. <i>Journal of Proteomics</i> , 2016, 130, 85-93.	1.2	13
5288	Adaptive selection and coevolution at the proteins of the Polycomb repressive complexes in <i>Drosophila</i> . <i>Heredity</i> , 2016, 116, 213-223.	1.2	4
5289	Single Active Site Mutation Causes Serious Resistance of HIV Reverse Transcriptase to Lamivudine: Insight from Multiple Molecular Dynamics Simulations. <i>Cell Biochemistry and Biophysics</i> , 2016, 74, 35-48.	0.9	8
5290	Transcriptome-Wide Differential Gene Expression in <i>Bicyclus anynana</i> Butterflies: Female Vision-Related Genes Are More Plastic. <i>Molecular Biology and Evolution</i> , 2016, 33, 79-92.	3.5	34
5291	miRNA-mRNA Interaction Network in Non-small Cell Lung Cancer. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 209-219.	2.2	40
5292	Interactive visual knowledge discovery from data-based temporal decision support system. <i>Information Visualization</i> , 2016, 15, 31-50.	1.2	15
5293	Ecological network analysis reveals the inter-connection between soil biodiversity and ecosystem function as affected by land use across Europe. <i>Applied Soil Ecology</i> , 2016, 97, 112-124.	2.1	184
5294	Analysis of Proteins That Rapidly Change Upon Mechanistic/Mammalian Target of Rapamycin Complex 1 (mTORC1) Repression Identifies Parkinson Protein 7 (PARK7) as a Novel Protein Aberrantly Expressed in Tuberous Sclerosis Complex (TSC). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 412-430.	2.5	31
5295	Gene network analysis reveals the association of important functional partners involved in antibiotic resistance: A report on an important pathogenic bacterium <i>Staphylococcus aureus</i> . <i>Gene</i> , 2016, 575, 253-263.	1.0	55
5296	A Genetic Network Associated With Stress Resistance, Longevity, and Cancer in Humans. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2016, 71, 703-712.	1.7	24
5297	Identification of the transcriptional regulators by expression profiling infected with hepatitis B virus. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2016, 40, 57-72.	0.7	1
5298	Temporal variation selects for diet-microbe co-metabolic traits in the gut of <i>Gorilla</i> spp. <i>ISME Journal</i> , 2016, 10, 514-526.	4.4	84
5299	miRNA-based drought regulation in wheat. <i>Functional and Integrative Genomics</i> , 2016, 16, 221-233.	1.4	202
5300	Using prior knowledge from cellular pathways and molecular networks for diagnostic specimen classification. <i>Briefings in Bioinformatics</i> , 2016, 17, 440-452.	3.2	25
5301	Function Nodes in Chinese Syntactic Networks. <i>Understanding Complex Systems</i> , 2016, , 187-201.	0.3	4
5302	Protein phosphorylation profiling identifies potential mechanisms for direct immunotoxicity. <i>Journal of Immunotoxicology</i> , 2016, 13, 97-107.	0.9	4
5303	Bioinformatics methods in drug repurposing for Alzheimer's disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 322-335.	3.2	78
5304	Computational Analysis of omics-Data to Identify Transcription Factors Regulating Secondary Metabolism in <i>Rauvolfia serpentina</i> . <i>Plant Molecular Biology Reporter</i> , 2016, 34, 283-302.	1.0	12

#	ARTICLE	IF	CITATIONS
5305	Organization Mining Using Online Social Networks. <i>Networks and Spatial Economics</i> , 2016, 16, 545-578.	0.7	37
5306	Toward Omics-Based, Systems Biomedicine, and Path and Drug Discovery Methodologies for Depression-Inflammation Research. <i>Molecular Neurobiology</i> , 2016, 53, 2927-2935.	1.9	40
5307	Identification of therapeutic targets for glioblastoma by network analysis. <i>Oncogene</i> , 2016, 35, 608-620.	2.6	18
5308	Identification of Phosphoribosyl-AMP cyclohydrolase, as drug target and its inhibitors in <i>Brucella melitensis</i> bv. 1 16M using metabolic pathway analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 287-299.	2.0	4
5309	On the Variable Ordering in Subgraph Isomorphism Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 193-203.	1.9	32
5310	Analysis of Organization of the Interactome Using Dominating Sets: A Case Study on Cell Cycle Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 282-289.	1.9	0
5311	Critical analysis of protein signaling networks involved in the regulation of plant secondary metabolism: focus on anthocyanins. <i>Critical Reviews in Biotechnology</i> , 2017, 37, 685-700.	5.1	41
5312	A Sparse Learning Framework for Joint Effect Analysis of Copy Number Variants. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1013-1027.	1.9	2
5313	CNS-wide Sexually Dimorphic Induction of the Major Histocompatibility Complex 1 Pathway With Aging. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, 16-29.	1.7	52
5314	Unwinding the Novel Genes Involved in the Differentiation of Embryonic Stem Cells into Insulin-Producing Cells: A Network-Based Approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 88-95.	2.2	7
5315	Network and Pathway-Based Analyses of Genes Associated with Parkinson's Disease. <i>Molecular Neurobiology</i> , 2017, 54, 4452-4465.	1.9	39
5316	Lipid and sterol gene sequence variation in autism and correlates with neurodevelopmental status: A pilot study. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 2, 137.	0.5	1
5317	Proteomic characterization of the internalization of <i>Opisthorchis viverrini</i> excretory/secretory products in human cells. <i>Parasitology International</i> , 2017, 66, 494-502.	0.6	18
5318	Differential Hive Plots: Seeing Networks Change. <i>Leonardo</i> , 2017, 50, 504-504.	0.2	1
5319	CNS repair and axon regeneration: Using genetic variation to determine mechanisms. <i>Experimental Neurology</i> , 2017, 287, 409-422.	2.0	24
5320	Pathways to smoking behaviours: biological insights from the Tobacco and Genetics Consortium meta-analysis. <i>Molecular Psychiatry</i> , 2017, 22, 82-88.	4.1	26
5321	Metabolomic network analysis of estrogen-stimulated MCF-7 cells: a comparison of overrepresentation analysis, quantitative enrichment analysis and pathway analysis versus metabolite network analysis. <i>Archives of Toxicology</i> , 2017, 91, 217-230.	1.9	13
5322	A Cyclin D2-derived peptide acts on specific cell cycle phases by activating ERK1/2 to cause the death of breast cancer cells. <i>Journal of Proteomics</i> , 2017, 151, 24-32.	1.2	21

#	ARTICLE	IF	CITATIONS
5323	Role of sequence evolution and conformational dynamics in the substrate specificity and oligomerization mode of thymidylate kinases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2136-2154.	2.0	1
5324	Integrated analysis of different microarray studies to identify candidate genes in type 1 diabetes. <i>Journal of Diabetes</i> , 2017, 9, 149-157.	0.8	8
5325	Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications. <i>Oncogene</i> , 2017, 36, 3375-3383.	2.6	14
5326	How semantic memory structure and intelligence contribute to creative thought: a network science approach. <i>Thinking and Reasoning</i> , 2017, 23, 158-183.	2.1	124
5327	Pathogenicity Genes in <i>Ustilagoidea virens</i> Revealed by a Predicted Protein-Protein Interaction Network. <i>Journal of Proteome Research</i> , 2017, 16, 1193-1206.	1.8	22
5328	MerR and ChrR mediate blue light induced photo-oxidative stress response at the transcriptional level in <i>Vibrio cholerae</i> . <i>Scientific Reports</i> , 2017, 7, 40817.	1.6	35
5329	Decoding Crucial LncRNAs Implicated in Neurogenesis and Neurological Disorders. <i>Stem Cells and Development</i> , 2017, 26, 541-553.	1.1	16
5330	Lithium reverses behavioral and axonal transport-related changes associated with ANK3 bipolar disorder gene disruption. <i>European Neuropsychopharmacology</i> , 2017, 27, 274-288.	0.3	20
5331	Long noncoding RNA LINC01186, regulated by TGF- $\beta$ /SMAD3, inhibits migration and invasion through Epithelial-Mesenchymal-Transition in lung cancer. <i>Gene</i> , 2017, 608, 1-12.	1.0	50
5332	Bacterial endophyte communities of three agricultural important grass species differ in their response towards management regimes. <i>Scientific Reports</i> , 2017, 7, 40914.	1.6	83
5333	Proteomic analysis of lysine succinylation of the human pathogen <i>Histoplasma capsulatum</i> . <i>Journal of Proteomics</i> , 2017, 154, 109-117.	1.2	23
5334	Bacterial Carriers for Glioblastoma Therapy. <i>Molecular Therapy - Oncolytics</i> , 2017, 4, 1-17.	2.0	26
5335	Mutations at protein-protein interfaces: Small changes over big surfaces have large impacts on human health. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 128, 3-13.	1.4	129
5336	Cross-Talk between Alternatively Spliced UGT1A Isoforms and Colon Cancer Cell Metabolism. <i>Molecular Pharmacology</i> , 2017, 91, 167-177.	1.0	16
5337	Proteomic characterization of microdissected breast tissue environment provides a protein-level overview of malignant transformation. <i>Proteomics</i> , 2017, 17, 1600213.	1.3	7
5338	Metabolites Associated With Lean Mass and Adiposity in Older Black Men. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, glw245.	1.7	32
5339	Measuring the contributions of Chinese scholars to the research field of systems biology from 2005 to 2013. <i>Scientometrics</i> , 2017, 110, 1615-1631.	1.6	6
5340	Integrative view of 2-oxoglutarate/Fe(II)-dependent oxygenase diversity and functions in bacteria. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 323-334.	1.1	31

#	ARTICLE	IF	CITATIONS
5341	Identifying Candidate Reprogramming Genes in Mouse Induced Pluripotent Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2017, 13, 532-541.	5.6	1
5342	Pathway analysis of complex diseases for GWAS, extending to consider rare variants, multi-omics and interactions. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 335-353.	1.1	54
5343	Inhibition of fat cell differentiation in 3T3-L1 pre-adipocytes by all-trans retinoic acid: Integrative analysis of transcriptomic and phenotypic data. <i>Biomolecular Detection and Quantification</i> , 2017, 11, 31-44.	7.0	9
5344	Context Specificity in Causal Signaling Networks Revealed by Phosphoprotein Profiling. <i>Cell Systems</i> , 2017, 4, 73-83.e10.	2.9	41
5345	Transcriptome analysis reveals common differential and global gene expression profiles in bluetongue virus serotype 16 (BTV-16) infected peripheral blood mononuclear cells (PBMCs) in sheep and goats. <i>Genomics Data</i> , 2017, 11, 62-72.	1.3	11
5346	Whole transcriptome analysis of three leaf stages in two cultivars and one of their F1 hybrid of <i>Camellia sinensis</i> L. with differing EGCG content. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
5347	SMAD transcription factors are altered in cell models of HD and regulate HTT expression. <i>Cellular Signalling</i> , 2017, 31, 1-14.	1.7	21
5348	Dissecting a co-expression network of basic helix-loop-helix ( bHLH ) genes from phosphate (Pi)-starved soybean ( <i>Glycine max</i> ). <i>Plant Gene</i> , 2017, 9, 19-25.	1.4	4
5349	Induction of resveratrol biosynthesis in <i>Vitis amurensis</i> cells by heterologous expression of the <i>Arabidopsis</i> constitutively active, Ca <sup>2+</sup> -independent form of the AtCPK1 gene. <i>Process Biochemistry</i> , 2017, 54, 144-155.	1.8	13
5350	Discovery of a small molecule targeting ULK1-modulated cell death of triple negative breast cancer in vitro and in vivo. <i>Chemical Science</i> , 2017, 8, 2687-2701.	3.7	120
5351	Evolutionary Conservation and Divergence of Gene Coexpression Networks in <i>Gossypium</i> (Cotton) Seeds. <i>Genome Biology and Evolution</i> , 2016, 8, evw280.	1.1	40
5352	Germline BRCA2 mutations drive prostate cancers with distinct evolutionary trajectories. <i>Nature Communications</i> , 2017, 8, 13671.	5.8	182
5353	Identification of temporal genes involved in the mechanisms of spinal cord injury. <i>Spinal Cord</i> , 2017, 55, 355-361.	0.9	6
5354	Computational polypharmacology: a new paradigm for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 279-291.	2.5	86
5355	Gene co-expression analysis for functional classification and gene-disease predictions. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw139.	3.2	718
5356	Identification and Characterization of MicroRNA Differentially Expressed in Macrophages Exposed to <i>Porphyromonas gingivalis</i> Infection. <i>Infection and Immunity</i> , 2017, 85, .	1.0	45
5357	Mechanistic Understanding of Lanthipeptide Biosynthetic Enzymes. <i>Chemical Reviews</i> , 2017, 117, 5457-5520.	23.0	375
5358	Identification and analysis of promiscuity cliffs formed by bioactive compounds and experimental implications. <i>RSC Advances</i> , 2017, 7, 58-66.	1.7	15



#	ARTICLE	IF	CITATIONS
5359	Phosphoproteome of crab-eating macaque cerebral cortex characterized through multidimensional reversed-phase liquid chromatography/mass spectrometry with tandem anion/cation exchange columns. <i>Journal of Chromatography A</i> , 2017, 1498, 196-206.	1.8	14
5360	Identification of biomarkers of intrahepatic cholangiocarcinoma via integrated analysis of mRNA and miRNA microarray data. <i>Molecular Medicine Reports</i> , 2017, 15, 1051-1056.	1.1	7
5361	An Interactive Macrophage Signal Transduction Map Facilitates Comparative Analyses of High-Throughput Data. <i>Journal of Immunology</i> , 2017, 198, 2191-2201.	0.4	21
5362	Mapping and Analysis. , 2017, , 101-116.		0
5363	Discovery and functional prioritization of Parkinson's disease candidate genes from large-scale whole exome sequencing. <i>Genome Biology</i> , 2017, 18, 22.	3.8	96
5364	Expression analysis of microRNAs and mRNAs in ovarian granulosa cells after microcystin-LR exposure. <i>Toxicol</i> , 2017, 129, 11-19.	0.8	18
5365	The structure of the yeast mitochondrial ribosome. <i>Science</i> , 2017, 355, 528-531.	6.0	161
5366	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
5367	Physiological Responses and Gene Co-Expression Network of Mycorrhizal Roots under K <sup>+</sup> Deprivation. <i>Plant Physiology</i> , 2017, 173, 1811-1823.	2.3	69
5368	The dynamics of the pulmonary microbiome during mechanical ventilation in the intensive care unit and the association with occurrence of pneumonia. <i>Thorax</i> , 2017, 72, 803-810.	2.7	118
5369	Gene networks in skeletal muscle following endurance exercise are coexpressed in blood neutrophils and linked with blood inflammation markers. <i>Journal of Applied Physiology</i> , 2017, 122, 752-766.	1.2	13
5370	Integrated analysis of differentially expressed genes and pathways in triple-negative breast cancer. <i>Molecular Medicine Reports</i> , 2017, 15, 1087-1094.	1.1	10
5371	An untargeted metabolomics method for archived newborn dried blood spots in epidemiologic studies. <i>Metabolomics</i> , 2017, 13, 1.	1.4	58
5372	Multiple resistance to pirimiphos-methyl and bifenthrin in <i>Tribolium castaneum</i> involves the activity of lipases, esterases, and laccase2. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 195, 27-43.	1.3	14
5373	Integrated mRNA and microRNA analysis identifies genes and small miRNA molecules associated with transcriptional and post-transcriptional-level responses to both drought stress and re-watering treatment in tobacco. <i>BMC Genomics</i> , 2017, 18, 62.	1.2	36
5374	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2017, 13, 674-688.	0.4	83
5375	Weighted Protein Interaction Network Analysis of Frontotemporal Dementia. <i>Journal of Proteome Research</i> , 2017, 16, 999-1013.	1.8	39
5376	Transcriptome and network analyses in <i>Saccharomyces cerevisiae</i> reveal that amphotericin B and lactoferrin synergy disrupt metal homeostasis and stress response. <i>Scientific Reports</i> , 2017, 7, 40232.	1.6	18



#	ARTICLE	IF	CITATIONS
5377	Establishment of a integrative multi-omics expression database CKDdb in the context of chronic kidney disease (CKD). <i>Scientific Reports</i> , 2017, 7, 40367.	1.6	24
5378	Combining Chemical Profiling and Network Analysis to Investigate the Pharmacology of Complex Prescriptions in Traditional Chinese Medicine. <i>Scientific Reports</i> , 2017, 7, 40529.	1.6	40
5379	Human Antiviral Protein IFIX Suppresses Viral Gene Expression during Herpes Simplex Virus 1 (HSV-1) Infection and Is Counteracted by Virus-induced Proteasomal Degradation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S200-S214.	2.5	27
5380	Different enhancer classes in <i>Drosophila</i> bind distinct architectural proteins and mediate unique chromatin interactions and 3D architecture. <i>Nucleic Acids Research</i> , 2017, 45, 1714-1730.	6.5	133
5381	Tissue and cell-type co-expression networks of transcription factors and wood component genes in <i>Populus trichocarpa</i> . <i>Planta</i> , 2017, 245, 927-938.	1.6	74
5382	A systems pharmacology perspective to decipher the mechanism of action of Parangichakkai chooranam , a Siddha formulation for the treatment of psoriasis. <i>Biomedicine and Pharmacotherapy</i> , 2017, 88, 74-86.	2.5	14
5383	Integrated, High-Throughput, Multiomics Platform Enables Data-Driven Construction of Cellular Responses and Reveals Global Drug Mechanisms of Action. <i>Journal of Proteome Research</i> , 2017, 16, 1364-1375.	1.8	34
5384	New insights into marine group III Euryarchaeota, from dark to light. <i>ISME Journal</i> , 2017, 11, 1102-1117.	4.4	72
5385	Host-Microbial Interactions in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1640-1650.	2.5	169
5386	Bioinformatic identification of candidate genes induced by trichostatin A in BGC-823 gastric cancer cells. <i>Oncology Letters</i> , 2017, 13, 777-783.	0.8	3
5387	Sequence, structure and function relationships in flaviviruses as assessed by evolutive aspects of its conserved non-structural protein domains. <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 565-571.	1.0	21
5388	A genome-wide scan for genes under balancing selection in <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 15.	3.2	30
5389	Fibrin hydrogels induce mixed dorsal/ventral spinal neuron identities during differentiation of human induced pluripotent stem cells. <i>Acta Biomaterialia</i> , 2017, 51, 237-245.	4.1	47
5390	Impacts of inorganic and organic fertilization treatments on bacterial and fungal communities in a paddy soil. <i>Applied Soil Ecology</i> , 2017, 112, 42-50.	2.1	208
5391	Brown Adipogenic Reprogramming Induced by a Small Molecule. <i>Cell Reports</i> , 2017, 18, 624-635.	2.9	48
5392	A Novel Group Wise-Based Method for Calculating Human miRNA Functional Similarity. <i>IEEE Access</i> , 2017, 5, 2364-2372.	2.6	8
5393	GenomeCAT: a versatile tool for the analysis and integrative visualization of DNA copy number variants. <i>BMC Bioinformatics</i> , 2017, 18, 19.	1.2	8
5394	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. <i>BMC Plant Biology</i> , 2017, 17, 17.	1.6	34

#	ARTICLE	IF	CITATIONS
5395	Oncogenes Activate an Autonomous Transcriptional Regulatory Circuit That Drives Glioblastoma. <i>Cell Reports</i> , 2017, 18, 961-976.	2.9	76
5396	Transcriptome sequencing analysis of porcine granulosa cells treated with an anti-inhibin antibody. <i>Reproductive Biology</i> , 2017, 17, 79-88.	0.9	6
5397	Genome Sequencing of the Behavior Manipulating Virus LbFV Reveals a Possible New Virus Family. <i>Genome Biology and Evolution</i> , 2016, 8, 3718-3739.	1.1	21
5398	Comparative analysis of RNA-Seq data from brain and blood samples of Parkinson's disease. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 557-564.	1.0	26
5399	Heterogeneous fractionation profiles of meta-analytic coactivation networks. <i>NeuroImage</i> , 2017, 149, 424-435.	2.1	6
5400	Differential sharing and distinct co-occurrence networks among spatially close bacterial microbiota of bark, mosses and lichens. <i>Molecular Ecology</i> , 2017, 26, 2826-2838.	2.0	79
5401	HAPPI-2: a Comprehensive and High-quality Map of Human Annotated and Predicted Protein Interactions. <i>BMC Genomics</i> , 2017, 18, 182.	1.2	35
5402	Proteomic analysis of the cullin 4B interactome using proximity-dependent biotinylation in living cells. <i>Proteomics</i> , 2017, 17, 1600163.	1.3	3
5403	Systems biology study of transcriptional and post-transcriptional co-regulatory network sheds light on key regulators involved in important biological processes in <i>Citrus sinensis</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 331-342.	1.4	5
5404	Sourdough-type propagation of faba bean flour: Dynamics of microbial consortia and biochemical implications. <i>International Journal of Food Microbiology</i> , 2017, 248, 10-21.	2.1	54
5405	Identification of miRNA-mRNA Modules in Colorectal Cancer Using Rough Hypercuboid Based Supervised Clustering. <i>Scientific Reports</i> , 2017, 7, 42809.	1.6	13
5406	Deep learning and 3D-DESI imaging reveal the hidden metabolic heterogeneity of cancer. <i>Chemical Science</i> , 2017, 8, 3500-3511.	3.7	117
5407	Identification of core gene networks and hub genes associated with progression of non-alcoholic fatty liver disease by RNA sequencing. <i>Hepatology Research</i> , 2017, 47, 1445-1458.	1.8	23
5408	compMS2Miner: An Automatable Metabolite Identification, Visualization, and Data-Sharing R Package for High-Resolution LC-MS Data Sets. <i>Analytical Chemistry</i> , 2017, 89, 3919-3928.	3.2	27
5409	A pan-cancer analysis of secreted Frizzled-related proteins: re-examining their proposed tumour suppressive function. <i>Scientific Reports</i> , 2017, 7, 42719.	1.6	50
5410	A Comprehensive Analysis of Metabolomics and Transcriptomics in Cervical Cancer. <i>Scientific Reports</i> , 2017, 7, 43353.	1.6	73
5411	Elucidating the biosynthetic pathways of volatile organic compounds in <i>Mycobacterium tuberculosis</i> through a computational approach. <i>Molecular BioSystems</i> , 2017, 13, 750-755.	2.9	6
5412	Abnormal epigenetic changes during differentiation of human skeletal muscle stem cells from obese subjects. <i>BMC Medicine</i> , 2017, 15, 39.	2.3	51

#	ARTICLE	IF	CITATIONS
5413	Aberrant expression of cell cycle and material metabolism related genes contributes to hepatocellular carcinoma occurrence. <i>Pathology Research and Practice</i> , 2017, 213, 316-321.	1.0	64
5414	Bacterial resistance to arsenic protects against protist killing. <i>BioMetals</i> , 2017, 30, 307-311.	1.8	13
5415	RNA-seq based detection of differentially expressed genes in the skeletal muscle of Duroc pigs with distinct lipid profiles. <i>Scientific Reports</i> , 2017, 7, 40005.	1.6	46
5416	The IQD Family of Calmodulin-Binding Proteins Links Calcium Signaling to Microtubules, Membrane Subdomains, and the Nucleus. <i>Plant Physiology</i> , 2017, 173, 1692-1708.	2.3	138
5417	Circulatory microRNA 23a and microRNA 23b and polycystic ovary syndrome (PCOS): the effects of body mass index and sex hormones in an Eastern Han Chinese population. <i>Journal of Ovarian Research</i> , 2017, 10, 10.	1.3	40
5418	Chilling Affects Phytohormone and Post-Embryonic Development Pathways during Bud Break and Fruit Set in Apple ( <i>Malus domestica</i> Borkh.). <i>Scientific Reports</i> , 2017, 7, 42593.	1.6	22
5419	Predictability of Genetic Interactions from Functional Gene Modules. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 617-624.	0.8	8
5420	Identification of potential therapeutic target genes, key miRNAs and mechanisms in oral lichen planus by bioinformatics analysis. <i>Archives of Oral Biology</i> , 2017, 78, 122-128.	0.8	5
5421	Whole-genome association analysis of pork meat pH revealed three significant regions and several potential genes in Finnish Yorkshire pigs. <i>BMC Genetics</i> , 2017, 18, 13.	2.7	20
5422	Microbial community compositions in different functional zones of Carrousel oxidation ditch system for domestic wastewater treatment. <i>AMB Express</i> , 2017, 7, 40.	1.4	73
5423	Global protein expression profile response of planktonic <i>Aeromonas hydrophila</i> exposed to chlortetracycline. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 68.	1.7	36
5424	Influence of Diet Composition on Cattle Rumen Methanogenesis: A Comparative Metagenomic Analysis in Indian and Exotic Cattle. <i>Indian Journal of Microbiology</i> , 2017, 57, 226-234.	1.5	11
5425	Data-Driven Discovery of Extravasation Pathway in Circulating Tumor Cells. <i>Scientific Reports</i> , 2017, 7, 43710.	1.6	32
5426	Dietary restriction protects against diethylnitrosamine-induced hepatocellular tumorigenesis by restoring the disturbed gene expression profile. <i>Scientific Reports</i> , 2017, 7, 43745.	1.6	16
5427	Identification of Topological Network Modules in Perturbed Protein Interaction Networks. <i>Scientific Reports</i> , 2017, 7, 43845.	1.6	29
5428	The origins and evolutionary history of human non-coding RNA regulatory networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750005.	0.3	16
5429	Revisiting Previously Investigated Plants: A Molecular Networking-Based Study of <i>Geissospermum laeve</i> . <i>Journal of Natural Products</i> , 2017, 80, 1007-1014.	1.5	45
5430	Gene expression profiles reveal key pathways and genes associated with neuropathic pain in patients with spinal cord injury. <i>Molecular Medicine Reports</i> , 2017, 15, 2120-2128.	1.1	12

#	ARTICLE	IF	CITATIONS
5431	Integrating untargeted metabonomics, partial least square regression analysis and MetPA to explore the targeted pathways involved into Huangqi Jiangzhong Tang against chronic atrophic gastritis rats. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2017, 164, 16-25.	1.8	16
5432	Transcriptome data analysis of grass carp ( <i>Ctenopharyngodon idella</i> ) infected by reovirus provides insights into two immune-related genes. <i>Fish and Shellfish Immunology</i> , 2017, 64, 68-77.	1.6	35
5433	Aberrant methylation patterns affect the molecular pathogenesis of rheumatoid arthritis. <i>International Immunopharmacology</i> , 2017, 46, 141-145.	1.7	11
5434	Effects of different kinds of essentiality on sequence evolution of human testis proteins. <i>Scientific Reports</i> , 2017, 7, 43534.	1.6	9
5435	Community dynamics drive punctuated engraftment of the fecal microbiome following transplantation using freeze-dried, encapsulated fecal microbiota. <i>Gut Microbes</i> , 2017, 8, 276-288.	4.3	39
5436	Bioinformatics analysis of the proteins interacting with LASP-1 and their association with HBV-related hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 44017.	1.6	8
5437	Toward deterministic and semiautomated SPADE analysis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017, 91, 281-289.	1.1	37
5438	Systems biology approach to late-onset Alzheimer's disease genome-wide association study identifies novel candidate genes validated using brain expression data and <i>Caenorhabditis elegans</i> experiments. , 2017, 13, 1133-1142.		40
5439	Proteome mining for the identification and in-silico characterization of putative drug targets of multi-drug resistant <i>Clostridium difficile</i> strain 630. <i>Journal of Microbiological Methods</i> , 2017, 136, 6-10.	0.7	3
5440	Global Gene Expression Patterns and Somatic Mutations in Sporadic Intracranial Aneurysms. <i>World Neurosurgery</i> , 2017, 100, 15-21.	0.7	6
5441	Insights into the molecular mechanisms of <i>Polygonum multiflorum</i> Thunb-induced liver injury: a computational systems toxicology approach. <i>Acta Pharmacologica Sinica</i> , 2017, 38, 719-732.	2.8	30
5442	Comparative transcriptomic analysis reveals the roles of overlapping heat-/drought-responsive genes in poplars exposed to high temperature and drought. <i>Scientific Reports</i> , 2017, 7, 43215.	1.6	72
5443	Previously unknown class of metalorganic compounds revealed in meteorites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2819-2824.	3.3	47
5444	Unexplored Archaeal Diversity in the Great Ape Gut Microbiome. <i>MSphere</i> , 2017, 2, .	1.3	76
5445	Downregulation of a novel long noncoding RNA TRPM2-AS promotes apoptosis in non-“small cell lung cancer. <i>Tumor Biology</i> , 2017, 39, 101042831769119.	0.8	32
5446	Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. <i>Nature Microbiology</i> , 2017, 2, 17022.	5.9	25
5447	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. <i>BMC Bioinformatics</i> , 2017, 18, 132.	1.2	16
5448	Network topology of NaV1.7 mutations in sodium channel-related painful disorders. <i>BMC Systems Biology</i> , 2017, 11, 28.	3.0	29

#	ARTICLE	IF	CITATIONS
5449	Characterization of chromosomal abnormalities in pregnancy losses reveals critical genes and loci for human early development. <i>Human Mutation</i> , 2017, 38, 669-677.	1.1	28
5450	Genetic separation of southern and northern soybean breeding programs in North America and their associated allelic variation at four maturity loci. <i>Molecular Breeding</i> , 2017, 37, 8.	1.0	32
5451	miR-600 Acts as a Bimodal Switch that Regulates Breast Cancer Stem Cell Fate through WNT Signaling. <i>Cell Reports</i> , 2017, 18, 2256-2268.	2.9	111
5452	TORC1-dependent sumoylation of Rpc82 promotes RNA polymerase III assembly and activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1039-1044.	3.3	38
5453	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in <i>Bacteroides coprocola</i> . <i>Microbiome</i> , 2017, 5, 15.	4.9	41
5454	Therapeutic properties of <i>Scutellaria baicalensis</i> in db/db mice evaluated using Connectivity Map and network pharmacology. <i>Scientific Reports</i> , 2017, 7, 41711.	1.6	19
5455	High-Throughput Phenotyping and QTL Mapping Reveals the Genetic Architecture of Maize Plant Growth. <i>Plant Physiology</i> , 2017, 173, 1554-1564.	2.3	179
5456	Estrogen receptor $\hat{\pm}$ yields treatment-specific enhancers between morphologically similar endometrial tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1316-E1325.	3.3	25
5457	The EGR2 targets LAG-3 and 4-1BB describe and regulate dysfunctional antigen-specific CD8+ T cells in the tumor microenvironment. <i>Journal of Experimental Medicine</i> , 2017, 214, 381-400.	4.2	154
5458	The Transcription Factor MYB29 Is a Regulator of <i>ALTERNATIVE OXIDASE1a</i> . <i>Plant Physiology</i> , 2017, 173, 1824-1843.	2.3	46
5459	<i>HIF1A</i> gene polymorphisms and human diseases: Graphical review of 97 association studies. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 439-452.	1.5	32
5460	Spontaneous ultra-weak photon emission in correlation to inflammatory metabolism and oxidative stress in a mouse model of collagen-induced arthritis. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2017, 168, 98-106.	1.7	14
5461	Integrated Analysis of LncRNA-mRNA Co-Expression Profiles in Patients with Moyamoya Disease. <i>Scientific Reports</i> , 2017, 7, 42421.	1.6	25
5462	A prominent glycol radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <i>proline</i> . <i>Science</i> , 2017, 355, .	6.0	126
5463	Systematic analysis of microarray datasets to identify Parkinson's disease-associated pathways and genes. <i>Molecular Medicine Reports</i> , 2017, 15, 1252-1262.	1.1	19
5464	Unboxing cluster heatmaps. <i>BMC Bioinformatics</i> , 2017, 18, 63.	1.2	26
5465	A taxonomy of visualization tasks for the analysis of biological pathway data. <i>BMC Bioinformatics</i> , 2017, 18, 21.	1.2	24
5466	Process assessment associated to microbial community response provides insight on possible mechanism of waste activated sludge digestion under typical chemical pretreatments. <i>Energy</i> , 2017, 137, 457-467.	4.5	26

#	ARTICLE	IF	CITATIONS
5467	The Human Adrenal Gland Proteome Defined by Transcriptomics and Antibody-Based Profiling. <i>Endocrinology</i> , 2017, 158, 239-251.	1.4	25
5468	A Systems Perspective of Signalling Networks in Host-Pathogen Interactions. <i>Journal of the Indian Institute of Science</i> , 2017, 97, 41-57.	0.9	0
5469	<sc>MALDI-TOF MS</sc> identification of microbiota associated with pest insect <i>Diabrotica speciosa</i>. <i>Agricultural and Forest Entomology</i> , 2017, 19, 408-417.	0.7	11
5470	Unity in defence: honeybee workers exhibit conserved molecular responses to diverse pathogens. <i>BMC Genomics</i> , 2017, 18, 207.	1.2	100
5471	Nitrate effects on chromate reduction in a methane-based biofilm. <i>Water Research</i> , 2017, 115, 130-137.	5.3	69
5472	Multiplex shRNA Screening of Germ Cell Development by <i>in Vivo</i> Transfection of Mouse Testis. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 247-255.	0.8	2
5473	Aberrant expression of microRNA induced by high-fructose diet: implications in the pathogenesis of hyperlipidemia and hepatic insulin resistance. <i>Journal of Nutritional Biochemistry</i> , 2017, 43, 125-131.	1.9	75
5474	Untangling the role of one-carbon metabolism in colorectal cancer risk: a comprehensive Bayesian network analysis. <i>Scientific Reports</i> , 2017, 7, 43434.	1.6	24
5475	Prediction of GCRV virus-host protein interactome based on structural motif-domain interactions. <i>BMC Bioinformatics</i> , 2017, 18, 145.	1.2	41
5476	Motor neurons control blood vessel patterning in the developing spinal cord. <i>Nature Communications</i> , 2017, 8, 14583.	5.8	57
5477	Characterization of gene expression profiles in HBV-related liver fibrosis patients and identification of ITGBL1 as a key regulator of fibrogenesis. <i>Scientific Reports</i> , 2017, 7, 43446.	1.6	68
5478	Continual Antigenic Diversification in China Leads to Global Antigenic Complexity of Avian Influenza H5N1 Viruses. <i>Scientific Reports</i> , 2017, 7, 43566.	1.6	21
5479	Phosphoproteins in extracellular vesicles as candidate markers for breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3175-3180.	3.3	328
5480	ChMYB1 regulates SCW stage-specific expression of the <i>GhGDSL</i> promoter in the fibres of <i>Gossypium hirsutum</i> L.. <i>Plant Biotechnology Journal</i> , 2017, 15, 1163-1174.	4.1	36
5481	Identification of therapeutic targets for Parkinson's disease via bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2017, 15, 731-735.	1.1	8
5482	Analysis of gene expression profiles of non-small cell lung cancer at different stages reveals significantly altered biological functions and candidate genes. <i>Oncology Reports</i> , 2017, 37, 1736-1746.	1.2	16
5483	Genome-Wide Sequencing Reveals MicroRNAs Downregulated in Cerebral Cavernous Malformations. <i>Journal of Molecular Neuroscience</i> , 2017, 61, 178-188.	1.1	31
5484	Comparative analysis of gene regulatory networks of highly metastatic breast cancer cells established by orthotopic transplantation and intra-circulation injection. <i>International Journal of Oncology</i> , 2017, 50, 497-504.	1.4	24



#	ARTICLE	IF	CITATIONS
5485	Metabolomics: A Primer. <i>Trends in Biochemical Sciences</i> , 2017, 42, 274-284.	3.7	273
5486	Quantitative Map of $\hat{I}^2$ -Lactone-Induced Virulence Regulation. <i>Journal of Proteome Research</i> , 2017, 16, 1180-1192.	1.8	25
5487	Blubber transcriptome response to acute stress axis activation involves transient changes in adipogenesis and lipolysis in a fasting-adapted marine mammal. <i>Scientific Reports</i> , 2017, 7, 42110.	1.6	40
5488	Extracellular RNAs Are Associated With Insulin Resistance and Metabolic Phenotypes. <i>Diabetes Care</i> , 2017, 40, 546-553.	4.3	73
5489	Exploration of bladder cancer molecular mechanisms based on miRNA-mRNA regulatory network. <i>Oncology Reports</i> , 2017, 37, 1461-1468.	1.2	10
5490	Rare copy number variants in patients with congenital conotruncal heart defects. <i>Birth Defects Research</i> , 2017, 109, 271-295.	0.8	15
5491	Metabolic perturbations of postnatal growth restriction and hyperoxia-induced pulmonary hypertension in a bronchopulmonary dysplasia model. <i>Metabolomics</i> , 2017, 13, 1.	1.4	23
5492	Expression profiling-based clustering of healthy subjects recapitulates classifications defined by clinical observation in Chinese medicine. <i>Journal of Genetics and Genomics</i> , 2017, 44, 191-197.	1.7	22
5493	Siderophore transport by MmpL5-MmpS5 protein complex in <i>Mycobacterium tuberculosis</i> . <i>Journal of Inorganic Biochemistry</i> , 2017, 170, 75-84.	1.5	19
5494	An adaptation of particle swarm clustering applied in basal cell carcinoma, squamous cell carcinoma of the skin and actinic keratosis. <i>Meta Gene</i> , 2017, 12, 72-77.	0.3	7
5495	Identification and characterization of the expression profile of the microRNAs in the Amazon species <i>Colossoma macropomum</i> by next generation sequencing. <i>Genomics</i> , 2017, 109, 67-74.	1.3	14
5496	Identification of neuron-related genes for cell therapy of neurological disorders by network analysis. <i>Journal of Zhejiang University: Science B</i> , 2017, 18, 172-182.	1.3	2
5497	Overcoming the divide between ataxias and spastic paraplegias: Shared phenotypes, genes, and pathways. <i>Movement Disorders</i> , 2017, 32, 332-345.	2.2	144
5498	Phenotype-Specific Association of Single-Nucleotide Polymorphisms with Heart Failure and Preserved Ejection Fraction: a Genome-Wide Association Analysis of the Cardiovascular Health Study. <i>Journal of Cardiovascular Translational Research</i> , 2017, 10, 285-294.	1.1	16
5499	Haploinsufficiency networks identify targetable patterns of allelic deficiency in low mutation ovarian cancer. <i>Nature Communications</i> , 2017, 8, 14423.	5.8	35
5500	Global Insight into Lysine Acetylation Events and Their Links to Biological Aspects in <i>Beauveria bassiana</i> , a Fungal Insect Pathogen. <i>Scientific Reports</i> , 2017, 7, 44360.	1.6	16
5501	Novel Indole-based Tambjamine-Analogues Induce Apoptotic Lung Cancer Cell Death through p38 Mitogen-Activated Protein Kinase Activation. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1224-1235.	1.9	24
5502	Structural and functional genomics analysis of methyltransferase genes and networks associate to understand antibiotic resistance inside the pangenome of <i>Pseudomonas aeruginosa</i> . <i>IFMBE Proceedings</i> , 2017, , 702-705.	0.2	1



#	ARTICLE	IF	CITATIONS
5503	Differential circRNA expression profiles during the BMP2-induced osteogenic differentiation of MC3T3-E1 cells. <i>Biomedicine and Pharmacotherapy</i> , 2017, 90, 492-499.	2.5	74
5504	Ecological dynamics and co-occurrence among marine phytoplankton, bacteria and myoviruses shows microdiversity matters. <i>ISME Journal</i> , 2017, 11, 1614-1629.	4.4	158
5505	Computational identification of mutually exclusive transcriptional drivers dysregulating metastatic microRNAs in prostate cancer. <i>Nature Communications</i> , 2017, 8, 14917.	5.8	16
5506	Genetic dissection of seed oil and protein content and identification of networks associated with oil content in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2017, 7, 46295.	1.6	112
5507	Soda pans of the Pannonian steppe harbor unique bacterial communities adapted to multiple extreme conditions. <i>Extremophiles</i> , 2017, 21, 639-649.	0.9	44
5508	Gene co-expression network reconstruction: a review on computational methods for inferring functional information from plant-based expression data. <i>Plant Biotechnology Reports</i> , 2017, 11, 71-86.	0.9	34
5509	Transcriptional Elongation of HSV Immediate Early Genes by the Super Elongation Complex Drives Lytic Infection and Reactivation from Latency. <i>Cell Host and Microbe</i> , 2017, 21, 507-517.e5.	5.1	32
5510	Integrated host and viral transcriptome analyses reveal pathology and inflammatory response mechanisms to ALV-J injection in SPF chickens. <i>Scientific Reports</i> , 2017, 7, 46156.	1.6	24
5511	Genome-wide analysis of cis-regulatory element structure and discovery of motif-driven gene co-expression networks in grapevine. <i>DNA Research</i> , 2017, 24, dsw061.	1.5	35
5512	An approach to infer putative disease-specific mechanisms using neighboring gene networks. <i>Bioinformatics</i> , 2017, 33, 1987-1994.	1.8	7
5513	Modeling Asymmetric Cell Division in <i>Caulobacter crescentus</i> Using a Boolean Logic Approach. <i>Results and Problems in Cell Differentiation</i> , 2017, 61, 1-21.	0.2	6
5514	Hidden Markov model and Chapman Kolmogorov for protein structures prediction from images. <i>Computational Biology and Chemistry</i> , 2017, 68, 231-244.	1.1	25
5515	Prediction of optimal gene functions for osteosarcoma using gene ontology and microarray profiles. <i>Journal of Bone Oncology</i> , 2017, 7, 18-22.	1.0	6
5516	Phylogenomic Analysis of the Microviridin Biosynthetic Pathway Coupled with Targeted Chemo-Enzymatic Synthesis Yields Potent Protease Inhibitors. <i>ACS Chemical Biology</i> , 2017, 12, 1538-1546.	1.6	45
5517	Automated analysis of high-content microscopy data with deep learning. <i>Molecular Systems Biology</i> , 2017, 13, 924.	3.2	220
5518	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. <i>Scientific Reports</i> , 2017, 7, 46539.	1.6	30
5519	Identification of potential biomarkers of sepsis using bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1689-1696.	0.8	16
5520	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. <i>Scientific Reports</i> , 2017, 7, 46562.	1.6	6

#	ARTICLE	IF	CITATIONS
5521	Metabolomics of fescue toxicosis in grazing beef steers. <i>Food and Chemical Toxicology</i> , 2017, 105, 285-299.	1.8	16
5522	Transcriptome sequencing combined with bioinformatics predicts potential genes and pathways associated with bupivacaine-induced apoptosis. <i>Animal Cells and Systems</i> , 2017, 21, 124-132.	0.8	0
5523	Mps1 Regulates Kinetochores-Microtubule Attachment Stability via the Ska Complex to Ensure Error-Free Chromosome Segregation. <i>Developmental Cell</i> , 2017, 41, 143-156.e6.	3.1	73
5524	Specific microRNA-mRNA Regulatory Network of Colon Cancer Invasion Mediated by Tissue Kallikrein-Related Peptidase 6. <i>Neoplasia</i> , 2017, 19, 396-411.	2.3	27
5525	High Influence: Identifying and Ranking Stability, Topological Significance, and Redundancies in Water Resource Networks. <i>Journal of Water Resources Planning and Management - ASCE</i> , 2017, 143, .	1.3	1
5526	Comparative Proteomics Uncovers Correlated Signaling Network and Potential Biomarkers for Progression of Prostate Cancer. <i>Cellular Physiology and Biochemistry</i> , 2017, 41, 1-9.	1.1	11
5527	Population Genomics of Paramecium Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1194-1216.	3.5	35
5528	WGCNA Application to Proteomic and Metabolomic Data Analysis. <i>Methods in Enzymology</i> , 2017, 585, 135-158.	0.4	244
5529	Genomic Responses of Mouse Synovial Fibroblasts During Tumor Necrosis Factor-Driven Arthritogenesis Greatly Mimic Those in Human Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 1588-1600.	2.9	29
5530	Systematically characterize the absorbed effective substances of Wutou Decoction and their metabolic pathways in rat plasma using UHPLC-Q-TOF-MS combined with a target network pharmacological analysis. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2017, 141, 95-107.	1.4	61
5531	Transcriptomic changes in an animal-bacterial symbiosis under modeled microgravity conditions. <i>Scientific Reports</i> , 2017, 7, 46318.	1.6	19
5532	Microbial communities associated with the anthropogenic, highly alkaline environment of a saline soda lime, Poland. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 945-962.	0.7	37
5533	Transcriptional regulatory networks underlying the reprogramming of spermatogonial stem cells to multipotent stem cells. <i>Experimental and Molecular Medicine</i> , 2017, 49, e315-e315.	3.2	13
5534	Integrated proteomic analysis of <i>Brachypodium distachyon</i> roots and leaves reveals a synergistic network in the response to drought stress and recovery. <i>Scientific Reports</i> , 2017, 7, 46183.	1.6	30
5535	Ethnicity influences gut metabolites and microbiota of the tribes of Assam, India. <i>Metabolomics</i> , 2017, 13, 1.	1.4	7
5536	Allosteric regulation of metabolism in cancer: endogenous mechanisms and considerations for drug design. <i>Current Opinion in Biotechnology</i> , 2017, 48, 102-110.	3.3	11
5537	Molecular dysexpression in gastric cancer revealed by integrated analysis of transcriptome data. <i>Oncology Letters</i> , 2017, 13, 3177-3185.	0.8	16
5538	Chemogenetic Interrogation of a Brain-wide Fear Memory Network in Mice. <i>Neuron</i> , 2017, 94, 363-374.e4.	3.8	211

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5539	Revealing inhibition difference between PFI-2 enantiomers against SETD7 by molecular dynamics simulations, binding free energy calculations and unbinding pathway analysis. <i>Scientific Reports</i> , 2017, 7, 46547.	1.6	25
5540	High-Throughput Sequencing and Co-Expression Network Analysis of lncRNAs and mRNAs in Early Brain Injury Following Experimental Subarachnoid Haemorrhage. <i>Scientific Reports</i> , 2017, 7, 46577.	1.6	42
5541	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	3.5	51
5542	Unraveling the complexity of transcriptomic, metabolomic and quality environmental response of tomato fruit. <i>BMC Plant Biology</i> , 2017, 17, 66.	1.6	48
5543	A subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	6.0	2,079
5544	Identification of potential crucial genes associated with steroid-induced necrosis of femoral head based on gene expression profile. <i>Gene</i> , 2017, 627, 322-326.	1.0	28
5545	From language identification to language distance. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2017, 484, 152-162.	1.2	33
5546	Dynamic Cytology and Transcriptional Regulation of Rice Lamina Joint Development. <i>Plant Physiology</i> , 2017, 174, 1728-1746.	2.3	53
5547	Transcriptomic alterations in the brain of painted turtles ( <i>Chrysemys picta</i> ) developmentally exposed to bisphenol A or ethinyl estradiol. <i>Physiological Genomics</i> , 2017, 49, 201-215.	1.0	18
5548	Clinical value of miR-452-5p expression in lung adenocarcinoma: A retrospective quantitative real-time polymerase chain reaction study and verification based on The Cancer Genome Atlas and Gene Expression Omnibus databases. <i>Tumor Biology</i> , 2017, 39, 101042831770575.	0.8	5
5549	Differential Network Analysis of Anti-sense Regulation. <i>Lecture Notes in Computer Science</i> , 2017, , 277-288.	1.0	0
5550	Systematic analysis of the lysine acetylome reveals diverse functions of lysine acetylation in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>AMB Express</i> , 2017, 7, 94.	1.4	16
5551	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2171-2184.	0.8	16
5552	Postzygotic single-nucleotide mosaicism contributes to the etiology of autism spectrum disorder and autistic traits and the origin of mutations. <i>Human Mutation</i> , 2017, 38, 1002-1013.	1.1	64
5553	Multipronged quantitative proteomics reveals serum proteome alterations in breast cancer intrinsic subtypes. <i>Journal of Proteomics</i> , 2017, 163, 1-13.	1.2	18
5554	Wounding induces dedifferentiation of epidermal Gata6+ cells and acquisition of stem cell properties. <i>Nature Cell Biology</i> , 2017, 19, 603-613.	4.6	138
5555	Involvement of a gut-retina axis in protection against dietary glycemia-induced age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4472-E4481.	3.3	179
5556	Protein-protein interactions and metabolite channelling in the plant tricarboxylic acid cycle. <i>Nature Communications</i> , 2017, 8, 15212.	5.8	103

#	ARTICLE	IF	CITATIONS
5557	Organ-specific transcriptome profiling of metabolic and pigment biosynthesis pathways in the floral ornamental progenitor species <i>Anthurium amnicola</i> Dressler. <i>Scientific Reports</i> , 2017, 7, 1596.	1.6	13
5558	Understanding the relative affinity and specificity of the substrate binding site of protein kinase B for substrate-mimetic inhibitors. <i>Molecular Simulation</i> , 2017, 43, 1459-1471.	0.9	0
5559	sfinx: an R package for the elimination of false positives from affinity purificationâ€“mass spectrometry datasets. <i>Bioinformatics</i> , 2017, 33, 1902-1904.	1.8	3
5560	MOST-visualization: software for producing automated textbook-style maps of genome-scale metabolic networks. <i>Bioinformatics</i> , 2017, 33, 2596-2597.	1.8	3
5561	A New Strategy for Deleting Animal drugs from Traditional Chinese Medicines based on Modified Yimusake Formula. <i>Scientific Reports</i> , 2017, 7, 1504.	1.6	45
5562	Identification of the zinc, copper and cadmium metalloproteome of the protozoan <i>Tetrahymena thermophila</i> by systematic bioinformatics. <i>Archives of Microbiology</i> , 2017, 199, 1141-1149.	1.0	24
5563	Egr2 and 3 control adaptive immune responses by temporally uncoupling expansion from T cell differentiation. <i>Journal of Experimental Medicine</i> , 2017, 214, 1787-1808.	4.2	66
5564	Identification of repaglinide as a therapeutic drug for glioblastoma multiforme. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 33-39.	1.0	23
5565	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , 2017, 19, 1268-1280.	2.9	79
5566	Polymerâ€“KLAK Peptide Conjugates Induce Cancer Cell Death through Synergistic Effects of Mitochondria Damage and Autophagy Blockage. <i>Bioconjugate Chemistry</i> , 2017, 28, 1709-1721.	1.8	18
5567	Selectivity determinants of GPCRâ€“G-protein binding. <i>Nature</i> , 2017, 545, 317-322.	13.7	297
5568	Comparative transcriptomic analysis of <i>Gardnerella vaginalis</i> biofilms vs. planktonic cultures using RNA-seq. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 3.	2.9	66
5569	Detecting the Molecular System Signatures of Idiopathic Pulmonary Fibrosis through Integrated Genomic Analysis. <i>Scientific Reports</i> , 2017, 7, 1554.	1.6	22
5570	Signature of Microbial Dysbiosis in Periodontitis. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	91
5571	Investigation of differentially-expressed microRNAs and genes in cervical cancer using an integrated bioinformatics analysis. <i>Oncology Letters</i> , 2017, 13, 2784-2790.	0.8	16
5572	Mass Spectrometric Analyses Reveal a Central Role for Ubiquitylation in Remodeling the <i>Arabidopsis</i> Proteome during Photomorphogenesis. <i>Molecular Plant</i> , 2017, 10, 846-865.	3.9	31
5573	Azathioprine with Allopurinol. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 946-955.	0.9	7
5574	Microarray Analysis Reveals Increased Expression of Matrix Metalloproteases and Cytokines of Interleukin-20 Subfamily in the Kidneys of Neonate Rats Underwent Unilateral Ureteral Obstruction: A Potential Role of IL-24 in the Regulation of Inflammation and Tissue Remodeling. <i>Kidney and Blood Pressure Research</i> , 2017, 42, 16-32.	0.9	6

#	ARTICLE	IF	CITATIONS
5575	Online Mentoring as an Extracurricular Measure to Encourage Talented Girls in STEM (Science,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 Mentoring. <i>Gifted Child Quarterly</i> , 2017, 61, 239-249.	1.2	45
5576	LRSSL: predict and interpret drug-disease associations based on data integration using sparse subspace learning. <i>Bioinformatics</i> , 2017, 33, 1187-1196.	1.8	106
5577	Integrated analysis of mRNA and miRNA expression profiles in pancreatic ductal adenocarcinoma. <i>Oncology Reports</i> , 2017, 37, 2779-2786.	1.2	11
5578	The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. <i>Cell</i> , 2017, 169, 679-692.e14.	13.5	48
5579	The centrosomal OFD1 protein interacts with the translation machinery and regulates the synthesis of specific targets. <i>Scientific Reports</i> , 2017, 7, 1224.	1.6	36
5580	Orthoscape: a cytoscape application for grouping and visualization KEGG based gene networks by taxonomy and homology principles. <i>BMC Bioinformatics</i> , 2017, 18, 1-9.	1.2	12
5581	Network-Based Gene Function Prediction in Mouse and Other Model Vertebrates Using MouseNet Server. <i>Methods in Molecular Biology</i> , 2017, 1611, 183-198.	0.4	3
5582	Genome-Wide Function Analysis of lincRNAs as miRNA Targets or Decoys in Plant. <i>RNA Technologies</i> , 2017, , 149-162.	0.2	3
5583	A comprehensive regional analysis of genome-wide expression profiles for major depressive disorder. <i>Journal of Affective Disorders</i> , 2017, 218, 86-92.	2.0	33
5584	Allosteric Autoinhibition Pathway in Transcription Factor ERG: Dynamics Network and Mutant Experimental Evaluations. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 1153-1165.	2.5	12
5585	The peripheral blood proteome signature of idiopathic pulmonary fibrosis is distinct from normal and is associated with novel immunological processes. <i>Scientific Reports</i> , 2017, 7, 46560.	1.6	51
5586	Dynamics of the Interaction between Cotton Bollworm <i>Helicoverpa armigera</i> and Nucleopolyhedrovirus as Revealed by Integrated Transcriptomic and Proteomic Analyses. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1009-1028.	2.5	40
5587	Prognostic Biomarker Identification Through Integrating the Gene Signatures of Hepatocellular Carcinoma Properties. <i>EBioMedicine</i> , 2017, 19, 18-30.	2.7	51
5588	In-depth analysis of the synaptic plasma membrane proteome of small hippocampal slices using an integrated approach. <i>Neuroscience</i> , 2017, 353, 119-132.	1.1	15
5589	The global expression profiling in esophageal squamous cell carcinoma. <i>Genomics</i> , 2017, 109, 241-250.	1.3	27
5590	Zika virus infection reprograms global transcription of host cells to allow sustained infection. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-10.	3.0	58
5591	Crosstalk of two-component signal transduction systems in regulating central carbohydrate and energy metabolism during autotrophic and photomixotrophic growth of <i>Synechocystis</i> sp. PCC 6803. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 485-496.	0.6	10
5592	Identification of Sequence Variants within Experimentally Validated Protein Interaction Sites Provides New Insights into Molecular Mechanisms of Disease Development. <i>Molecular Informatics</i> , 2017, 36, 1700017.	1.4	4

#	ARTICLE	IF	CITATIONS
5593	Metabolomic changes and metabolic responses to expression of heterologous biosynthetic genes for lycopene production in <i>Yarrowia lipolytica</i> . <i>Journal of Biotechnology</i> , 2017, 251, 174-185.	1.9	15
5594	Disturbance-induced phytoplankton regime shifts and recovery of cyanobacteria dominance in two subtropical reservoirs. <i>Water Research</i> , 2017, 120, 52-63.	5.3	151
5595	Metabolomics Study of the Effects of Inflammation, Hypoxia, and High Glucose on Isolated Human Pancreatic Islets. <i>Journal of Proteome Research</i> , 2017, 16, 2294-2306.	1.8	35
5596	Comprehensive quantitative lipidomic approach to investigate serum phospholipid alterations in breast cancer. <i>Metabolomics</i> , 2017, 13, 1.	1.4	8
5597	Identification of OtpR regulated sRNAs in <i>Brucella melitensis</i> expressed under acidic stress and their roles in pathogenesis and metabolism. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2017, 50, 40-47.	0.7	6
5598	Type 2 Diabetes Inhibited Human Mesenchymal Stem Cells Angiogenic Response by Overactivity of the Autophagic Pathway. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 1518-1530.	1.2	52
5599	Complement Protein C1q Enhances Macrophage Foam Cell Survival and Efferocytosis. <i>Journal of Immunology</i> , 2017, 198, 472-480.	0.4	44
5600	Working with Ontologies. <i>Methods in Molecular Biology</i> , 2017, 1525, 123-135.	0.4	6
5601	Old age and the associated impairment of bones' adaptation to loading are associated with transcriptomic changes in cellular metabolism, cell-matrix interactions and the cell cycle. <i>Gene</i> , 2017, 599, 36-52.	1.0	42
5602	A Comprehensively Curated Genome-Scale Two-Cell Model for the Heterocystous Cyanobacterium <i>Anabaena</i> sp. PCC 7120. <i>Plant Physiology</i> , 2017, 173, 509-523.	2.3	39
5603	Large-scale transcriptome analysis reveals arabidopsis metabolic pathways are frequently influenced by different pathogens. <i>Plant Molecular Biology</i> , 2017, 94, 453-467.	2.0	16
5604	Heterogeneous Ribosomes Preferentially Translate Distinct Subpools of mRNAs Genome-wide. <i>Molecular Cell</i> , 2017, 67, 71-83.e7.	4.5	480
5605	Grazing of leaf-associated Cercomonads (Protists: Rhizaria: Cercozoa) structures bacterial community composition and function. <i>Environmental Microbiology</i> , 2017, 19, 3297-3309.	1.8	87
5606	The genomic mosaicism of hybrid speciation. <i>Science Advances</i> , 2017, 3, e1602996.	4.7	138
5607	Analysis of protein complexes in Arabidopsis leaves using size exclusion chromatography and label-free protein correlation profiling. <i>Journal of Proteomics</i> , 2017, 166, 8-18.	1.2	48
5608	Screening the key microRNAs and transcription factors in prostate cancer based on microRNA functional synergistic relationships. <i>Medicine (United States)</i> , 2017, 96, e5679.	0.4	17
5609	Single-cell profiling reveals heterogeneity and functional patterning of GPCR expression in the vascular system. <i>Nature Communications</i> , 2017, 8, 15700.	5.8	80
5610	Comparative Genomic Analysis Reveals Habitat-Specific Genes and Regulatory Hubs within the Genus <i>Novosphingobium</i> . <i>MSystems</i> , 2017, 2, .	1.7	75



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5611	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017, 16, 2887-2898.	1.8	25
5612	Cerebrospinal fluid microRNAs are potential biomarkers of temporal lobe epilepsy and status epilepticus. <i>Scientific Reports</i> , 2017, 7, 3328.	1.6	93
5613	Genetic Variants Within Key Nodes of the Cascade of Antipsychotic Mechanisms: Effects on Antipsychotic Response and Schizophrenia Psychopathology in a Naturalistic Treatment Setting in Two Independent Korean and Italian Samples. <i>Advances in Therapy</i> , 2017, 34, 1482-1497.	1.3	3
5614	Huntington's Disease iPSC-Derived Brain Microvascular Endothelial Cells Reveal WNT-Mediated Angiogenic and Blood-Brain Barrier Deficits. <i>Cell Reports</i> , 2017, 19, 1365-1377.	2.9	199
5615	Establishment of a Strong Link Between Smoking and Cancer Pathogenesis through DNA Methylation Analysis. <i>Scientific Reports</i> , 2017, 7, 1811.	1.6	59
5616	Genome-wide DNA methylation analysis in lung fibroblasts co-cultured with silica-exposed alveolar macrophages. <i>Respiratory Research</i> , 2017, 18, 91.	1.4	22
5617	Clustering and Network Analysis of Reverse Phase Protein Array Data. <i>Methods in Molecular Biology</i> , 2017, 1606, 171-191.	0.4	6
5618	Overexpression of GSK3-like Kinase 5 (OsGSK5) in rice ( <i>Oryza sativa</i> ) enhances salinity tolerance in part via preferential carbon allocation to root starch. <i>Functional Plant Biology</i> , 2017, 44, 705.	1.1	22
5619	Identification of the abiotic stress-related transcription in little Neptune grass <i>Cymodocea nodosa</i> with RNA-seq. <i>Marine Genomics</i> , 2017, 34, 47-56.	0.4	16
5620	The best models of metabolism. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2017, 9, e1391.	6.6	37
5621	SCENERY: a web application for (causal) network reconstruction from cytometry data. <i>Nucleic Acids Research</i> , 2017, 45, W270-W275.	6.5	9
5622	The Mapping of Predicted Triplex DNA:RNA in the <i>Drosophila</i> Genome Reveals a Prominent Location in Development- and Morphogenesis-Related Genes. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2295-2304.	0.8	8
5623	Using PFP and ESG Protein Function Prediction Web Servers. <i>Methods in Molecular Biology</i> , 2017, 1611, 1-14.	0.4	7
5624	Macroanalysis in the Arts and Sciences. , 2017, , 87-100.		0
5625	Longitudinal variation of microbial communities in benthic biofilms and association with hydrological and physicochemical conditions in glacier-fed streams. <i>Freshwater Science</i> , 2017, 36, 479-490.	0.9	26
5626	Oviduct extracellular vesicles protein content and their role during oviduct's embryo cross-talk. <i>Reproduction</i> , 2017, 154, 253-268.	1.1	157
5627	MiR529a modulates panicle architecture through regulating SQUAMOSA PROMOTER BINDING-LIKE genes in rice ( <i>Oryza sativa</i> ). <i>Plant Molecular Biology</i> , 2017, 94, 469-480.	2.0	45
5628	Bamboo invasion of broadleaf forests altered soil fungal community closely linked to changes in soil organic C chemical composition and mineral N production. <i>Plant and Soil</i> , 2017, 418, 507-521.	1.8	54



#	ARTICLE	IF	CITATIONS
5629	Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. <i>Neurobiology of Aging</i> , 2017, 57, 104-119.	1.5	24
5630	Coupling Targeted and Untargeted Mass Spectrometry for Metabolome-Microbiome-Wide Association Studies of Human Fecal Samples. <i>Analytical Chemistry</i> , 2017, 89, 7549-7559.	3.2	62
5631	Identification of oral cancer related candidate genes by integrating protein-protein interactions, gene ontology, pathway analysis and immunohistochemistry. <i>Scientific Reports</i> , 2017, 7, 2472.	1.6	27
5632	Establishment of the model system between phytochemicals and gene expression profiles in Macrosclereid cells of <i>Medicago truncatula</i> . <i>Scientific Reports</i> , 2017, 7, 2580.	1.6	14
5633	TCM-Mesh: The database and analytical system for network pharmacology analysis for TCM preparations. <i>Scientific Reports</i> , 2017, 7, 2821.	1.6	168
5634	Reconstruction of pathway modification induced by nicotinamide using multi-omic network analyses in triple negative breast cancer. <i>Scientific Reports</i> , 2017, 7, 3466.	1.6	15
5635	Integrated analysis and transcript abundance modelling of H3K4me3 and H3K27me3 in developing secondary xylem. <i>Scientific Reports</i> , 2017, 7, 3370.	1.6	32
5636	Machine Learning and Network Analysis of Molecular Dynamics Trajectories Reveal Two Chains of Red/Ox-specific Residue Interactions in Human Protein Disulfide Isomerase. <i>Scientific Reports</i> , 2017, 7, 3666.	1.6	33
5637	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	1.6	24
5638	Conformation dynamics of the intrinsically disordered protein c-Myb with the ff99IDPs force field. <i>RSC Advances</i> , 2017, 7, 29713-29721.	1.7	17
5639	GeNICE: A Novel Framework for Gene Network Inference by Clustering, Exhaustive Search, and Multivariate Analysis. <i>Journal of Computational Biology</i> , 2017, 24, 809-830.	0.8	2
5640	Transcriptome of <i>Pterospermum kingtungense</i> provides implications on the mechanism underlying its rapid vegetative growth and limestone adaption. <i>Scientific Reports</i> , 2017, 7, 3198.	1.6	5
5641	Functional dissection of human targets for KSHV-encoded miRNAs using network analysis. <i>Scientific Reports</i> , 2017, 7, 3159.	1.6	4
5642	Identification of novel dysregulated key genes in Breast cancer through high throughput ChIP-Seq data analysis. <i>Scientific Reports</i> , 2017, 7, 3229.	1.6	10
5643	Fetal Metabolic Stress Disrupts Immune Homeostasis and Induces Proinflammatory Responses in Human Immunodeficiency Virus Type 1 and Combination Antiretroviral Therapy Exposed Infants. <i>Journal of Infectious Diseases</i> , 2017, 216, 436-446.	1.9	26
5644	GRIK3: A novel oncogenic protein related to tumor TNM stage, lymph node metastasis, and poor prognosis of GC. <i>Tumor Biology</i> , 2017, 39, 101042831770436.	0.8	13
5645	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower ( <i>Helianthus annuus</i> L.). <i>Plant Molecular Biology</i> , 2017, 94, 549-564.	2.0	51
5646	Unravelling the complexity of signalling networks in cancer: A review of the increasing role for computational modelling. <i>Critical Reviews in Oncology/Hematology</i> , 2017, 117, 73-113.	2.0	15

#	ARTICLE	IF	CITATIONS
5647	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	5.8	165
5648	ceRNAs in plants: computational approaches and associated challenges for target mimic research. <i>Briefings in Bioinformatics</i> , 2017, 19, 1273-1289.	3.2	16
5649	Global identification, structural analysis and expression characterization of bHLH transcription factors in wheat. <i>BMC Plant Biology</i> , 2017, 17, 90.	1.6	51
5650	Abnormal expression of long non-coding RNAs in myocardial infarction. <i>Heart and Vessels</i> , 2017, 32, 1253-1261.	0.5	8
5651	IL15RA is required for osteoblast function and bone mineralization. <i>Bone</i> , 2017, 103, 20-30.	1.4	37
5652	A systems level analysis of epileptogenesis-associated proteome alterations. <i>Neurobiology of Disease</i> , 2017, 105, 164-178.	2.1	25
5653	MIDAS: Mining differentially activated subpaths of KEGG pathways from multi-class RNA-seq data. <i>Methods</i> , 2017, 124, 13-24.	1.9	15
5654	Structure and specificity of a new class of Ca <sup>2+</sup> -independent housekeeping sortase from <i>Streptomyces avermitilis</i> provide insights into its non-canonical substrate preference. <i>Journal of Biological Chemistry</i> , 2017, 292, 7244-7257.	1.6	15
5655	Bioinformatics analysis of gene expression profiles of esophageal squamous cell carcinoma. <i>Ecological Management and Restoration</i> , 2017, 30, 1-8.	0.2	20
5656	Phylogenomic Synteny Network Analysis of MADS-Box Transcription Factor Genes Reveals Lineage-Specific Transpositions, Ancient Tandem Duplications, and Deep Positional Conservation. <i>Plant Cell</i> , 2017, 29, 1278-1292.	3.1	106
5657	Inferring miRNA sponge co-regulation of protein-protein interactions in human breast cancer. <i>BMC Bioinformatics</i> , 2017, 18, 243.	1.2	20
5658	Genetic Dissection of Morphometric Traits Reveals That Phytochrome B Affects Nucleus Size and Heterochromatin Organization in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2519-2531.	0.8	14
5659	Identification of critical genes in nucleus pulposus cells isolated from degenerated intervertebral discs using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 553-564.	1.1	12
5660	Comparative functional genomic screens of three yeast deletion collections reveal unexpected effects of genotype in response to diverse stress. <i>Open Biology</i> , 2017, 7, 160330.	1.5	12
5661	Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. <i>Molecular Systems Biology</i> , 2017, 13, 932.	3.2	177
5662	Identification of potential target genes associated with the effect of propranolol on angiosarcoma via microarray analysis. <i>Oncology Letters</i> , 2017, 13, 4267-4275.	0.8	4
5663	Microproteome of dentoalveolar tissues. <i>Bone</i> , 2017, 101, 219-229.	1.4	26
5664	Repression of Interstitial Identity in Nephron Progenitor Cells by Pax2 Establishes the Nephron-Interstitial Boundary during Kidney Development. <i>Developmental Cell</i> , 2017, 41, 349-365.e3.	3.1	61

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5665	Genome-wide identification and phylogenetic, comparative genomic, alternative splicing, and expression analyses of TCP genes in plants. <i>Plant Gene</i> , 2017, 12, 23-32.	1.4	6
5666	Reconstructing context-specific gene regulatory network and identifying modules and network rewiring through data integration. <i>Methods</i> , 2017, 124, 36-45.	1.9	2
5667	Proteomic analysis of JAK2V617F-induced changes identifies potential new combinatorial therapeutic approaches. <i>Leukemia</i> , 2017, 31, 2717-2725.	3.3	10
5668	The complex genetics of hypoplastic left heart syndrome. <i>Nature Genetics</i> , 2017, 49, 1152-1159.	9.4	177
5669	System analysis identifies distinct and common functional networks governed by transcription factor ASCL1, in glioma and small cell lung cancer. <i>Molecular BioSystems</i> , 2017, 13, 1481-1494.	2.9	4
5670	Identification of potential gene targets in systemic vasculitis using DNA microarray analysis. <i>Molecular Medicine Reports</i> , 2017, 15, 3665-3673.	1.1	2
5671	Evolutionary, computational, and biochemical studies of the salicylaldehyde dehydrogenases in the naphthalene degradation pathway. <i>Scientific Reports</i> , 2017, 7, 43489.	1.6	18
5672	Single-cell DNA sequencing reveals a late-dissemination model in metastatic colorectal cancer. <i>Genome Research</i> , 2017, 27, 1287-1299.	2.4	189
5673	Impacts of diet on hindgut microbiota and short-chain fatty acids in grass carp ( <i>Ctenopharyngodon idellus</i> ). <i>Aquaculture Research</i> , 2017, 48, 5595-5605.	0.9	60
5674	Effects of ecological restoration on soil microbial diversity in a temperate grassy woodland. <i>Applied Soil Ecology</i> , 2017, 117-118, 117-128.	2.1	28
5675	Lysine Acetylome Analysis Reveals Photosystem II Manganese-stabilizing Protein Acetylation is Involved in Negative Regulation of Oxygen Evolution in Model Cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1297-1311.	2.5	26
5676	Characterization of the CLASP2 Protein Interaction Network Identifies SOGA1 as a Microtubule-Associated Protein. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1718-1735.	2.5	41
5677	Altered long non-coding RNA expression profile in rabbit atria with atrial fibrillation: TCONS_00075467 modulates atrial electrical remodeling by sponging miR-328 to regulate CACNA1C. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 108, 73-85.	0.9	64
5678	Identifying miRNA-mRNA regulation network of chronic pancreatitis based on the significant functional expression. <i>Medicine (United States)</i> , 2017, 96, e6668.	0.4	24
5679	Single-Cell RNA Sequencing Reveals Expanded Clones of Islet Antigen-Reactive CD4+ T Cells in Peripheral Blood of Subjects with Type 1 Diabetes. <i>Journal of Immunology</i> , 2017, 199, 323-335.	0.4	62
5680	The response of archaeal species to seasonal variables in a subtropical aerated soil: insight into the low abundant methanogens. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6505-6515.	1.7	7
5681	Synergistic effects of Chuanxiong-Chishao herb-pair on promoting angiogenesis at network pharmacological and pharmacodynamic levels. <i>Chinese Journal of Integrative Medicine</i> , 2017, 23, 654-662.	0.7	22
5682	vhfRNAi: a web-platform for analysis of host genes involved in viral infections discovered by genome wide RNAi screens. <i>Molecular BioSystems</i> , 2017, 13, 1377-1387.	2.9	3

#	ARTICLE	IF	CITATIONS
5683	Identification of key genes and pathways for peri-implantitis through the analysis of gene expression data. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1832-1840.	0.8	14
5684	Gene networks for total number born in pigs across divergent environments. <i>Mammalian Genome</i> , 2017, 28, 426-435.	1.0	3
5685	Deep sequencing reveals a global reprogramming of lncRNA transcriptome during EMT. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1703-1713.	1.9	18
5686	Network propagation: a universal amplifier of genetic associations. <i>Nature Reviews Genetics</i> , 2017, 18, 551-562.	7.7	514
5687	High glucose increases the formation and pro-oxidative activity of endothelial microparticles. <i>Diabetologia</i> , 2017, 60, 1791-1800.	2.9	79
5688	Alignment of the transcriptome with individual variation in animals selectively bred for High Drinking-In-the-Dark (HDID). <i>Alcohol</i> , 2017, 60, 115-120.	0.8	8
5689	Intertumoral Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2017, 31, 737-754.e6.	7.7	836
5690	Upregulation of cyclin B1 plays potential roles in the invasiveness of pituitary adenomas. <i>Journal of Clinical Neuroscience</i> , 2017, 43, 267-273.	0.8	20
5691	Functional proteogenomics reveals biomarkers and therapeutic targets in lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6581-6586.	3.3	32
5692	A Key Role for Apoplastic H <sub>2</sub> O <sub>2</sub> in Norway Spruce Phenolic Metabolism. <i>Plant Physiology</i> , 2017, 174, 1449-1475.	2.3	46
5693	Genetic diversity patterns of microeukaryotic plankton communities in Shenhu Bay, southeast China. <i>Continental Shelf Research</i> , 2017, 141, 68-75.	0.9	8
5694	Integrated metagenomic analysis of the rumen microbiome of cattle reveals key biological mechanisms associated with methane traits. <i>Methods</i> , 2017, 124, 108-119.	1.9	21
5695	Deciphering the Mechanism of Action of <i>Wrightia tinctoria</i> for Psoriasis Based on Systems Pharmacology Approach. <i>Journal of Alternative and Complementary Medicine</i> , 2017, 23, 866-878.	2.1	2
5696	Prediction of marker genes associated with hypertension by bioinformatics analyses. <i>International Journal of Molecular Medicine</i> , 2017, 40, 137-145.	1.8	5
5697	Zika Virus Infects Human Fetal Brain Microglia and Induces Inflammation. <i>Clinical Infectious Diseases</i> , 2017, 64, 914-920.	2.9	133
5698	Visualization and Analysis of MicroRNAs within KEGG Pathways using VANESA. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	11
5699	Serotonin Transporter Associated Protein Complexes Are Enriched in Synaptic Vesicle Proteins and Proteins Involved in Energy Metabolism and Ion Homeostasis. <i>ACS Chemical Neuroscience</i> , 2017, 8, 1101-1116.	1.7	15
5700	Structural intermediates and directionality of the swiveling motion of Pyruvate Phosphate Dikinase. <i>Scientific Reports</i> , 2017, 7, 45389.	1.6	16

#	ARTICLE	IF	CITATIONS
5701	Design, Network Analysis and In Silico Modeling of Biologically Significant 4-(substituted) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td (	0.7	2
5702	Morphoproteomic Characterization of Lung Squamous Cell Carcinoma Fragmentation, a Histological Marker of Increased Tumor Invasiveness. <i>Cancer Research</i> , 2017, 77, 2585-2593.	0.4	15
5703	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. <i>Human Molecular Genetics</i> , 2017, 26, 1219-1229.	1.4	73
5704	A microRNA regulates the response of corals to thermal stress. <i>Molecular Ecology</i> , 2017, 26, 3472-3483.	2.0	31
5705	Chromatin-remodeling factor SMARCD2 regulates transcriptional networks controlling differentiation of neutrophil granulocytes. <i>Nature Genetics</i> , 2017, 49, 742-752.	9.4	87
5706	Microbial Biogeography and Core Microbiota of the Rat Digestive Tract. <i>Scientific Reports</i> , 2017, 7, 45840.	1.6	127
5707	Tracking the evolution of 3D gene organization demonstrates its connection to phenotypic divergence. <i>Nucleic Acids Research</i> , 2017, 45, 4330-4343.	6.5	7
5708	Chemical-agnostic hazard prediction: Statistical inference of in vitro toxicity pathways from proteomics responses to chemical mixtures. <i>Computational Toxicology</i> , 2017, 2, 39-44.	1.8	0
5709	Differential expression of novel metabolic and immunological biomarkers in oysters challenged with a virulent strain of OsHV-1. <i>Developmental and Comparative Immunology</i> , 2017, 73, 229-245.	1.0	50
5710	Proteomic insight into the mitigation of wheat root drought stress by arbuscular mycorrhizae. <i>Journal of Proteomics</i> , 2017, 169, 21-32.	1.2	75
5711	Molecular phenotyping of multiple mouse strains under metabolic challenge uncovers a role for Elov12 in glucose-induced insulin secretion. <i>Molecular Metabolism</i> , 2017, 6, 340-351.	3.0	42
5712	EDTA-functionalized magnetic nanoparticles: A suitable platform for the analysis of low abundance urinary proteins. <i>Talanta</i> , 2017, 170, 81-88.	2.9	5
5713	The impact of micronutrient status on health: correlation network analysis to understand the role of micronutrients in metabolic-inflammatory processes regulating homeostasis and phenotypic flexibility. <i>Genes and Nutrition</i> , 2017, 12, 5.	1.2	18
5714	Gene networks show associations with seed region connectivity. <i>Human Brain Mapping</i> , 2017, 38, 3126-3140.	1.9	32
5715	Assessing the miRNA sponge potential of RUNX1T1 in t(8;21) acute myeloid leukemia. <i>Gene</i> , 2017, 615, 35-40.	1.0	12
5716	metaX: a flexible and comprehensive software for processing metabolomics data. <i>BMC Bioinformatics</i> , 2017, 18, 183.	1.2	489
5717	Systems Pharmacology-based strategy to screen new adjuvant for hepatitis B vaccine from Traditional Chinese Medicine <i>Ophiocordyceps sinensis</i> . <i>Scientific Reports</i> , 2017, 7, 44788.	1.6	13
5718	In Silico Approaches Toward Combating Antibiotic Resistance. , 2017, , 577-593.		2

#	ARTICLE	IF	CITATIONS
5719	The miRNAome of <i>Catharanthus roseus</i> : identification, expression analysis, and potential roles of microRNAs in regulation of terpenoid indole alkaloid biosynthesis. <i>Scientific Reports</i> , 2017, 7, 43027.	1.6	39
5720	Resolving protein structure–function–binding site relationships from a binding site similarity network perspective. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1319-1335.	1.5	14
5721	Systematic Investigation of <i>Ginkgo Biloba</i> Leaves for Treating Cardio-cerebrovascular Diseases in an Animal Model. <i>ACS Chemical Biology</i> , 2017, 12, 1363-1372.	1.6	77
5722	rNAV 2.0: a visualization tool for bacterial sRNA-mediated regulatory networks mining. <i>BMC Bioinformatics</i> , 2017, 18, 188.	1.2	6
5724	Identification of likely associations between cerebral folate deficiency and complex genetic and metabolic pathogenesis of autism spectrum disorders by utilization of a pilot interaction modeling approach. <i>Autism Research</i> , 2017, 10, 1424-1435.	2.1	15
5725	Multiple stressors in sediments impact adjacent hard substrate habitats and across biological domains. <i>Science of the Total Environment</i> , 2017, 592, 295-305.	3.9	20
5726	Machine Learning of Global Phosphoproteomic Profiles Enables Discrimination of Direct versus Indirect Kinase Substrates. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 786-798.	2.5	32
5727	Malonylome Analysis Reveals the Involvement of Lysine Malonylation in Metabolism and Photosynthesis in Cyanobacteria. <i>Journal of Proteome Research</i> , 2017, 16, 2030-2043.	1.8	28
5728	Genome-wide DNA methylation profiles reveal novel candidate genes associated with meat quality at different age stages in hens. <i>Scientific Reports</i> , 2017, 7, 45564.	1.6	61
5729	An interaction network of mental disorder proteins in neural stem cells. <i>Translational Psychiatry</i> , 2017, 7, e1082-e1082.	2.4	22
5730	PopNet: A Markov Clustering Approach to Study Population Genetic Structure. <i>Molecular Biology and Evolution</i> , 2017, 34, 1799-1811.	3.5	5
5731	Potential Regulators Driving the Transition in Nonalcoholic Fatty Liver Disease: a Stage-Based View. <i>Cellular Physiology and Biochemistry</i> , 2017, 41, 239-251.	1.1	16
5732	Science Mapping: A Systematic Review of the Literature. <i>Journal of Data and Information Science</i> , 2017, 2, 1-40.	0.5	830
5733	Molecular Evolutionary Constraints that Determine the Avirulence State of <i>Clostridium botulinum</i> C2 Toxin. <i>Journal of Molecular Evolution</i> , 2017, 84, 174-186.	0.8	12
5734	A phosphoproteomic landscape of rice ( <i>Oryza sativa</i> ) tissues. <i>Physiologia Plantarum</i> , 2017, 160, 458-475.	2.6	28
5735	Modified mesenchymal stem cells using miRNA transduction alter lung injury in a bleomycin model. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2017, 313, L92-L103.	1.3	32
5736	Connecting myelin-related and synaptic dysfunction in schizophrenia with SNP-rich gene expression hubs. <i>Scientific Reports</i> , 2017, 7, 45494.	1.6	9
5737	Cooperative Metabolism in a Three-Partner Insect-Bacterial Symbiosis Revealed by Metabolic Modeling. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	72



#	ARTICLE	IF	CITATIONS
5738	Identification of a six-lncRNA signature associated with recurrence of ovarian cancer. <i>Scientific Reports</i> , 2017, 7, 752.	1.6	52
5739	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. <i>Bioinformatics</i> , 2017, 33, 1418-1420.	1.8	5
5740	Powerful differential expression analysis incorporating network topology for next-generation sequencing data. <i>Bioinformatics</i> , 2017, 33, 1505-1513.	1.8	20
5741	A Pan-Genomic Approach to Understand the Basis of Host Adaptation in <i>Achromobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1030-1046.	1.1	40
5742	Anthropogenic shift of planktonic food web structure in a coastal lagoon by freshwater flow regulation. <i>Scientific Reports</i> , 2017, 7, 44441.	1.6	21
5743	Defining the Core Citrus Leaf- and Root-Associated Microbiota: Factors Associated with Community Structure and Implications for Managing Huanglongbing (Citrus Greening) Disease. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	78
5744	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2017, 16, 1988-2003.	1.8	17
5745	Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation. <i>Scientific Reports</i> , 2017, 7, 63.	1.6	67
5746	Transcriptional regulatory dynamics drive coordinated metabolic and neural response to social challenge in mice. <i>Genome Research</i> , 2017, 27, 959-972.	2.4	54
5747	PINTnet: construction of condition-specific pathway interaction network by computing shortest paths on weighted PPI. <i>BMC Systems Biology</i> , 2017, 11, 15.	3.0	12
5748	Potential protective function of the sterol regulatory element binding factor 1â€“fatty acid desaturase 1/2 axis in early-stage age-related macular degeneration. <i>Heliyon</i> , 2017, 3, e00266.	1.4	18
5749	Analyzing trapped protein complexes by Virotrap and SFINX. <i>Nature Protocols</i> , 2017, 12, 881-898.	5.5	15
5750	A Computational Approach to Study Gene Expression Networks. <i>Methods in Molecular Biology</i> , 2017, 1471, 325-334.	0.4	0
5751	RNA Seq analysis for transcriptome profiling in response to classical swine fever vaccination in indigenous and crossbred pigs. <i>Functional and Integrative Genomics</i> , 2017, 17, 607-620.	1.4	13
5752	Bacterioplankton assembly and interspecies interaction indicating increasing coastal eutrophication. <i>Chemosphere</i> , 2017, 177, 317-325.	4.2	70
5753	Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. <i>Nature Microbiology</i> , 2017, 2, 17033.	5.9	17
5754	Generating testable hypotheses for schizophrenia and rheumatoid arthritis pathogenesis by integrating epidemiological, genomic, and protein interaction data. <i>NPJ Schizophrenia</i> , 2017, 3, 11.	2.0	45
5755	Harnessing the power of proteomics for identification of oncogenic, druggable signalling pathways in cancer. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 431-447.	2.5	15



#	ARTICLE	IF	CITATIONS
5756	Comparison and visualisation of agreement for paired lists of rankings. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 31-45.	0.2	0
5757	<i>Bacillus licheniformis</i> affects the microbial community and metabolic profile in the spontaneous fermentation of Daqu starter for Chinese liquor making. <i>International Journal of Food Microbiology</i> , 2017, 250, 59-67.	2.1	145
5758	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. <i>Journal of Biomedical Informatics</i> , 2017, 68, 71-82.	2.5	7
5759	Spatial confluence of psychological and anatomical network constructs in the human brain revealed by a mass meta-analysis of fMRI activation. <i>Scientific Reports</i> , 2017, 7, 44259.	1.6	7
5760	Chemometric analysis reveals links in the formation of fragrant bio-molecules during agarwood ( <i>Aquilaria malaccensis</i> ) and fungal interactions. <i>Scientific Reports</i> , 2017, 7, 44406.	1.6	38
5761	Network-Guided GWAS Improves Identification of Genes Affecting Free Amino Acids. <i>Plant Physiology</i> , 2017, 173, 872-886.	2.3	52
5762	Systematic and functional identification of small non-coding RNAs associated with exogenous biofuel stress in cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Biotechnology for Biofuels</i> , 2017, 10, 57.	6.2	36
5763	Functional Connectivity of Multiple Brain Regions Required for the Consolidation of Social Recognition Memory. <i>Journal of Neuroscience</i> , 2017, 37, 4103-4116.	1.7	170
5764	Hyphenated hydrology: Interdisciplinary evolution of water resource science. <i>Water Resources Research</i> , 2017, 53, 2972-2982.	1.7	16
5765	Modeling anorexia nervosa: transcriptional insights from human iPSC-derived neurons. <i>Translational Psychiatry</i> , 2017, 7, e1060-e1060.	2.4	22
5766	The AP-1 Transcription Factor c-Jun Promotes Arthritis by Regulating Cyclooxygenase-2 and Arginase-1 Expression in Macrophages. <i>Journal of Immunology</i> , 2017, 198, 3605-3614.	0.4	67
5767	Calcium dependent regulation of protein ubiquitination – Interplay between E3 ligases and calcium binding proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1227-1235.	1.9	25
5768	Evidencing 98 secondary metabolites of <i>Penicillium verrucosum</i> using substrate isotopic labeling and high-resolution mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1071, 29-43.	1.2	12
5769	Molecular Classification of Lobular Carcinoma of the Breast. <i>Scientific Reports</i> , 2017, 7, 43265.	1.6	10
5770	HBV quasispecies composition in Lamivudine-failed chronic hepatitis B patients and its influence on virological response to Tenofovir-based rescue therapy. <i>Scientific Reports</i> , 2017, 7, 44742.	1.6	6
5771	Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 855-872.	2.5	27
5772	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , 2017, 77, 3057-3069.	0.4	33
5773	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017, 4, 430-444.e5.	2.9	65

#	ARTICLE	IF	CITATIONS
5774	Comparative analysis of protein evolution in the genome of pre-epidemic and epidemic Zika virus. <i>Infection, Genetics and Evolution</i> , 2017, 51, 74-85.	1.0	23
5775	Synergistic drug combinations for cancer identified in a CRISPR screen for pairwise genetic interactions. <i>Nature Biotechnology</i> , 2017, 35, 463-474.	9.4	408
5776	In vivo microsampling to capture the elusive exposome. <i>Scientific Reports</i> , 2017, 7, 44038.	1.6	30
5777	Networking in microbes: conjugative elements and plasmids in the genus <i>Alteromonas</i> . <i>BMC Genomics</i> , 2017, 18, 36.	1.2	39
5778	Integrative Diffusion-Weighted Imaging and Radiogenomic Network Analysis of Glioblastoma multiforme. <i>Scientific Reports</i> , 2017, 7, 43523.	1.6	20
5779	Unique Physiological and Transcriptional Shifts under Combinations of Salinity, Drought, and Heat. <i>Plant Physiology</i> , 2017, 174, 421-434.	2.3	97
5780	The pangenome of the genus <i>Clostridium</i> . <i>Environmental Microbiology</i> , 2017, 19, 2588-2603.	1.8	43
5781	Identifying candidate positive selection genes in Korean imported pig breeds. <i>Genes and Genomics</i> , 2017, 39, 557-565.	0.5	7
5782	Diel-scale temporal dynamics recorded for bacterial groups in Namib Desert soil. <i>Scientific Reports</i> , 2017, 7, 40189.	1.6	42
5783	Molecular mechanisms underlying the positive role of treadmill training in locomotor recovery after spinal cord injury. <i>Spinal Cord</i> , 2017, 55, 441-446.	0.9	10
5784	High-Fiber Diet and Acetate Supplementation Change the Gut Microbiota and Prevent the Development of Hypertension and Heart Failure in Hypertensive Mice. <i>Circulation</i> , 2017, 135, 964-977.	1.6	695
5785	Differential Expression and Functional Analysis of High-Throughput -Omics Data Using Open Source Tools. <i>Methods in Molecular Biology</i> , 2017, 1537, 327-345.	0.4	6
5786	Comparative and temporal transcriptome analysis of peste des petits ruminants virus infected goat peripheral blood mononuclear cells. <i>Virus Research</i> , 2017, 229, 28-40.	1.1	38
5787	Defining the human copper proteome and analysis of its expression variation in cancers. <i>Metallomics</i> , 2017, 9, 112-123.	1.0	168
5788	Effect of Aggregation Operators on Network-Based Disease Gene Prioritization: A Case Study on Blood Disorders. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1276-1287.	1.9	9
5789	Cardiac inflammation in genetic dilated cardiomyopathy caused by MYBPC3 mutation. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 102, 83-93.	0.9	39
5790	Altered mucosal expression of microRNAs in pediatric patients with inflammatory bowel disease. <i>Digestive and Liver Disease</i> , 2017, 49, 378-387.	0.4	27
5791	A decade of irrigation transforms the soil microbiome of a semi-arid pine forest. <i>Molecular Ecology</i> , 2017, 26, 1190-1206.	2.0	163

#	ARTICLE	IF	CITATIONS
5792	miRNA mediated gene regulatory network analysis of <i>Cichorium intybus</i> (chicory). <i>Agri Gene</i> , 2017, 3, 37-45.	1.9	6
5793	Identification of the potential biomarkers for the metastasis of rectal adenocarcinoma. <i>Apmis</i> , 2017, 125, 93-100.	0.9	16
5794	Proteomic profile of susceptible and multidrug-resistant clinical isolates of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> using label-free and immunoproteomic strategies. <i>Research in Microbiology</i> , 2017, 168, 222-233.	1.0	8
5795	HMGB1 downregulation mediates terameprocol vascular anti-proliferative effect in experimental pulmonary hypertension. <i>Journal of Cellular Physiology</i> , 2017, 232, 3128-3138.	2.0	5
5796	Environmental DNA metabarcoding reveals primary chemical contaminants in freshwater sediments from different land-use types. <i>Chemosphere</i> , 2017, 172, 201-209.	4.2	41
5797	sbml-diff: A Tool for Visually Comparing SBML Models in Synthetic Biology. <i>ACS Synthetic Biology</i> , 2017, 6, 1225-1229.	1.9	3
5798	Gene expression profile changes in rat dorsal horn after sciatic nerve injury. <i>Neurological Research</i> , 2017, 39, 176-182.	0.6	14
5799	Ecogenomic responses of benthic communities under multiple stressors along the marine and adjacent riverine areas of northern Bohai Sea, China. <i>Chemosphere</i> , 2017, 172, 166-174.	4.2	31
5800	Transcriptomic analysis of gene expression profiles of stomach carcinoma reveal abnormal expression of mitotic components. <i>Life Sciences</i> , 2017, 170, 41-49.	2.0	17
5801	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. <i>Soil Biology and Biochemistry</i> , 2017, 105, 227-235.	4.2	72
5802	Identification of the fitness determinants of budding yeast on a natural substrate. <i>ISME Journal</i> , 2017, 11, 959-971.	4.4	21
5803	Modeling and Extending Ecological Networks Using Land Similarity. <i>Studies in Computational Intelligence</i> , 2017, , 709-718.	0.7	1
5804	Lactate signalling regulates fungal $\beta$ -glucan masking and immune evasion. <i>Nature Microbiology</i> , 2017, 2, 16238.	5.9	197
5805	Mapping of inhibitors and activity data to the human kinome and exploring promiscuity from a ligand and target perspective. <i>Chemical Biology and Drug Design</i> , 2017, 89, 834-845.	1.5	16
5806	Major intrinsic proteins repertoire of <i>Morus notabilis</i> and their expression profiles in different species. <i>Plant Physiology and Biochemistry</i> , 2017, 111, 304-317.	2.8	5
5807	BioBlocks: Programming Protocols in Biology Made Easier. <i>ACS Synthetic Biology</i> , 2017, 6, 1230-1232.	1.9	20
5808	The metastasis suppressor RARRES3 as an endogenous inhibitor of the immunoproteasome expression in breast cancer cells. <i>Scientific Reports</i> , 2017, 7, 39873.	1.6	21
5809	Integrated analysis reveals candidate mRNA and their potential roles in uterine leiomyomas. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 149-156.	0.6	8

#	ARTICLE	IF	CITATIONS
5810	Linking the Transcriptional Landscape of Bone Induction to Biomaterial Design Parameters. <i>Advanced Materials</i> , 2017, 29, 1603259.	11.1	34
5811	PlaNet: Comparative Co-Expression Network Analyses for Plants. <i>Methods in Molecular Biology</i> , 2017, 1533, 213-227.	0.4	42
5812	Practical Utilization of OryzaExpress and Plant Omics Data Center Databases to Explore Gene Expression Networks in <i>Oryza Sativa</i> and Other Plant Species. <i>Methods in Molecular Biology</i> , 2017, 1533, 229-240.	0.4	2
5813	Dynamic landscape of alternative polyadenylation during retinal development. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 1721-1739.	2.4	20
5814	Imbalance of bacteriome profiles within the Finnish Diabetes Prediction and Prevention study: Parallel use of 16S profiling and virome sequencing in stool samples from children with islet autoimmunity and matched controls. <i>Pediatric Diabetes</i> , 2017, 18, 588-598.	1.2	44
5815	miRNA profiling of human naive CD4 T cells links miR-34c-5p to cell activation and HIV replication. <i>EMBO Journal</i> , 2017, 36, 346-360.	3.5	32
5816	Proteomic Data Storage and Sharing. <i>Methods in Molecular Biology</i> , 2017, 1549, 5-15.	0.4	2
5817	Rhizosphere microbiomes of potato cultivated in the High Andes show stable and dynamic core microbiomes with different responses to plant development. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw242.	1.3	114
5818	A Luciferase-fragment Complementation Assay to Detect Lipid Droplet-associated Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 329-345.	2.5	24
5819	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368.	6.5	6,303
5820	Comparative analysis of hepatocellular carcinoma and cirrhosis gene expression profiles. <i>Molecular Medicine Reports</i> , 2017, 15, 380-386.	1.1	16
5821	The Underlying Ecological Processes of Gut Microbiota Among Cohabiting Retarded, Overgrown and Normal Shrimp. <i>Microbial Ecology</i> , 2017, 73, 988-999.	1.4	102
5822	Long-Term Nickel Contamination Increases the Occurrence of Antibiotic Resistance Genes in Agricultural Soils. <i>Environmental Science &amp; Technology</i> , 2017, 51, 790-800.	4.6	240
5823	Epigenetic Networks Regulate the Transcriptional Program in Memory and Terminally Differentiated CD8+ T Cells. <i>Journal of Immunology</i> , 2017, 198, 937-949.	0.4	55
5824	Network Tools for the Analysis of Proteomic Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 177-197.	0.4	17
5825	Protein kinase C $\delta$ -dependent regulation of Ubiquitin-proteasome system function in breast cancer. <i>Cancer Biomarkers</i> , 2017, 21, 1-9.	0.8	21
5826	Identification of potential therapeutic targets for gliomas by bioinformatics analysis. <i>Oncology Letters</i> , 2017, 14, 5203-5210.	0.8	3
5827	Meta-analysis of transcriptomic datasets identifies genes enriched in the mammalian circadian pacemaker. <i>Nucleic Acids Research</i> , 2017, 45, 9860-9873.	6.5	29

#	ARTICLE	IF	CITATIONS
5828	Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. <i>Nucleic Acids Research</i> , 2017, 45, 11622-11642.	6.5	46
5829	Architecture of eukaryotic mRNA 3' end processing machinery. <i>Science</i> , 2017, 358, 1056-1059.	6.0	124
5830	Combined analysis of ChIP-seq and gene microarray datasets identify the E2-mediated genes in ER $\alpha$ -dependent manner in osteosarcoma. <i>Oncology Reports</i> , 2017, 38, 2335-2342.	1.2	2
5831	Effects of Shu Gan Jian Pi formula on rats with carbon tetrachloride-induced liver fibrosis using serum metabolomics based on gas chromatography-time of flight mass spectrometry. <i>Molecular Medicine Reports</i> , 2017, 16, 3901-3909.	1.1	11
5832	Screening and identification of critical transcription factors involved in the protection of cardiomyocytes against hydrogen peroxide-induced damage by Yixin-shu. <i>Scientific Reports</i> , 2017, 7, 13867.	1.6	13
5833	Dysregulation of Cortical Neuron DNA Methylation Profile in Autism Spectrum Disorder. <i>Cerebral Cortex</i> , 2017, 27, 5739-5754.	1.6	118
5834	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. <i>Science Signaling</i> , 2017, 10, .	1.6	52
5835	Multi-level differential network analysis of COPD exacerbations. <i>European Respiratory Journal</i> , 2017, 50, 1700075.	3.1	38
5836	Molecular mechanisms underlying gliomas and glioblastoma pathogenesis revealed by bioinformatics analysis of microarray data. <i>Medical Oncology</i> , 2017, 34, 182.	1.2	44
5837	Radiation alters the cargo of exosomes released from squamous head and neck cancer cells to promote migration of recipient cells. <i>Scientific Reports</i> , 2017, 7, 12423.	1.6	92
5838	Transcriptomic analysis of juvenile wood formation during the growing season in <i>Pinus canariensis</i> . <i>Holzforschung</i> , 2017, 71, 919-937.	0.9	11
5839	Transcriptomic signature of Fusarium toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery. <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 163-177.	1.3	4
5840	Omega-6 and omega-3 oxylipins are implicated in soybean oil-induced obesity in mice. <i>Scientific Reports</i> , 2017, 7, 12488.	1.6	46
5841	Framework for gradual progression of cell ontogeny in the <i>Arabidopsis</i> root meristem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8922-E8929.	3.3	46
5842	Elucidating <i>Escherichia coli</i> Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database. <i>Journal of Proteome Research</i> , 2017, 16, 4156-4165.	1.8	32
5843	Gaining insights into cancer biology through exploration of the cancer secretome using proteomic and bioinformatic tools. <i>Expert Review of Proteomics</i> , 2017, 14, 1021-1035.	1.3	21
5844	Characterization of the human DNA gut virome across populations with different subsistence strategies and geographical origin. <i>Environmental Microbiology</i> , 2017, 19, 4728-4735.	1.8	32
5845	The dynamic landscape of gene regulation during <i>Bombyx mori</i> oogenesis. <i>BMC Genomics</i> , 2017, 18, 714.	1.2	11

#	ARTICLE	IF	CITATIONS
5846	Dynamic metabolic reprogramming of steroidal glycol-alkaloid and phenylpropanoid biosynthesis may impart early blight resistance in wild tomato ( <i>Solanum arcanum</i> Peralta). <i>Plant Molecular Biology</i> , 2017, 95, 411-423.	2.0	41
5847	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. <i>Nature Communications</i> , 2017, 8, 767.	5.8	67
5848	Whole-genome scale identification of methylation markers specific for cerebral palsy in monozygotic discordant twins. <i>Molecular Medicine Reports</i> , 2017, 16, 9423-9430.	1.1	18
5849	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017, 8, 1186.	5.8	78
5850	Functional classification of protein toxins as a basis for bioinformatic screening. <i>Scientific Reports</i> , 2017, 7, 13940.	1.6	19
5851	Alterations in the proteome of wheat primary roots after wortmannin application during seed germination. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	3
5852	Heterogeneous circRNA expression profiles and regulatory functions among HEK293T single cells. <i>Scientific Reports</i> , 2017, 7, 14393.	1.6	5
5853	Biological network border detection. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 947-955.	0.6	1
5854	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2017, 1666, 539-556.	0.4	11
5855	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 989, 93-107.	0.8	3
5856	Multi-omic network-based interrogation of rat liver metabolism following gastric bypass surgery featuring SWATH proteomics. <i>Technology</i> , 2017, 05, 139-184.	1.4	5
5857	Foxp1 in Forebrain Pyramidal Neurons Controls Gene Expression Required for Spatial Learning and Synaptic Plasticity. <i>Journal of Neuroscience</i> , 2017, 37, 10917-10931.	1.7	48
5858	Hub nodes in the network of human Mitogen-Activated Protein Kinase (MAPK) pathways: Characteristics and potential as drug targets. <i>Informatics in Medicine Unlocked</i> , 2017, 9, 173-180.	1.9	5
5859	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. <i>Trends in Genetics</i> , 2017, 33, 960-970.	2.9	165
5860	Natural product diversity associated with the nematode symbionts <i>Photorhabdus</i> and <i>Xenorhabdus</i> . <i>Nature Microbiology</i> , 2017, 2, 1676-1685.	5.9	136
5861	Evaluating the toxicity of silicon dioxide nanoparticles on neural stem cells using RNA-Seq. <i>RSC Advances</i> , 2017, 7, 47552-47564.	1.7	14
5862	The Induction of Oxalate Metabolism <i>in Vivo</i> Is More Effective with Functional Microbial Communities than with Functional Microbial Species. <i>MSystems</i> , 2017, 2, .	1.7	33
5863	EulerianGrapher. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
5864	Characteristic analyses of a neural differentiation model from iPSC-derived neuron according to morphology, physiology, and global gene expression pattern. <i>Scientific Reports</i> , 2017, 7, 12233.	1.6	73
5865	Topology of protein-protein interaction network and edge reduction co-efficiency in VEGF signaling of breast cancer. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2017, 6, 1.	1.2	3
5866	Functional proteomics outlines the complexity of breast cancer molecular subtypes. <i>Scientific Reports</i> , 2017, 7, 10100.	1.6	50
5867	Monitoring storage induced changes in the platelet proteome employing label free quantitative mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 11045.	1.6	27
5868	Integrated strategy of differentially expressed genes associated with ulcerative colitis. <i>Molecular Medicine Reports</i> , 2017, 16, 7479-7489.	1.1	6
5869	Screening of potential genes contributing to the macrocycle drug resistance of <i>C. albicans</i> via microarray analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 7527-7533.	1.1	4
5870	Inflammasome-driven catecholamine catabolism in macrophages blunts lipolysis during ageing. <i>Nature</i> , 2017, 550, 119-123.	13.7	329
5871	Identification of key genes associated with the effect of osmotic stimuli on intervertebral discs using microarray analysis. <i>Oncology Letters</i> , 2017, 14, 4249-4255.	0.8	4
5872	Study of microRNA mediated gene regulation in <i>Striga hermonthica</i> through in-silico approach. <i>Agri Gene</i> , 2017, 6, 47-53.	1.9	1
5873	Alteration of soil bacterial interaction networks driven by different long-term fertilization management practices in the red soil of South China. <i>Applied Soil Ecology</i> , 2017, 120, 128-134.	2.1	41
5874	Coordinated Splicing of Regulatory Detained Introns within Oncogenic Transcripts Creates an Exploitable Vulnerability in Malignant Glioma. <i>Cancer Cell</i> , 2017, 32, 411-426.e11.	7.7	161
5875	Temporal Control of Mammalian Cortical Neurogenesis by m6A Methylation. <i>Cell</i> , 2017, 171, 877-889.e17.	13.5	567
5876	Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons. <i>Cell Reports</i> , 2017, 20, 3236-3247.	2.9	121
5877	Chromatographic unsupervised classification of olive and non-olive oil samples with the aid of graph theory. <i>Analytical Methods</i> , 2017, 9, 6267-6272.	1.3	1
5878	Genome-wide association study and annotating candidate gene networks affecting age at first calving in Nellore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 484-492.	0.8	42
5879	<i>Stenotrophomonas</i> -Like Bacteria Are Widespread Symbionts in Cone Snail Venom Ducts. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	10
5880	Microarray expression profile analysis of long non-coding RNAs in optineurin E50K mutant transgenic mice. <i>Molecular Medicine Reports</i> , 2017, 16, 1255-1261.	1.1	7
5881	Integrating networks and comparative genomics reveals retroelement proliferation dynamics in hominid genomes. <i>Science Advances</i> , 2017, 3, e1701256.	4.7	16



#	ARTICLE	IF	CITATIONS
5882	RiceAntherNet: a gene co-expression network for identifying anther and pollen development genes. <i>Plant Journal</i> , 2017, 92, 1076-1091.	2.8	34
5883	Triosâ€”promising in silico biomarkers for differentiating the effect of disease on the human microbiome network. <i>Scientific Reports</i> , 2017, 7, 13259.	1.6	13
5884	Transcription profiling analysis of genes and pathomechanisms underlying the defense response against Tobacco Etch Virus infection in <i>Arabidopsis thaliana</i> . <i>Russian Journal of Plant Physiology</i> , 2017, 64, 930-938.	0.5	1
5885	Effects of anticholinergic agent on miRNA profiles and transcriptomes in a murine model of allergic rhinitis. <i>Molecular Medicine Reports</i> , 2017, 16, 6558-6569.	1.1	14
5886	Plastic Transcriptomes Stabilize Immunity to Pathogen Diversity: The Jasmonic Acid and Salicylic Acid Networks within the <i>Arabidopsis</i> / <i>Botrytis</i> Pathosystem. <i>Plant Cell</i> , 2017, 29, 2727-2752.	3.1	84
5887	Identification of potential transcriptomic markers in developing asthma: An integrative analysis of gene expression profiles. <i>Molecular Immunology</i> , 2017, 92, 38-44.	1.0	8
5888	New strategies to understand platelet storage lesion. <i>ISBT Science Series</i> , 2017, 12, 496-500.	1.1	6
5889	Interactions of plant growth-promoting rhizobacteria and soil factors in two leguminous plants. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8485-8497.	1.7	76
5890	FN1, FOS, and ITGA5 induce preeclampsia: Abnormal expression and methylation. <i>Hypertension in Pregnancy</i> , 2017, 36, 302-309.	0.5	17
5891	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	1.8	219
5892	Identification of prostate cancer hub genes and therapeutic agents using bioinformatics approach. <i>Cancer Biomarkers</i> , 2017, 20, 553-561.	0.8	20
5893	A Padawan Programmerâ€™s Guide to Developing Software Libraries. <i>Cell Systems</i> , 2017, 5, 431-437.	2.9	14
5894	Identifying key genes associated with acute myocardial infarction. <i>Medicine (United States)</i> , 2017, 96, e7741.	0.4	28
5895	iPhemap: an atlas of phenotype to genotype relationships of human iPSC models of neurological diseases. <i>EMBO Molecular Medicine</i> , 2017, 9, 1742-1762.	3.3	24
5896	Dynamic and Modularized MicroRNA Regulation and Its Implication in Human Cancers. <i>Scientific Reports</i> , 2017, 7, 13356.	1.6	60
5897	Network analysis of EMT and MET micro-RNA regulation in breast cancer. <i>Scientific Reports</i> , 2017, 7, 13534.	1.6	48
5898	Reverse Nearest Neighbor Search on a Protein-Protein Interaction Network to Infer Protein-Disease Associations. <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221772040.	1.0	10
5899	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099

#	ARTICLE	IF	CITATIONS
5900	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
5901	The basic tilted helix bundle domain of the prolyl isomerase FKBP25 is a novel double-stranded RNA binding module. <i>Nucleic Acids Research</i> , 2017, 45, 11989-12004.	6.5	15
5902	Computing Prediction and Functional Analysis of Prokaryotic Propionylation. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2896-2904.	2.5	7
5903	Cardamonin inhibits colonic neoplasia through modulation of MicroRNA expression. <i>Scientific Reports</i> , 2017, 7, 13945.	1.6	37
5904	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	3.3	111
5905	The IBD interactome: an integrated view of aetiology, pathogenesis and therapy. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017, 14, 739-749.	8.2	301
5906	iCAVE: an open source tool for visualizing biomolecular networks in 3D, stereoscopic 3D and immersive 3D. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	21
5907	Bioinformatics analysis of gene expression profiling for identification of potential key genes among ischemic stroke. <i>Medicine (United States)</i> , 2017, 96, e7564.	0.4	10
5908	Mortality and transcriptional effects of inorganic mercury in the marine copepod <i>Calanus finmarchicus</i> . <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2017, 80, 845-861.	1.1	11
5909	Large-scale examination of functional and sequence diversity of 2-oxoglutarate/Fe(II)-dependent oxygenases in Metazoa. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2922-2933.	1.1	31
5910	Genome-wide association study and gene set analysis for understanding candidate genes involved in salt tolerance at the rice seedling stage. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1391-1403.	1.0	37
5911	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. <i>Cell Stem Cell</i> , 2017, 21, 349-358.e6.	5.2	163
5912	Malagasy traditional treatments for food crops: A tool to control potato bacterial diseases?. <i>Crop Protection</i> , 2017, 102, 49-55.	1.0	2
5913	mRNA-Seq reveals accumulation followed by reduction of small nuclear and nucleolar RNAs in yeast exposed to antiviral ribavirin. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	1
5914	Systematic Identification of Determinants for Single-Strand Annealing-Mediated Deletion Formation in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3269-3279.	0.8	1
5915	Differences between Platelets Derived from Neonatal Cord Blood and Adult Peripheral Blood Assessed by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3567-3575.	1.8	28
5916	Combinatorial ensemble miRNA target prediction of co-regulation networks with non-prediction data. <i>Nucleic Acids Research</i> , 2017, 45, 8745-8757.	6.5	21
5917	Architecture and Dynamics of the Jasmonic Acid Gene Regulatory Network. <i>Plant Cell</i> , 2017, 29, 2086-2105.	3.1	220

#	ARTICLE	IF	CITATIONS
5918	Paradigm of Biased PAR1 (Protease-Activated Receptor-1) Activation and Inhibition in Endothelial Cells Dissected by Phosphoproteomics. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 1891-1902.	1.1	18
5919	Illumina deep sequencing reveals conserved and novel microRNAs involved in the response to X-ray irradiation after peripheral nerve injury in rats. <i>Neuroscience Letters</i> , 2017, 658, 12-18.	1.0	2
5920	Toward the Standardization of Mitochondrial Proteomics: The Italian Mitochondrial Human Proteome Project Initiative. <i>Journal of Proteome Research</i> , 2017, 16, 4319-4329.	1.8	66
5921	Genome-Scale Genetic Interactions and Cell Imaging Confirm Cytokinesis as Deleterious to Transient Topoisomerase II Deficiency in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3379-3391.	0.8	8
5922	Evolutionarily Conserved Alternative Splicing Across Monocots. <i>Genetics</i> , 2017, 207, 465-480.	1.2	47
5923	Exposure to BMAA mirrors molecular processes linked to neurodegenerative disease. <i>Proteomics</i> , 2017, 17, 1700161.	1.3	29
5924	Navigating freely-available software tools for metabolomics analysis. <i>Metabolomics</i> , 2017, 13, 106.	1.4	173
5925	TAF10 and TAF10b partially redundant roles during <i>Drosophila melanogaster</i> morphogenesis. <i>Transcription</i> , 2017, 8, 297-306.	1.7	2
5926	DNA methyltransferase homologue TRDMT1 in <i>Plasmodium falciparum</i> specifically methylates endogenous aspartic acid tRNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1047-1057.	0.9	20
5927	Defining Human Tyrosine Kinase Phosphorylation Networks Using Yeast as an In Vivo Model Substrate. <i>Cell Systems</i> , 2017, 5, 128-139.e4.	2.9	20
5928	Liver cyst gene knockout in cholangiocytes inhibits cilium formation and Wnt signaling. <i>Human Molecular Genetics</i> , 2017, 26, 4190-4202.	1.4	10
5929	Genome-Wide Analysis and Expression Profiles of the MYB Genes in <i>Brachypodium distachyon</i> . <i>Plant and Cell Physiology</i> , 2017, 58, 1777-1788.	1.5	41
5930	Molecular mechanisms of breast cancer metastasis by gene expression profile analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 4671-4677.	1.1	31
5931	Identification of Salinity Stress Tolerant Proteins in <i>Sorghum Bicolor</i> Computational Approach. <i>Lecture Notes in Computer Science</i> , 2017, , 318-325.	1.0	1
5932	Identification of prognostic markers of high grade prostate cancer through an integrated bioinformatics approach. <i>Journal of Cancer Research and Clinical Oncology</i> , 2017, 143, 2571-2579.	1.2	34
5933	Downregulation of miR-136-5p in hepatocellular carcinoma and its clinicopathological significance. <i>Molecular Medicine Reports</i> , 2017, 16, 5393-5405.	1.1	28
5934	Personalized analysis of pathway aberrance induced by sevoflurane and propofol. <i>Molecular Medicine Reports</i> , 2017, 16, 5312-5320.	1.1	0
5935	Functional Analysis of OMICs Data and Small Molecule Compounds in an Integrated Knowledge-Based Platform. <i>Methods in Molecular Biology</i> , 2017, 1613, 101-124.	0.4	19

#	ARTICLE	IF	CITATIONS
5936	YAP/TAZ Orchestrate VEGF Signaling during Developmental Angiogenesis. <i>Developmental Cell</i> , 2017, 42, 462-478.e7.	3.1	249
5937	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. <i>MBio</i> , 2017, 8, .	1.8	42
5938	P-body proteins regulate transcriptional rewiring to promote DNA replication stress resistance. <i>Nature Communications</i> , 2017, 8, 558.	5.8	32
5939	Digging into the low molecular weight peptidome with the OligoNet web server. <i>Scientific Reports</i> , 2017, 7, 11692.	1.6	11
5940	MPZL1 forms a signalling complex with GRB2 adaptor and PTPN11 phosphatase in HER2-positive breast cancer cells. <i>Scientific Reports</i> , 2017, 7, 11514.	1.6	21
5941	Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. <i>Journal of Biological Chemistry</i> , 2017, 292, 18240-18255.	1.6	52
5942	Systems genetics identifies a co-regulated module of liver microRNAs associated with plasma LDL cholesterol in murine diet-induced dyslipidemia. <i>Physiological Genomics</i> , 2017, 49, 618-629.	1.0	13
5943	Extracellular vesicle-packaged miRNA release after short-term exposure to particulate matter is associated with increased coagulation. <i>Particle and Fibre Toxicology</i> , 2017, 14, 32.	2.8	85
5944	Differential Expression of miRNAs in the Respiratory Tree of the Sea Cucumber <i>Apostichopus japonicus</i> Under Hypoxia Stress. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3681-3692.	0.8	28
5945	GRID-seq reveals the global RNA-chromatin interactome. <i>Nature Biotechnology</i> , 2017, 35, 940-950.	9.4	233
5946	Culture independent assessment of human milk microbial community in lactational mastitis. <i>Scientific Reports</i> , 2017, 7, 7804.	1.6	133
5947	Transcriptome analysis of genes involved in secondary cell wall biosynthesis in developing internodes of <i>Miscanthus lutarioriparius</i> . <i>Scientific Reports</i> , 2017, 7, 9034.	1.6	55
5948	Environmentally Friendly Procedure Based on Supercritical Fluid Chromatography and Tandem Mass Spectrometry Molecular Networking for the Discovery of Potent Antiviral Compounds from <i>Euphorbia semiperfoliata</i> . <i>Journal of Natural Products</i> , 2017, 80, 2620-2629.	1.5	51
5949	N <sup>1</sup> - and O-Acetylation in <i>Mycobacterium tuberculosis</i> Lineage 7 and Lineage 4 Strains: Proteins Involved in Bioenergetics, Virulence, and Antimicrobial Resistance Are Acetylated. <i>Journal of Proteome Research</i> , 2017, 16, 4045-4059.	1.8	37
5950	Predicted effects of observed changes in the mRNA and microRNA transcriptome of lung neutrophils during <i>S. pneumoniae</i> pneumonia in mice. <i>Scientific Reports</i> , 2017, 7, 11258.	1.6	17
5951	Protein complexes, big data, machine learning and integrative proteomics: lessons learned over a decade of systematic analysis of protein interaction networks. <i>Expert Review of Proteomics</i> , 2017, 14, 845-855.	1.3	19
5952	Integrated analysis of microRNA and gene expression profiles reveals a functional regulatory module associated with liver fibrosis. <i>Gene</i> , 2017, 636, 87-95.	1.0	53
5953	Comprehensive analysis of lncRNAs and mRNAs in skeletal muscle of rainbow trout ( <i>Oncorhynchus</i> ) TJ ETQq1 1 0.784314 rgBT /Overl	1.6	9

#	ARTICLE	IF	CITATIONS
5954	RNA Sequencing and Co-expressed Long Non-coding RNA in Modern and Wild Wheats. <i>Scientific Reports</i> , 2017, 7, 10670.	1.6	64
5955	Unravelling diversity and metabolic potential of microbial consortia at each stage of leather sewage treatment. <i>RSC Advances</i> , 2017, 7, 41727-41737.	1.7	14
5956	Detection of dysregulated protein-association networks by high-throughput proteomics predicts cancer vulnerabilities. <i>Nature Biotechnology</i> , 2017, 35, 983-989.	9.4	138
5957	A mouse model for embryonal tumors with multilayered rosettes uncovers the therapeutic potential of Sonic-hedgehog inhibitors. <i>Nature Medicine</i> , 2017, 23, 1191-1202.	15.2	38
5958	Network-based machine learning and graph theory algorithms for precision oncology. <i>Npj Precision Oncology</i> , 2017, 1, 25.	2.3	74
5959	Using the Contextual Hub Analysis Tool (CHAT) in Cytoscape to Identify Contextually Relevant Network Hubs. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 8.24.1-8.24.13.	25.8	6
5960	Determinants and Regulation of Protein Turnover in Yeast. <i>Cell Systems</i> , 2017, 5, 283-294.e5.	2.9	85
5961	Host Genetic Control of the Oral Microbiome in Health and Disease. <i>Cell Host and Microbe</i> , 2017, 22, 269-278.e3.	5.1	165
5962	(Re-)programming of subtype specific cardiomyocytes. <i>Advanced Drug Delivery Reviews</i> , 2017, 120, 142-167.	6.6	13
5963	A Link between Linearmycin Biosynthesis and Extracellular Vesicle Genesis Connects Specialized Metabolism and Bacterial Membrane Physiology. <i>Cell Chemical Biology</i> , 2017, 24, 1238-1249.e7.	2.5	41
5964	Toxicogenomic and bioinformatics platforms to identify key molecular mechanisms of a curcumin-analogue DM-1 toxicity in melanoma cells. <i>Pharmacological Research</i> , 2017, 125, 178-187.	3.1	15
5965	The <i>Schistosoma mansoni</i> genome encodes thousands of long non-coding RNAs predicted to be functional at different parasite life-cycle stages. <i>Scientific Reports</i> , 2017, 7, 10508.	1.6	48
5966	Dynamic Changes in the Splenic Transcriptome of Chickens during the Early Infection and Progress of Marek's Disease. <i>Scientific Reports</i> , 2017, 7, 11648.	1.6	6
5967	Screening candidate microRNA-mRNA regulatory pairs for predicting the response to chemoradiotherapy in rectal cancer by a bioinformatics approach. <i>Scientific Reports</i> , 2017, 7, 11312.	1.6	4
5969	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017, 26, 6170-6182.	2.0	299
5970	Seasonal rather than spatial variability drives planktonic and benthic bacterial diversity in a microtidal lagoon and the adjacent open sea. <i>Molecular Ecology</i> , 2017, 26, 5961-5973.	2.0	35
5971	Proteomes of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> LBB.B5 Incubated in Milk at Optimal and Low Temperatures. <i>MSystems</i> , 2017, 2, .	1.7	8
5972	Predictive and Comparative Network Analysis of the Gut Microbiota in Type 2 Diabetes. , 2017, , .		2

#	ARTICLE	IF	CITATIONS
5973	Structure of an Insecticide Sequestering Carboxylesterase from the Disease Vector <i>Culex quinquefasciatus</i> : What Makes an Enzyme a Good Insecticide Sponge?. <i>Biochemistry</i> , 2017, 56, 5512-5525.	1.2	24
5974	Hotspots of aberrant enhancer activity punctuate the colorectal cancer epigenome. <i>Nature Communications</i> , 2017, 8, 14400.	5.8	93
5975	Toward Neuroproteomics in Biological Psychiatry: A Systems Approach Unravels Okadaic Acid-Induced Alterations in the Neuronal Phosphoproteome. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 550-563.	1.0	8
5976	Identification of novel methylated targets in colorectal cancer by microarray analysis and construction of co-expression network. <i>Oncology Letters</i> , 2017, 14, 2643-2648.	0.8	14
5977	RNase H1 Cooperates with DNA Gyrases to Restrict R-Loops and Maintain Genome Integrity in Arabidopsis Chloroplasts. <i>Plant Cell</i> , 2017, 29, 2478-2497.	3.1	66
5978	Identification of key genes and pathways in Parkinson's disease through integrated analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 3769-3776.	1.1	17
5979	Three Faces of N-Acetylaspartate: Activator, Substrate, and Inhibitor of Human Aspartoacylase. <i>Journal of Physical Chemistry B</i> , 2017, 121, 9389-9397.	1.2	13
5980	Microbial communities with distinct denitrification potential in spruce and beech soils differing in nitrate leaching. <i>Scientific Reports</i> , 2017, 7, 9738.	1.6	34
5981	Joint inflammation related citrullination of functional arginines in extracellular proteins. <i>Scientific Reports</i> , 2017, 7, 8246.	1.6	18
5982	Integrated analysis of mRNA and miRNA expression in HeLa cells expressing low levels of Nucleolin. <i>Scientific Reports</i> , 2017, 7, 9017.	1.6	22
5983	Proteomic and network analysis of human serum albuminome by integrated use of quick crosslinking and two-step precipitation. <i>Scientific Reports</i> , 2017, 7, 9856.	1.6	11
5984	Marked seasonality and high spatial variation in estuarine ciliates are driven by exchanges between the $\alpha$ -abundant and $\alpha$ -intermediate biospheres. <i>Scientific Reports</i> , 2017, 7, 9494.	1.6	27
5985	Niche harmony search algorithm for detecting complex disease associated high-order SNP combinations. <i>Scientific Reports</i> , 2017, 7, 11529.	1.6	36
5986	Computational Cell Cycle Profiling of Cancer Cells for Prioritizing FDA-Approved Drugs with Repurposing Potential. <i>Scientific Reports</i> , 2017, 7, 11261.	1.6	27
5987	Differential expression and co-expression gene networks reveal candidate biomarkers of boar taint in non-castrated pigs. <i>Scientific Reports</i> , 2017, 7, 12205.	1.6	46
5988	Proteome-wide acetylation dynamics in human cells. <i>Scientific Reports</i> , 2017, 7, 10296.	1.6	42
5989	Transcriptomic profiling of Tibetan highland fish ( <i>Gymnocypris przewalskii</i> ) in response to the infection of parasite ciliate <i>Ichthyophthirius multifiliis</i> . <i>Fish and Shellfish Immunology</i> , 2017, 70, 524-535.	1.6	23
5990	Modeling the peak of emergence in systems: Design and katachi. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 131, 213-241.	1.4	3

#	ARTICLE	IF	CITATIONS
5991	Transcriptome-based network analysis reveals renal cell type-specific dysregulation of hypoxia-associated transcripts. <i>Scientific Reports</i> , 2017, 7, 8576.	1.6	62
5992	Combined transcriptome and metabolome analyses of metformin effects reveal novel links between metabolic networks in steroidogenic systems. <i>Scientific Reports</i> , 2017, 7, 8652.	1.6	16
5993	Bioinformatics analyses of pathways and gene predictions in IL-1 $\beta$ and IL-1 $\beta$ knockout mice with spinal cord injury. <i>Acta Histochemica</i> , 2017, 119, 663-670.	0.9	10
5994	Identifying the miRNA signature associated with survival time in patients with lung adenocarcinoma using miRNA expression profiles. <i>Scientific Reports</i> , 2017, 7, 7507.	1.6	60
5995	The global view of mRNA-related ceRNA cross-talks across cardiovascular diseases. <i>Scientific Reports</i> , 2017, 7, 10185.	1.6	30
5996	Genotype-specific physiological and transcriptomic responses to drought stress in <i>Setaria italica</i> (an) Tj ETQq1 1 0.784314 rgBT /Overl 1.6 51	1.6	51
5997	Gene expression associated with suicide attempts in US veterans. <i>Translational Psychiatry</i> , 2017, 7, e1226-e1226.	2.4	20
5998	Identification of the active compounds and significant pathways of yinchenhao decoction based on network pharmacology. <i>Molecular Medicine Reports</i> , 2017, 16, 4583-4592.	1.1	105
5999	Investigating the microRNA-mRNA regulatory network in acute myeloid leukemia. <i>Oncology Letters</i> , 2017, 14, 3981-3988.	0.8	13
6000	Total Synthesis and Biological Assessment of Novel Albicidins Discovered by Mass Spectrometric Networking. <i>Chemistry - A European Journal</i> , 2017, 23, 15316-15321.	1.7	29
6001	Human protein secretory pathway genes are expressed in a tissue-specific pattern to match processing demands of the secretome. <i>Npj Systems Biology and Applications</i> , 2017, 3, 22.	1.4	32
6002	Integrated Analysis of Copy Number Variations and Gene Expression Profiling in Hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 10570.	1.6	33
6003	An overview of posttraumatic stress disorder genetic studies by analyzing and integrating genetic data into genetic database PTSDgene. <i>Neuroscience and Biobehavioral Reviews</i> , 2017, 83, 647-656.	2.9	17
6004	Phenotype-driven precision oncology as a guide for clinical decisions one patient at a time. <i>Nature Communications</i> , 2017, 8, 435.	5.8	75
6005	Transcriptome analysis of inflammation-related gene expression in endothelial cells activated by complement MASP-1. <i>Scientific Reports</i> , 2017, 7, 10462.	1.6	14
6006	<i>Bifidobacterium pseudocatenulatum</i> LI09 and <i>Bifidobacterium catenulatum</i> LI10 attenuate D-galactosamine-induced liver injury by modifying the gut microbiota. <i>Scientific Reports</i> , 2017, 7, 8770.	1.6	70
6007	The yeast noncoding RNA interaction network. <i>Rna</i> , 2017, 23, 1479-1492.	1.6	25
6008	Mining databases for protein aggregation: a review. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 143-152.	1.4	11



#	ARTICLE	IF	CITATIONS
6009	Bioinformatics analysis to identify the critical genes, microRNAs and long noncoding RNAs in melanoma. <i>Medicine (United States)</i> , 2017, 96, e7497.	0.4	17
6010	Conformational plasticity and evolutionary analysis of the myotilin tandem Ig domains. <i>Scientific Reports</i> , 2017, 7, 3993.	1.6	11
6011	MYC and hsa-miRNA-423-5p as biomarkers in nasopharyngeal carcinoma revealed by miRNA-mRNA-pathway network integrated analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 1039-1046.	1.1	6
6012	Transcription factor-microRNA associations and their impact on colorectal cancer survival. <i>Molecular Carcinogenesis</i> , 2017, 56, 2512-2526.	1.3	13
6013	Effect of social interactions on hippocampal protein expression in animal dominant and submissive model of behavioral disorders. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1700089.	0.8	4
6014	Seed desiccation mechanisms co-opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i> . <i>Plant, Cell and Environment</i> , 2017, 40, 2292-2306.	2.8	49
6015	Exploration of the sequential gene changes in epithelial ovarian cancer induced by carboplatin via microarray analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 3155-3160.	1.1	4
6016	Microbiota, metabolome, and immune alterations in obese mice fed a high-fat diet containing type 2 resistant starch. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700184.	1.5	81
6017	Microarray analysis reveals key genes and pathways in Tetralogy of Fallot. <i>Molecular Medicine Reports</i> , 2017, 16, 2707-2713.	1.1	1
6018	Investigation of naphthofuran moiety as potential dual inhibitor against BACE-1 and GSK-3 $\beta$ : molecular dynamics simulations, binding energy, and network analysis to identify first-in-class dual inhibitors against Alzheimer's disease. <i>Journal of Molecular Modeling</i> , 2017, 23, 239.	0.8	20
6019	A Method to Assess Bacteriocin Effects on the Gut Microbiota of Mice. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	3
6020	Biological analysis of cancer specific microRNAs on function modeling in osteosarcoma. <i>Scientific Reports</i> , 2017, 7, 5382.	1.6	23
6021	Fungal communities are differentially affected by conventional and biodynamic agricultural management approaches in vineyard ecosystems. <i>Agriculture, Ecosystems and Environment</i> , 2017, 246, 306-313.	2.5	94
6022	Proteomics analysis of human placenta reveals glutathione metabolism dysfunction as the underlying pathogenesis for preeclampsia. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1207-1214.	1.1	26
6023	Volatile metabolite profiling reveals the changes in the volatile compounds of new spontaneously generated loquat cultivars. <i>Food Research International</i> , 2017, 100, 234-243.	2.9	9
6024	Clinical Metabolomics to Segregate Aromatic Amino Acid Decarboxylase Deficiency From Drug-Induced Metabolite Elevations. <i>Pediatric Neurology</i> , 2017, 75, 66-72.	1.0	19
6025	Full Characterization of Localization Diversity in the Human Protein Interactome. <i>Journal of Proteome Research</i> , 2017, 16, 3019-3029.	1.8	22
6026	Vertically and horizontally transmitted microbial symbionts shape the gut microbiota ontogenesis of a skin-mucus feeding discus fish progeny. <i>Scientific Reports</i> , 2017, 7, 5263.	1.6	65

#	ARTICLE	IF	CITATIONS
6027	Genome-wide identification and characterization of circular RNAs by high throughput sequencing in soybean. <i>Scientific Reports</i> , 2017, 7, 5636.	1.6	108
6028	Microarray analysis of copy-number variations and gene expression profiles in prostate cancer. <i>Medicine (United States)</i> , 2017, 96, e7264.	0.4	7
6029	Biotic interactions in a Mediterranean oak forest: role of allelopathy along phenological development of woody species. <i>European Journal of Forest Research</i> , 2017, 136, 699-710.	1.1	18
6030	Meta-analysis of microarray datasets for the risk assessment of coplanar polychlorinated biphenyl 77 (PCB77) on human health. <i>Toxicology and Environmental Health Sciences</i> , 2017, 9, 161-168.	1.1	6
6031	Coupling sugarcane yield to soil nematodes: Implications from different fertilization regimes and growth stages. <i>Agriculture, Ecosystems and Environment</i> , 2017, 247, 157-165.	2.5	6
6032	Dual RNA-Seq of <i>Lysobacter capsici</i> AZ78 " <i>Phytophthora infestans</i> interaction shows the implementation of attack strategies by the bacterium and unsuccessful oomycete defense responses. <i>Environmental Microbiology</i> , 2017, 19, 4113-4125.	1.8	30
6033	Network based subcellular proteomics in monocyte membrane revealed novel candidate genes involved in osteoporosis. <i>Osteoporosis International</i> , 2017, 28, 3033-3042.	1.3	14
6034	Bam35 Tectivirus Intraviral Interaction Map Unveils New Function and Localization of Phage ORFan Proteins. <i>Journal of Virology</i> , 2017, 91, .	1.5	20
6035	Improved prediction of breast cancer outcome by identifying heterogeneous biomarkers. <i>Bioinformatics</i> , 2017, 33, 3619-3626.	1.8	35
6036	Interplay between the gut microbiota and immune responses of ayu ( <i>Plecoglossus altivelis</i> ) during <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2017, 68, 479-487.	1.6	100
6037	Do manure-borne or indigenous soil microorganisms influence the spread of antibiotic resistance genes in manured soil?. <i>Soil Biology and Biochemistry</i> , 2017, 114, 229-237.	4.2	170
6038	Detecting gene subnetworks under selection in biological pathways. <i>Nucleic Acids Research</i> , 2017, 45, e149-e149.	6.5	48
6039	Bacterial Signaling Nucleotides Inhibit Yeast Cell Growth by Impacting Mitochondrial and Other Specifically Eukaryotic Functions. <i>MBio</i> , 2017, 8, .	1.8	10
6040	Novel chaperonins are prevalent in the viroplankton and demonstrate links to viral biology and ecology. <i>ISME Journal</i> , 2017, 11, 2479-2491.	4.4	31
6041	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. <i>Nature Communications</i> , 2017, 8, 198.	5.8	84
6042	Partial microduplication in the histone acetyltransferase complex member KANSL1 is associated with congenital heart defects in 22q11.2 microdeletion syndrome patients. <i>Scientific Reports</i> , 2017, 7, 1795.	1.6	28
6043	Characterization of developmental defects in the forebrain resulting from hyperactivated mTOR signaling by integrative analysis of transcriptomic and proteomic data. <i>Scientific Reports</i> , 2017, 7, 2826.	1.6	15
6044	Analysis of aquaporins in Brassicaceae species reveals high-level of conservation and dynamic role against biotic and abiotic stress in canola. <i>Scientific Reports</i> , 2017, 7, 2771.	1.6	84

#	ARTICLE	IF	CITATIONS
6045	Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network. <i>Scientific Reports</i> , 2017, 7, 2919.	1.6	13
6046	NEK1 kinase domain structure and its dynamic protein interactome after exposure to Cisplatin. <i>Scientific Reports</i> , 2017, 7, 5445.	1.6	29
6047	Neuron-autonomous transcriptome changes upon ischemia/reperfusion injury. <i>Scientific Reports</i> , 2017, 7, 5800.	1.6	15
6048	Imaging mass spectrometry and MS/MS molecular networking reveals chemical interactions among cuticular bacteria and pathogenic fungi associated with fungus-growing ants. <i>Scientific Reports</i> , 2017, 7, 5604.	1.6	60
6049	Benchmarking selected computational gene network growing tools in context of virus-host interactions. <i>Scientific Reports</i> , 2017, 7, 5805.	1.6	13
6050	Microbiome analysis and confocal microscopy of used kitchen sponges reveal massive colonization by <i>Acinetobacter</i> , <i>Moraxella</i> and <i>Chryseobacterium</i> species. <i>Scientific Reports</i> , 2017, 7, 5791.	1.6	41
6051	High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. <i>Scientific Reports</i> , 2017, 7, 6731.	1.6	11
6052	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017, 7, 6037.	1.6	12
6053	Transcriptome profiling of monocytes from XLA patients revealed the innate immune function dysregulation due to the BTK gene expression deficiency. <i>Scientific Reports</i> , 2017, 7, 6836.	1.6	19
6054	Post-hypoxia Invasion of the fetal brain by multidrug resistant <i>Staphylococcus</i> . <i>Scientific Reports</i> , 2017, 7, 6458.	1.6	17
6055	A systems approach to a spatio-temporal understanding of the drought stress response in maize. <i>Scientific Reports</i> , 2017, 7, 6590.	1.6	68
6056	Genome-wide Analysis and Expression Divergence of the Trihelix family in <i>Brassica Rapa</i> : Insight into the Evolutionary Patterns in Plants. <i>Scientific Reports</i> , 2017, 7, 6463.	1.6	37
6057	Integration of miRNA and mRNA expression profiles reveals microRNA-regulated networks during muscle wasting in cardiac cachexia. <i>Scientific Reports</i> , 2017, 7, 6998.	1.6	42
6058	Enriching Traditional Protein-protein Interaction Networks with Alternative Conformations of Proteins. <i>Scientific Reports</i> , 2017, 7, 7180.	1.6	15
6059	Informatics Support for Basic Research in Biomedicine. <i>ILAR Journal</i> , 2017, 58, 80-89.	1.8	6
6060	An underappreciated hotspot of antibiotic resistance: The groundwater near the municipal solid waste landfill. <i>Science of the Total Environment</i> , 2017, 609, 966-973.	3.9	133
6061	Non-interacting proteins may resemble interacting proteins: prevalence and implications. <i>Scientific Reports</i> , 2017, 7, 40419.	1.6	12
6062	Connections between the human gut microbiome and gestational diabetes mellitus. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	204

#	ARTICLE	IF	CITATIONS
6063	Construction and Optimization of a Large Gene Coexpression Network in Maize Using RNA-Seq Data. <i>Plant Physiology</i> , 2017, 175, 568-583.	2.3	55
6064	Evidence of microbial rhodopsins in <scp>A</scp>antarctic <scp>D</scp>ry <scp>V</scp>alley edaphic systems. <i>Environmental Microbiology</i> , 2017, 19, 3755-3767.	1.8	17
6065	Ulva biomass as a co-substrate for stable anaerobic digestion of spent coffee grounds in continuous mode. <i>Bioresource Technology</i> , 2017, 241, 1182-1190.	4.8	14
6066	Genomic and phenotypic signatures of climate adaptation in an <i>Anolis</i> lizard. <i>Ecology and Evolution</i> , 2017, 7, 6390-6403.	0.8	26
6067	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	1.3	25
6068	Induction of senescence in cancer cells by 5-azadeoxycytidine: Bioinformatics and experimental insights to its targets. <i>Computational Biology and Chemistry</i> , 2017, 70, 49-55.	1.1	17
6069	Identification of key genes associated with rheumatoid arthritis with bioinformatics approach. <i>Medicine (United States)</i> , 2017, 96, e7673.	0.4	15
6070	Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. <i>MSystems</i> , 2017, 2, .	1.7	30
6071	Architecture and dynamics of overlapped RNA regulatory networks. <i>Rna</i> , 2017, 23, 1636-1647.	1.6	32
6072	Apple, from omics to systemic function. <i>Plant Growth Regulation</i> , 2017, 83, 1-11.	1.8	21
6073	Circular RNAs in rat models of cardiovascular and renal diseases. <i>Physiological Genomics</i> , 2017, 49, 484-490.	1.0	33
6074	Quantitative Proteomics Reveals Temporal Proteomic Changes in Signaling Pathways during BV2 Mouse Microglial Cell Activation. <i>Journal of Proteome Research</i> , 2017, 16, 3419-3432.	1.8	21
6075	NaviCom: a web application to create interactive molecular network portraits using multi-level omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
6076	GeneHancer: genome-wide integration of enhancers and target genes in GeneCards. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	820
6077	NutriChem 2.0: exploring the effect of plant-based foods on human health and drug efficacy. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	14
6078	A Web Tool for Generating High Quality Machine-readable Biological Pathways. <i>Journal of Visualized Experiments</i> , 2017, .	0.2	6
6079	Genetic Architecture and Molecular Networks Underlying Leaf Thickness in Desert-Adapted Tomato <i>Solanum pennellii</i>. <i>Plant Physiology</i> , 2017, 175, 376-391.	2.3	38
6080	mRNA-miRNA bipartite network reconstruction to predict prognostic module biomarkers in colorectal cancer stage differentiation. <i>Molecular BioSystems</i> , 2017, 13, 2168-2180.	2.9	33

#	ARTICLE	IF	CITATIONS
6081	Environmental Selection, Dispersal, and Organism Interactions Shape Community Assembly in High-Throughput Enrichment Culturing. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	12
6082	RNA Sequencing and Bioinformatics Analysis Implicate the Regulatory Role of a Long Noncoding RNA-mRNA Network in Hepatic Stellate Cell Activation. <i>Cellular Physiology and Biochemistry</i> , 2017, 42, 2030-2042.	1.1	22
6083	Nuclear FAK and Runx1 Cooperate to Regulate IGFBP3, Cell-Cycle Progression, and Tumor Growth. <i>Cancer Research</i> , 2017, 77, 5301-5312.	0.4	48
6084	Identification of key genes and pathways associated with obesity in children. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 1065-1073.	0.8	38
6085	Map the gap: alternative visualisations of geographic knowledge production. <i>Geo: Geography and Environment</i> , 2017, 4, e00038.	0.5	4
6086	Genome-wide characterization of the WRKY gene family in radish ( <i>Raphanus sativus</i> L.) reveals its critical functions under different abiotic stresses. <i>Plant Cell Reports</i> , 2017, 36, 1757-1773.	2.8	41
6087	Cell Surface Proteomics of N-Linked Glycoproteins for Typing of Human Lymphocytes. <i>Proteomics</i> , 2017, 17, 1700156.	1.3	18
6088	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1647, 267-295.	0.4	1
6089	Overexpression of Topoisomerase 2-Alpha Confers a Poor Prognosis in Pancreatic Adenocarcinoma Identified by Co-Expression Analysis. <i>Digestive Diseases and Sciences</i> , 2017, 62, 2790-2800.	1.1	27
6090	An integrated approach to identify critical transcription factors in the protection against hydrogen peroxide-induced oxidative stress by Danhong injection. <i>Free Radical Biology and Medicine</i> , 2017, 112, 480-493.	1.3	17
6091	The Human Serum Metabolome of Vitamin B-12 Deficiency and Repletion, and Associations with Neurological Function in Elderly Adults. <i>Journal of Nutrition</i> , 2017, 147, 1839-1849.	1.3	18
6092	Label-free quantitative proteomic analysis of <i>Lactobacillus fermentum</i> NCDC 400 during bile salt exposure. <i>Journal of Proteomics</i> , 2017, 167, 36-45.	1.2	32
6093	Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6.	4.5	47
6094	Identification of breast cancer mechanism based on weighted gene coexpression network analysis. <i>Cancer Gene Therapy</i> , 2017, 24, 333-341.	2.2	62
6095	Functional prediction of miR-3144-5p in human cardiac myocytes based on transcriptome sequencing and bioinformatics. <i>Medicine (United States)</i> , 2017, 96, e7539.	0.4	3
6096	Global mRNA polarization regulates translation efficiency in the intestinal epithelium. <i>Science</i> , 2017, 357, 1299-1303.	6.0	140
6097	Comprehensive Metabolomics Study To Assess Longitudinal Biochemical Changes and Potential Early Biomarkers in Nonobese Diabetic Mice That Progress to Diabetes. <i>Journal of Proteome Research</i> , 2017, 16, 3873-3890.	1.8	13
6098	Quantitative proteomic analysis of host responses triggered by <i>Mycobacterium tuberculosis</i> infection in human macrophage cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 835-844.	0.9	23

#	ARTICLE	IF	CITATIONS
6099	Retrovirus-Based Virus-Like Particle Immunogenicity and Its Modulation by Toll-Like Receptor Activation. <i>Journal of Virology</i> , 2017, 91, .	1.5	18
6100	Crotonases: Nature's Exceedingly Convertible Catalysts. <i>ACS Catalysis</i> , 2017, 7, 6587-6599.	5.5	14
6101	Examination of pathways involved in leukemia inhibitory factor (LIF)-induced cell growth arrest using label-free proteomics approach. <i>Journal of Proteomics</i> , 2017, 168, 37-52.	1.2	40
6102	Systems Pharmacology Dissection of Multiscale Mechanisms of Action for Herbal Medicines in Treating Rheumatoid Arthritis. <i>Molecular Pharmaceutics</i> , 2017, 14, 3201-3217.	2.3	38
6103	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017, 35, 747-756.	9.4	340
6104	A gene network regulated by FGF signalling during ear development. <i>Scientific Reports</i> , 2017, 7, 6162.	1.6	29
6105	Transcriptome Analysis of Three Sheep Intestinal Regions reveals Key Pathways and Hub Regulatory Genes of Large Intestinal Lipid Metabolism. <i>Scientific Reports</i> , 2017, 7, 5345.	1.6	18
6106	Genome-wide RNA-Sequencing analysis identifies a distinct fibrosis gene signature in the conjunctiva after glaucoma surgery. <i>Scientific Reports</i> , 2017, 7, 5644.	1.6	16
6107	The Epigenetic Landscape of Promoter Genome-wide Analysis in Breast Cancer. <i>Scientific Reports</i> , 2017, 7, 6597.	1.6	25
6108	Dietary perturbations alter the ecological significance of ingested <i>Lactobacillus plantarum</i> in the digestive tract. <i>Scientific Reports</i> , 2017, 7, 7267.	1.6	9
6109	Regulation of gene expression is associated with tolerance of the Arctic copepod <i>Calanus glacialis</i> to acidified sea water. <i>Ecology and Evolution</i> , 2017, 7, 7145-7160.	0.8	53
6110	PDTM: a systems pharmacology platform of traditional Chinese medicine for psoriasis. <i>Annals of Medicine</i> , 2017, 49, 652-660.	1.5	16
6111	Deciphering transcriptional regulation in human embryonic stem cells specified towards a trophoblast fate. <i>Scientific Reports</i> , 2017, 7, 17257.	1.6	28
6112	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. <i>Cell Reports</i> , 2017, 21, 3317-3328.	2.9	68
6113	Interactome Analysis of Microtubule-targeting Agents Reveals Cytotoxicity Bases in Normal Cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 352-360.	3.0	2
6114	Ensemble Modeling Approach Targeting Heterogeneous RNA-Seq data: Application to Melanoma Pseudogenes. <i>Scientific Reports</i> , 2017, 7, 17344.	1.6	2
6115	Tear proteome analysis in ocular surface diseases using label-free LC-MS/MS and multiplexed-microarray biomarker validation. <i>Scientific Reports</i> , 2017, 7, 17478.	1.6	69
6116	Diverging mRNA and Protein Networks in Activated Microglia Reveal SRSF3 Suppresses Translation of Highly Upregulated Innate Immune Transcripts. <i>Cell Reports</i> , 2017, 21, 3220-3233.	2.9	70



#	ARTICLE	IF	CITATIONS
6117	Profiling invasive <i>Plasmodium falciparum</i> merozoites using an integrated omics approach. <i>Scientific Reports</i> , 2017, 7, 17146.	1.6	9
6118	Modeling of the jasmonate signaling pathway in <i>Arabidopsis thaliana</i> with respect to pathophysiology of <i>Alternaria</i> blight in Brassica. <i>Scientific Reports</i> , 2017, 7, 16790.	1.6	28
6119	Epigenetic Drug Repositioning for Alzheimer's Disease Based on Epigenetic Targets in Human Interactome. <i>Journal of Alzheimer's Disease</i> , 2017, 61, 53-65.	1.2	20
6120	Identification of molecular mechanisms of glutamine in pancreatic cancer. <i>Oncology Letters</i> , 2017, 14, 6395-6402.	0.8	4
6121	Isolation and characterization of mesenchymal stem cells and its antitumor application on ovarian cancer cell line. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2018, 46, 1-10.	1.9	4
6122	IL-33 and ST2 mediate FAK-dependent antitumor immune evasion through transcriptional networks. <i>Science Signaling</i> , 2017, 10, .	1.6	64
6123	An integrated bioinformatical analysis of miR-19a target genes in multiple myeloma. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 4711-4720.	0.8	8
6124	Modulation of Immune Signaling and Metabolism Highlights Host and Fungal Transcriptional Responses in Mouse Models of Invasive Pulmonary Aspergillosis. <i>Scientific Reports</i> , 2017, 7, 17096.	1.6	33
6125	Longitudinal exome-wide association study to identify genetic susceptibility loci for hypertension in a Japanese population. <i>Experimental and Molecular Medicine</i> , 2017, 49, e409-e409.	3.2	8
6126	A Cell-Line-Specific Atlas of PARP-Mediated Protein Asp/Glu-ADP-Ribosylation in Breast Cancer. <i>Cell Reports</i> , 2017, 21, 2326-2337.	2.9	51
6127	Dysbiosis of the microbiome in gastric carcinogenesis. <i>Scientific Reports</i> , 2017, 7, 15957.	1.6	172
6128	Computational derivation of a molecular framework for hair follicle biology from disease genes. <i>Scientific Reports</i> , 2017, 7, 16303.	1.6	4
6129	From word models to executable models of signaling networks using automated assembly. <i>Molecular Systems Biology</i> , 2017, 13, 954.	3.2	137
6130	Machine Learning Approach for Identification of miRNA-mRNA Regulatory Modules in Ovarian Cancer. <i>Lecture Notes in Computer Science</i> , 2017, , 438-447.	1.0	1
6131	Discovery of a Small-Molecule Bromodomain-Containing Protein 4 (BRD4) Inhibitor That Induces AMP-Activated Protein Kinase-Modulated Autophagy-Associated Cell Death in Breast Cancer. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 9990-10012.	2.9	103
6132	Interplay of neuronal and non-neuronal genes regulates intestinal DAF-16-mediated immune response during <i>Fusarium</i> infection of <i>Caenorhabditis elegans</i> . <i>Cell Death Discovery</i> , 2017, 3, 17073.	2.0	8
6133	Csl2, a novel chimeric bacteriophage lysin to fight infections caused by <i>Streptococcus suis</i> , an emerging zoonotic pathogen. <i>Scientific Reports</i> , 2017, 7, 16506.	1.6	25
6134	Increased Biosynthetic Gene Dosage in a Genome-Reduced Defensive Bacterial Symbiont. <i>MSystems</i> , 2017, 2, .	1.7	46



#	ARTICLE	IF	CITATIONS
6135	Exploration of the mechanism of colorectal cancer metastasis using microarray analysis. <i>Oncology Letters</i> , 2017, 14, 6671-6677.	0.8	13
6136	Foxp1 regulation of neonatal vocalizations via cortical development. <i>Genes and Development</i> , 2017, 31, 2039-2055.	2.7	52
6137	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. <i>MBio</i> , 2017, 8, .	1.8	169
6138	Quantitative Extracellular Matrix Proteomics Suggests Cell Wall Reprogramming in Host-Specific Immunity During Vascular Wilt Caused by <i>Fusarium oxysporum</i> in Chickpea. <i>Proteomics</i> , 2017, 17, 1600374.	1.3	10
6139	Extracellular miR-145, miR-223 and miR-326 expression signature allow for differential diagnosis of immune-mediated neuroinflammatory diseases. <i>Journal of the Neurological Sciences</i> , 2017, 383, 188-198.	0.3	36
6140	Urothelial cancer proteomics provides both prognostic and functional information. <i>Scientific Reports</i> , 2017, 7, 15819.	1.6	20
6141	Carina. , 2017, , .		5
6142	Investigation of candidate genes and mechanisms underlying postmenopausal osteoporosis using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2017, 17, 1561-1572.	1.1	3
6143	Identification of the key miRNAs associated with survival time in stomach adenocarcinoma. <i>Oncology Letters</i> , 2017, 14, 4563-4572.	0.8	10
6144	Common mechanism of pathogenesis in various types of metastatic osteosarcoma. <i>Oncology Letters</i> , 2017, 14, 6307-6313.	0.8	6
6145	Comparative Analysis of Tocopherol Biosynthesis Genes and Its Transcriptional Regulation in Soybean Seeds. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 11054-11064.	2.4	14
6146	Geochemical and Microbial Community Attributes in Relation to Hyporheic Zone Geological Facies. <i>Scientific Reports</i> , 2017, 7, 12006.	1.6	40
6147	Analysis of gene expression profiling variations induced by hsa-miR-145-5p-overexpression in laryngeal squamous cell carcinoma cell line Tu-177. <i>Molecular Medicine Reports</i> , 2017, 16, 5863-5870.	1.1	7
6148	Dataset generated for Dissection of mechanisms of Trypanothione Reductase and Tryparedoxin Peroxidase through dynamic network analysis and simulations in leishmaniasis. <i>Data in Brief</i> , 2017, 15, 757-769.	0.5	6
6149	Genomic Subtypes of Non-invasive Bladder Cancer with Distinct Metabolic Profile and Female Gender Bias in KDM6A Mutation Frequency. <i>Cancer Cell</i> , 2017, 32, 701-715.e7.	7.7	224
6150	Application of a co-expression network for the analysis of aggressive and non-aggressive breast cancer cell lines to predict the clinical outcome of patients. <i>Molecular Medicine Reports</i> , 2017, 16, 7967-7978.	1.1	24
6151	Bacteriome genetic structures of urban deposits are indicative of their origin and impacted by chemical pollutants. <i>Scientific Reports</i> , 2017, 7, 13219.	1.6	24
6152	Quantitative proteomic Analysis Reveals up-regulation of caveolin-1 in FOXP3-overexpressed human gastric cancer cells. <i>Scientific Reports</i> , 2017, 7, 14460.	1.6	5

#	ARTICLE	IF	CITATIONS
6153	Fungal networks serve as novel ecological routes for enrichment and dissemination of antibiotic resistance genes as exhibited by microcosm experiments. <i>Scientific Reports</i> , 2017, 7, 15457.	1.6	20
6154	Research synergy and drug development: Bright stars in neighboring constellations. <i>Heliyon</i> , 2017, 3, e00442.	1.4	7
6155	NDEx 2.0: A Clearinghouse for Research on Cancer Pathways. <i>Cancer Research</i> , 2017, 77, e58-e61.	0.4	63
6156	Preliminary identification of key miRNAs, signaling pathways, and genes associated with Hirschsprung's disease by analysis of tissue microRNA expression profiles. <i>World Journal of Pediatrics</i> , 2017, 13, 489-495.	0.8	11
6157	Identification and functional analysis of risk-related microRNAs for the prognosis of patients with bladder urothelial carcinoma. <i>Oncology Letters</i> , 2017, 14, 7297-7303.	0.8	5
6158	Prediction of Host-Pathogen Interactions for <i>Helicobacter pylori</i> by Interface Mimicry and Implications to Gastric Cancer. <i>Journal of Molecular Biology</i> , 2017, 429, 3925-3941.	2.0	28
6159	Hypoxia tolerance, longevity and cancer-resistance in the mole rat <i>Spalax</i> – a liver transcriptomics approach. <i>Scientific Reports</i> , 2017, 7, 14348.	1.6	38
6160	Specific eukaryotic plankton are good predictors of net community production in the Western Antarctic Peninsula. <i>Scientific Reports</i> , 2017, 7, 14845.	1.6	28
6161	Characterization of the zinc-induced Shank3 interactome of mouse synaptosome. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 581-586.	1.0	13
6162	New microbial resource: microbial diversity, function and dynamics in Chinese liquor starter. <i>Scientific Reports</i> , 2017, 7, 14577.	1.6	64
6163	Establishment of a de novo Reference Transcriptome of <i>Histomonas meleagridis</i> Reveals Basic Insights About Biological Functions and Potential Pathogenic Mechanisms of the Parasite. <i>Protist</i> , 2017, 168, 663-685.	0.6	28
6164	Competing endogenous RNA screening based on long noncoding RNA-messenger RNA co-expression profile in Hepatitis B virus-associated hepatocarcinogenesis. <i>Journal of Traditional Chinese Medicine = Chung I Tsa Chih Ying Wen Pan / Sponsored By All-China Association of Traditional Chinese Medicine, Academy of Traditional Chinese Medicine</i> , 2017, 37, 510-521.	0.4	13
6165	Mammalian $\beta$ 2 AMPK regulates intrinsic heart rate. <i>Nature Communications</i> , 2017, 8, 1258.	5.8	43
6166	Identification of miRNAs involved in DRG neurite outgrowth and their putative targets. <i>FEBS Letters</i> , 2017, 591, 2091-2105.	1.3	25
6167	Phylogenomic Insight into <i>Salinispora</i> (Bacteria, Actinobacteria) Species Designations. <i>Scientific Reports</i> , 2017, 7, 3564.	1.6	27
6168	Genome-wide analysis of banana MADS-box family closely related to fruit development and ripening. <i>Scientific Reports</i> , 2017, 7, 3467.	1.6	36
6169	Quantitative Proteomics Analysis Reveals Novel Targets of miR-21 in Zebrafish Embryos. <i>Scientific Reports</i> , 2017, 7, 4022.	1.6	9
6170	Inhibition of CDK4/6 by Palbociclib Significantly Extends Survival in Medulloblastoma Patient-Derived Xenograft Mouse Models. <i>Clinical Cancer Research</i> , 2017, 23, 5802-5813.	3.2	74

#	ARTICLE	IF	CITATIONS
6171	Gene Expression Profiling in Human Lung Cells Exposed to Isoprene-Derived Secondary Organic Aerosol. <i>Environmental Science &amp; Technology</i> , 2017, 51, 8166-8175.	4.6	53
6172	Quantitative Phosphoproteomics Reveals a Role for Collapsin Response Mediator Protein 2 in PDGF-Induced Cell Migration. <i>Scientific Reports</i> , 2017, 7, 3970.	1.6	8
6173	A cross-species approach to identify transcriptional regulators exemplified for Dnajc22 and Hnf4a. <i>Scientific Reports</i> , 2017, 7, 4056.	1.6	3
6174	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. <i>Nature Methods</i> , 2017, 14, 819-825.	9.0	157
6175	Spatiotemporal profile of postsynaptic interactomes integrates components of complex brain disorders. <i>Nature Neuroscience</i> , 2017, 20, 1150-1161.	7.1	104
6176	PCDH18 is frequently inactivated by promoter methylation in colorectal cancer. <i>Scientific Reports</i> , 2017, 7, 2819.	1.6	17
6177	Protein homeostasis of a metastable subproteome associated with Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5703-E5711.	3.3	77
6178	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , 2017, 174, 2376-2396.	2.3	121
6179	Seed weight differences between wild and domesticated soybeans are associated with specific changes in gene expression. <i>Plant Cell Reports</i> , 2017, 36, 1417-1426.	2.8	14
6180	Analysis of culm elongation in photoheterotrophic status of <i>Dendrocalamus sinicus</i> by comparative proteomics. <i>Trees - Structure and Function</i> , 2017, 31, 687-704.	0.9	3
6181	Modelling APOE ε3/ε4 allele-associated sporadic Alzheimer's disease in an induced neuron. <i>Brain</i> , 2017, 140, 2193-2209.	3.7	21
6182	Identification of PEG-induced water stress responsive transcripts using co-expression network in <i>Eucalyptus grandis</i> . <i>Gene</i> , 2017, 627, 393-407.	1.0	6
6183	Physiological characteristics of <i>Magnetospirillum gryphiswaldense</i> MSR-1 that control cell growth under high-iron and low-oxygen conditions. <i>Scientific Reports</i> , 2017, 7, 2800.	1.6	19
6184	Benchmarking Water Quality from Wastewater to Drinking Waters Using Reduced Transcriptome of Human Cells. <i>Environmental Science &amp; Technology</i> , 2017, 51, 9318-9326.	4.6	45
6185	From ranking and clustering of evolving networks to patent citation analysis. , 2017, , .		3
6186	Maternal chromium restriction modulates miRNA profiles related to lipid metabolism disorder in mice offspring. <i>Experimental Biology and Medicine</i> , 2017, 242, 1444-1452.	1.1	10
6187	Transcriptome Sequencing Reveals Astrocytes as a Therapeutic Target in Heat-Stroke. <i>Neuroscience Bulletin</i> , 2017, 33, 627-640.	1.5	13
6188	Human Regulatory Protein Ki-1/57 Is a Target of SUMOylation and Affects PML Nuclear Body Formation. <i>Journal of Proteome Research</i> , 2017, 16, 3147-3157.	1.8	9

#	ARTICLE	IF	CITATIONS
6189	Investigating the regulatory roles of the microRNAs and the Argonaute 1-enriched small RNAs in plant metabolism. <i>Gene</i> , 2017, 628, 180-189.	1.0	1
6190	Effects of suspended sediments on the sponge holobiont with implications for dredging management. <i>Scientific Reports</i> , 2017, 7, 4925.	1.6	52
6191	The gut eukaryotic microbiota influences the growth performance among cohabitating shrimp. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6447-6457.	1.7	77
6192	Elucidating Protein-DNA Interactions in Human Aliphoid Chromatin via Hybridization Capture and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3433-3442.	1.8	12
6193	Selective Deamination of Mutagens by a Mycobacterial Enzyme. <i>Journal of the American Chemical Society</i> , 2017, 139, 10762-10768.	6.6	5
6194	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
6195	Effects of sediment smothering on the sponge holobiont with implications for dredging management. <i>Scientific Reports</i> , 2017, 7, 5156.	1.6	29
6196	Molecular inter-kingdom interactions of endophytes isolated from <i>Lichnophora ericoides</i> . <i>Scientific Reports</i> , 2017, 7, 5373.	1.6	19
6197	Systems-level organization of non-alcoholic fatty liver disease progression network. <i>Molecular BioSystems</i> , 2017, 13, 1898-1911.	2.9	22
6198	Quantitative proteomic analysis identifies proteins and pathways related to neuronal development in differentiated SH-SY5Y neuroblastoma cells. <i>EuPA Open Proteomics</i> , 2017, 16, 1-11.	2.5	48
6199	Enterprise map construction based on EOLN model. , 2017, , .		0
6200	Randomization Strategies Affect Motif Significance Analysis in TF-miRNA-Gene Regulatory Networks. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	1
6201	Pathway-related modules involved in the application of sevoflurane or propofol in off-pump coronary artery bypass graft surgery. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 97-106.	0.8	6
6202	Effect of drought stress on metabolite contents in barley recombinant inbred line population revealed by untargeted GC-MS profiling. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	22
6203	Diet-induced reconstruction of mucosal microbiota associated with alterations of epithelium lectin expression and regulation in the maintenance of rumen homeostasis. <i>Scientific Reports</i> , 2017, 7, 3941.	1.6	5
6204	Integrated analysis of the potential roles of miRNA-mRNA networks in triple negative breast cancer. <i>Molecular Medicine Reports</i> , 2017, 16, 1139-1146.	1.1	18
6205	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	1.6	21
6206	Main and epistatic loci studies in soybean for <i>Sclerotinia sclerotiorum</i> resistance reveal multiple modes of resistance in multi-environments. <i>Scientific Reports</i> , 2017, 7, 3554.	1.6	57

#	ARTICLE	IF	CITATIONS
6207	Transcriptome and metabolome analysis of <i>Ferula gummosa</i> Boiss. to reveal major biosynthetic pathways of galbanum compounds. <i>Functional and Integrative Genomics</i> , 2017, 17, 725-737.	1.4	17
6208	Computational modelling of genome-scale metabolic networks and its application to CHO cell cultures. <i>Computers in Biology and Medicine</i> , 2017, 88, 150-160.	3.9	24
6210	Association of MITF loci with coat color spotting patterns in Ethiopian cattle. <i>Genes and Genomics</i> , 2017, 39, 285-293.	0.5	7
6211	Functional models and extending strategies for ecological networks. <i>Applied Network Science</i> , 2017, 2, 10.	0.8	3
6212	Bioinformatic Approaches Including Predictive Metagenomic Profiling Reveal Characteristics of Bacterial Response to Petroleum Hydrocarbon Contamination in Diverse Environments. <i>Scientific Reports</i> , 2017, 7, 1108.	1.6	135
6213	Deciphering biodiversity and interactions between bacteria and microeukaryotes within epilithic biofilms from the Loue River, France. <i>Scientific Reports</i> , 2017, 7, 4344.	1.6	34
6214	Uterine responses to early pre-attachment embryos in the domestic dog and comparisons with other domestic animal species. <i>Biology of Reproduction</i> , 2017, 97, 197-216.	1.2	22
6215	Meta-analysis of microarray and RNA-Seq gene expression datasets for carcinogenic risk: An assessment of Bisphenol A. <i>Molecular and Cellular Toxicology</i> , 2017, 13, 239-249.	0.8	15
6216	Complex network analysis of thermostable mutants of <i>Bacillus subtilis</i> Lipase A. <i>Applied Network Science</i> , 2017, 2, 18.	0.8	7
6217	Integrated transcriptomics and metabolomics analysis to characterize cold stress responses in <i>Nicotiana tabacum</i> . <i>BMC Genomics</i> , 2017, 18, 496.	1.2	83
6218	Mov10 suppresses retroelements and regulates neuronal development and function in the developing brain. <i>BMC Biology</i> , 2017, 15, 54.	1.7	40
6219	Integrative information theoretic network analysis for genome-wide association study of aspirin exacerbated respiratory disease in Korean population. <i>BMC Medical Genomics</i> , 2017, 10, 31.	0.7	12
6220	Systemic analysis of genome-wide expression profiles identified potential therapeutic targets of demethylation drugs for glioblastoma. <i>Gene</i> , 2017, 627, 387-392.	1.0	3
6221	Isolation of Premyrasinane, Myrsinane, and Tiglane Diterpenoids from <i>Euphorbia pithyusa</i> Using a Chikungunya Virus Cell-Based Assay and Analogue Annotation by Molecular Networking. <i>Journal of Natural Products</i> , 2017, 80, 2051-2059.	1.5	37
6222	Comparative Expression Analysis of Rice and Arabidopsis Peroxiredoxin Genes Suggests Conserved or Diversified Roles Between the Two Species and Leads to the Identification of Tandemly Duplicated Rice Peroxiredoxin Genes Differentially Expressed in Seeds. <i>Rice</i> , 2017, 10, 30.	1.7	20
6223	Comparison of tissue/disease specific integrated networks using directed graphlet signatures. <i>BMC Bioinformatics</i> , 2017, 18, 135.	1.2	9
6224	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. <i>BMC Bioinformatics</i> , 2017, 18, 177.	1.2	53
6225	ATria: a novel centrality algorithm applied to biological networks. <i>BMC Bioinformatics</i> , 2017, 18, 239.	1.2	10

#	ARTICLE	IF	CITATIONS
6226	WebGVI: a web-based gene enrichment analysis and visualization tool. <i>BMC Bioinformatics</i> , 2017, 18, 237.	1.2	12
6227	Microbial composition of spiny ants (Hymenoptera: Formicidae: Polyrhachis) across their geographic range. <i>BMC Evolutionary Biology</i> , 2017, 17, 96.	3.2	42
6228	Active module identification in intracellular networks using a memetic algorithm with a new binary decoding scheme. <i>BMC Genomics</i> , 2017, 18, 209.	1.2	7
6229	Chronic nicotine differentially affects murine transcriptome profiling in isolated cortical interneurons and pyramidal neurons. <i>BMC Genomics</i> , 2017, 18, 194.	1.2	7
6230	Membrane-enriched proteome changes and prion protein expression during neural differentiation and in neuroblastoma cells. <i>BMC Genomics</i> , 2017, 18, 319.	1.2	2
6231	Global analysis of protein lysine succinylation profiles in common wheat. <i>BMC Genomics</i> , 2017, 18, 309.	1.2	46
6232	Label-free quantitative proteomics of <i>Corynebacterium pseudotuberculosis</i> isolates reveals differences between Biovars ovis and equi strains. <i>BMC Genomics</i> , 2017, 18, 451.	1.2	17
6233	Comparative proteomic analysis of <i>Neisseria meningitidis</i> wildtype and dprA null mutant strains links DNA processing to pilus biogenesis. <i>BMC Microbiology</i> , 2017, 17, 96.	1.3	8
6234	Transcriptomic changes reveal gene networks responding to the overexpression of a blueberry DWARF AND DELAYED FLOWERING 1 gene in transgenic blueberry plants. <i>BMC Plant Biology</i> , 2017, 17, 106.	1.6	18
6235	Prior knowledge guided active modules identification: an integrated multi-objective approach. <i>BMC Systems Biology</i> , 2017, 11, 8.	3.0	14
6236	Rewiring of the inferred protein interactome during blood development studied with the tool PPICompare. <i>BMC Systems Biology</i> , 2017, 11, 44.	3.0	6
6237	Network reconstruction of the mouse secretory pathway applied on CHO cell transcriptome data. <i>BMC Systems Biology</i> , 2017, 11, 37.	3.0	14
6238	Systematic identification of an integrative network module during senescence from time-series gene expression. <i>BMC Systems Biology</i> , 2017, 11, 36.	3.0	8
6239	Parameter identifiability analysis and visualization in large-scale kinetic models of biosystems. <i>BMC Systems Biology</i> , 2017, 11, 54.	3.0	92
6240	Exploring the FGFR3-related oncogenic mechanism in bladder cancer using bioinformatics strategy. <i>World Journal of Surgical Oncology</i> , 2017, 15, 66.	0.8	13
6241	Specific circulating microRNA signature of bicuspid aortic valve disease. <i>Journal of Translational Medicine</i> , 2017, 15, 76.	1.8	60
6242	Astrocyte-specific overexpressed gene signatures in response to methamphetamine exposure in vitro. <i>Journal of Neuroinflammation</i> , 2017, 14, 49.	3.1	34
6243	Identification of host cellular proteins that interact with the M protein of a highly pathogenic porcine reproductive and respiratory syndrome virus vaccine strain. <i>Virology Journal</i> , 2017, 14, 39.	1.4	6

#	ARTICLE	IF	CITATIONS
6244	A transcriptome profile in hepatocellular carcinomas based on integrated analysis of microarray studies. <i>Diagnostic Pathology</i> , 2017, 12, 4.	0.9	34
6245	A comparison of gene expression profiles in patients with coronary artery disease, type 2 diabetes, and their coexisting conditions. <i>Diagnostic Pathology</i> , 2017, 12, 44.	0.9	16
6246	Computational dynamic approaches for temporal omics data with applications to systems medicine. <i>BioData Mining</i> , 2017, 10, 20.	2.2	23
6247	Modeling environmental risk factors of autism in mice induces IBD-related gut microbial dysbiosis and hyperserotonemia. <i>Molecular Brain</i> , 2017, 10, 14.	1.3	56
6248	Differential correlation for sequencing data. <i>BMC Research Notes</i> , 2017, 10, 54.	0.6	24
6249	Analyzing the genes related to Alzheimer's disease via a network and pathway-based approach. <i>Alzheimer's Research and Therapy</i> , 2017, 9, 29.	3.0	87
6250	A game-theory modeling approach to utility and strength of interactions dynamics in biomedical research social networks. <i>Complex Adaptive Systems Modeling</i> , 2017, 5, .	1.6	1
6251	QSP Toolbox: Computational Implementation of Integrated Workflow Components for Deploying Multi-Scale Mechanistic Models. <i>AAPS Journal</i> , 2017, 19, 1002-1016.	2.2	47
6252	Shifts in rhizosphere fungal community during secondary succession following abandonment from agriculture. <i>ISME Journal</i> , 2017, 11, 2294-2304.	4.4	177
6253	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. <i>Nature Methods</i> , 2017, 14, 645-646.	9.0	160
6254	Inherited determinants of early recurrent somatic mutations in prostate cancer. <i>Nature Communications</i> , 2017, 8, 48.	5.8	23
6255	Expression and integrated network analyses revealed functional divergence of NHX-type Na <sup>+</sup> /H <sup>+</sup> exchanger genes in poplar. <i>Scientific Reports</i> , 2017, 7, 2607.	1.6	50
6256	Korean Variant Archive (KOVA): a reference database of genetic variations in the Korean population. <i>Scientific Reports</i> , 2017, 7, 4287.	1.6	60
6257	Investigation of association estimators in network inference algorithms on breast cancer proteomic data. , 2017, , .		0
6258	Nutritional metabolomics and breast cancer risk in a prospective study. <i>American Journal of Clinical Nutrition</i> , 2017, 106, 637-649.	2.2	128
6259	Dereplication of natural products from complex extracts by regression analysis and molecular networking: case study of redox-active compounds from <i>Viola alba</i> subsp. <i>dehnhardtii</i> . <i>Metabolomics</i> , 2017, 13, 1.	1.4	12
6260	In silico search of inhibitors of <i>Streptococcus mutans</i> for the control of dental plaque. <i>Archives of Oral Biology</i> , 2017, 83, 68-75.	0.8	4
6261	Protein network construction using reverse phase protein array data. <i>Methods</i> , 2017, 124, 89-99.	1.9	5



#	ARTICLE	IF	CITATIONS
6262	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	6.5	116
6263	Graph theoretical analysis, <i>in silico</i> modeling, design, and synthesis of compounds containing benzimidazole skeleton as antidepressant agents. <i>Chemical Biology and Drug Design</i> , 2017, 89, 714-722.	1.5	11
6264	Dereplication of Flavonoid Glycoconjugates from <i>Adenocalymma imperatoris-maximilianii</i> by Untargeted Tandem Mass Spectrometry-Based Molecular Networking. <i>Planta Medica</i> , 2017, 83, 636-646.	0.7	29
6265	Cancer-associated fibroblasts regulate keratinocyte cell-cell adhesion via TGF- $\beta$ -dependent pathways in genotype-specific oral cancer. <i>Carcinogenesis</i> , 2017, 38, 76-85.	1.3	40
6266	Proteomes and Ubiquitylomes Analysis Reveals the Involvement of Ubiquitination in Protein Degradation in <i>Petunias</i> . <i>Plant Physiology</i> , 2017, 173, 668-687.	2.3	80
6267	Analysis of the interplay between methylation and expression reveals its potential role in cancer aetiology. <i>Functional and Integrative Genomics</i> , 2017, 17, 53-68.	1.4	14
6268	Bridging the gap between morphological species and molecular barcodes – Exemplified by loricate choanoflagellates. <i>European Journal of Protistology</i> , 2017, 57, 26-37.	0.5	26
6269	Visualization and Analysis of miRNA-Targets Interactions Networks. <i>Methods in Molecular Biology</i> , 2017, 1509, 209-220.	0.4	16
6270	Anti-obesity effect of radix <i>Angelica sinensis</i> and candidate causative genes in transcriptome analyses of adipose tissues in high-fat diet-induced mice. <i>Gene</i> , 2017, 599, 92-98.	1.0	14
6271	Expression Data Analysis for the Identification of Potential Biomarker of Pregnancy Associated Breast Cancer. <i>Pathology and Oncology Research</i> , 2017, 23, 537-544.	0.9	8
6272	Molecular alterations in bone marrow mesenchymal stromal cells derived from acute myeloid leukemia patients. <i>Leukemia</i> , 2017, 31, 1069-1078.	3.3	81
6273	Molecular Networking As a Drug Discovery, Drug Metabolism, and Precision Medicine Strategy. <i>Trends in Pharmacological Sciences</i> , 2017, 38, 143-154.	4.0	250
6274	Identifying miRNA regulatory mechanisms in preeclampsia by systems biology approaches. <i>Hypertension in Pregnancy</i> , 2017, 36, 90-99.	0.5	28
6275	Does organically produced lettuce harbor higher abundance of antibiotic resistance genes than conventionally produced?. <i>Environment International</i> , 2017, 98, 152-159.	4.8	205
6276	Global gene expression profile of peripheral blood mononuclear cells challenged with <i>Theileria annulata</i> in crossbred and indigenous cattle. <i>Infection, Genetics and Evolution</i> , 2017, 47, 9-18.	1.0	13
6277	Proteomic and physiological approach reveals drought-induced changes in rapeseeds: Water-saver and water-spender strategy. <i>Journal of Proteomics</i> , 2017, 152, 188-205.	1.2	39
6278	Domain-agnostic discovery of similarities and concepts at scale. <i>Knowledge and Information Systems</i> , 2017, 51, 531-560.	2.1	2
6279	Weighted Epistatic Analysis of NSAIDs Hypersensitivity Data. <i>Engineering Applications of Artificial Intelligence</i> , 2017, 62, 312-319.	4.3	0

#	ARTICLE	IF	CITATIONS
6280	Differentially Expressed Long Non-Coding RNAs Were Predicted to Be Involved in the Control of Signaling Pathways in Pediatric Astrocytoma. <i>Molecular Neurobiology</i> , 2017, 54, 6598-6608.	1.9	10
6281	Gut content microbiota of introduced bigheaded carps ( <i>Hypophthalmichthys</i> spp.) inhabiting the largest shallow lake in Central Europe. <i>Microbiological Research</i> , 2017, 195, 40-50.	2.5	25
6282	Environmental spread of microbes impacts the development of metabolic phenotypes in mice transplanted with microbial communities from humans. <i>ISME Journal</i> , 2017, 11, 676-690.	4.4	63
6283	Prediction of microRNAs involved in immune system diseases through network based features. <i>Journal of Biomedical Informatics</i> , 2017, 65, 34-45.	2.5	9
6284	Transforming growth factor- $\beta$ 1 regulation of ATF-3, c-Jun and JunB proteins for activation of matrix metalloproteinase-13 gene in human breast cancer cells. <i>International Journal of Biological Macromolecules</i> , 2017, 94, 370-377.	3.6	31
6285	PROFEAT Update: A Protein Features Web Server with Added Facility to Compute Network Descriptors for Studying Omics-Derived Networks. <i>Journal of Molecular Biology</i> , 2017, 429, 416-425.	2.0	36
6286	Seasonality of freshwater bacterioplankton diversity in two tropical shallow lakes from the Brazilian Atlantic Forest. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw218.	1.3	31
6287	Spatial and temporal structure of the clinical research based on mesenchymal stromal cells: A network analysis. <i>Cytotherapy</i> , 2017, 19, 47-60.	0.3	3
6288	MicroRNA and protein profiles in invasive versus non-invasive oral tongue squamous cell carcinoma cells in vitro. <i>Experimental Cell Research</i> , 2017, 350, 9-18.	1.2	16
6289	Spinal Cord Transcriptomic and Metabolomic Analysis after Excitotoxic Injection Injury Model of Syringomyelia. <i>Journal of Neurotrauma</i> , 2017, 34, 720-733.	1.7	18
6290	ASEAN centrality amidst economic integration in the Asia Pacific region. <i>Journal of the Asia Pacific Economy</i> , 2017, 22, 273-290.	1.0	5
6291	Positive cooperative regulation of double binding sites for human acetylcholinesterase. <i>Chemical Biology and Drug Design</i> , 2017, 89, 694-704.	1.5	9
6292	Identification of the miRNA-mRNA regulatory network in multiple sclerosis. <i>Neurological Research</i> , 2017, 39, 142-151.	0.6	42
6293	Network Pharmacology. , 2017, , 127-164.		61
6294	Identification of upstream transcription factors (TFs) for expression signature genes in breast cancer. <i>Gynecological Endocrinology</i> , 2017, 33, 193-198.	0.7	14
6295	Changes in mammary histology and transcriptome profiles by low-dose exposure to environmental phenols at critical windows of development. <i>Environmental Research</i> , 2017, 152, 233-243.	3.7	26
6296	PhenoStacks: Cross-Sectional Cohort Phenotype Comparison Visualizations. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2017, 23, 191-200.	2.9	19
6297	Global molecular changes in a tibial compression induced ACL rupture model of post-traumatic osteoarthritis. <i>Journal of Orthopaedic Research</i> , 2017, 35, 474-485.	1.2	48

#	ARTICLE	IF	CITATIONS
6298	Identification of Transcription Factor-Gene Regulatory Network in Acute Myocardial Infarction. <i>Heart Lung and Circulation</i> , 2017, 26, 343-353.	0.2	11
6299	Network ethnopharmacological evaluation of the immunomodulatory activity of <i>Withania somnifera</i> . <i>Journal of Ethnopharmacology</i> , 2017, 197, 250-256.	2.0	64
6300	CD4-gp120 interaction interface - a gateway for HIV-1 infection in human: molecular network, modeling and docking studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2631-2644.	2.0	5
6301	Antigen-presenting human B cells are expanded in inflammatory conditions. <i>Journal of Leukocyte Biology</i> , 2017, 101, 577-587.	1.5	28
6302	Omics to Explore Amyotrophic Lateral Sclerosis Evolution: the Central Role of Arginine and Proline Metabolism. <i>Molecular Neurobiology</i> , 2017, 54, 5361-5374.	1.9	40
6303	Combined Analysis of ChIP Sequencing and Gene Expression Dataset in Breast Cancer. <i>Pathology and Oncology Research</i> , 2017, 23, 361-368.	0.9	14
6304	The "heritability"™ of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017, 118, 160-168.	1.2	7
6305	Antibiotics and iron-limiting conditions and their effect on the production and composition of outer membrane vesicles secreted from clinical isolates of extraintestinal pathogenic <i>E. coli</i> . <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600091.	0.8	20
6306	MicroRNA mediated network motifs in autoimmune diseases and its crosstalk between genes, functions and pathways. <i>Journal of Immunological Methods</i> , 2017, 440, 19-26.	0.6	18
6307	Key species and impact of fishery through food web analysis: A case study from Baja California Sur, Mexico. <i>Journal of Marine Systems</i> , 2017, 165, 92-102.	0.9	18
6308	Determination of differentially regulated proteins upon proteasome inhibition in AML cell lines by the combination of large-scale and targeted quantitative proteomics. <i>Proteomics</i> , 2017, 17, 1600089.	1.3	11
6309	Relation of Transcriptional Factors to the Expression and Activity of Cytochrome P450 and UDP-Glucuronosyltransferases 1A in Human Liver: Co-Expression Network Analysis. <i>AAPS Journal</i> , 2017, 19, 203-214.	2.2	14
6310	Network analyses reveal intra- and interspecific differences in behaviour when passing a complex migration obstacle. <i>Journal of Applied Ecology</i> , 2017, 54, 836-845.	1.9	10
6311	Efficacy of ARACNE algorithm for inferring canine B-cell lymphoma gene regulatory network (GRN). <i>Comparative Clinical Pathology</i> , 2017, 26, 121-125.	0.3	1
6312	In-Depth Cerebrospinal Fluid Quantitative Proteome and Deglycoproteome Analysis: Presenting a Comprehensive Picture of Pathways and Processes Affected by Multiple Sclerosis. <i>Journal of Proteome Research</i> , 2017, 16, 179-194.	1.8	29
6313	RelSim: An integrated method to identify disease genes using gene expression profiles and PPIN based similarity measure. <i>Information Sciences</i> , 2017, 384, 110-125.	4.0	26
6314	Structural insight into GRIP1-PDZ6 in Alzheimer's™ disease: study from protein expression data to molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2235-2247.	2.0	3
6315	Bioinformatics exploration of PAK1 (P21-activated kinase-1) revealed potential network gene elements in breast invasive carcinoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2269-2279.	2.0	7

#	ARTICLE	IF	CITATIONS
6316	Pediatric obesity is associated with an altered gut microbiota and discordant shifts in <sc>Firmicutes</sc> populations. <i>Environmental Microbiology</i> , 2017, 19, 95-105.	1.8	326
6317	Gene Expression Profile of Extracellular Matrix and Adhesion Molecules in the Human Normal Corneal Stroma. <i>Current Eye Research</i> , 2017, 42, 520-527.	0.7	7
6318	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	107
6319	Genomic diversity in <i>Onchocerca volvulus</i> and its <i>Wolbachia</i> endosymbiont. <i>Nature Microbiology</i> , 2017, 2, 16207.	5.9	53
6320	Dual-specificity phosphatase 6 deficiency regulates gut microbiome and transcriptome response against diet-induced obesity in mice. <i>Nature Microbiology</i> , 2017, 2, 16220.	5.9	47
6321	Profiling the Serum Albumin Cys34 Adductome of Solid Fuel Users in Xuanwei and Fuyuan, China. <i>Environmental Science &amp; Technology</i> , 2017, 51, 46-57.	4.6	33
6322	Systems Genetics Identifies a Novel Regulatory Domain of Amylose Synthesis. <i>Plant Physiology</i> , 2017, 173, 887-906.	2.3	71
6323	Visualization of Biomolecular Structures: State of the Art Revisited. <i>Computer Graphics Forum</i> , 2017, 36, 178-204.	1.8	69
6324	Drought-related secondary metabolites of barley ( <i>Hordeum vulgare</i> L.) leaves and their metabolomic quantitative trait loci. <i>Plant Journal</i> , 2017, 89, 898-913.	2.8	83
6325	Genomic amplification of Fanconi anemia complementation group A (FancA) in head and neck squamous cell carcinoma (HNSCC): Cellular mechanisms of radioresistance and clinical relevance. <i>Cancer Letters</i> , 2017, 386, 87-99.	3.2	21
6326	Identification of clinically predictive metagenes that encode components of a network coupling cell shape to transcription by image-omics. <i>Genome Research</i> , 2017, 27, 196-207.	2.4	33
6327	Proteome and Secretome Characterization of Glioblastoma-Derived Neural Stem Cells. <i>Stem Cells</i> , 2017, 35, 967-980.	1.4	40
6328	Network pharmacology-based study on the mechanism of action for herbal medicines in Alzheimer treatment. <i>Journal of Ethnopharmacology</i> , 2017, 196, 281-292.	2.0	96
6329	A network biology approach to understanding the importance of chameleon proteins in human physiology and pathology. <i>Amino Acids</i> , 2017, 49, 303-315.	1.2	3
6330	Identification of new key genes for type 1 diabetes through construction and analysis of protein-protein interaction networks based on blood and pancreatic islet transcriptomes. <i>Journal of Diabetes</i> , 2017, 9, 764-777.	0.8	43
6331	Coupling between ATP hydrolysis and protein conformational change in maltose transporter. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 207-220.	1.5	0
6332	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	1.4	34
6333	Extracellular vesicles released by hepatocytes from gastric infusion model of alcoholic liver disease contain a MicroRNA barcode that can be detected in blood. <i>Hepatology</i> , 2017, 65, 475-490.	3.6	91

#	ARTICLE	IF	CITATIONS
6334	Integrative genomic and network analysis identified novel genes associated with the development of advanced cervical squamous cell carcinoma. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2899-2911.	1.1	9
6335	Phylogenomic networks reveal limited phylogenetic range of lateral gene transfer by transduction. <i>ISME Journal</i> , 2017, 11, 543-554.	4.4	81
6336	Microbial co-presence and mutual-exclusion networks in the Bovine rumen microbiome. , 2017, , .		3
6337	Harnessing the microbiomes of Brassica vegetables for health issues. <i>Scientific Reports</i> , 2017, 7, 17649.	1.6	47
6338	Identifying hub genes and potential mechanisms associated with senescence in human annulus cells by gene expression profiling and bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 17, 3465-3472.	1.1	4
6339	The epitranscriptome m6A writer METTL3 promotes chemo- and radioresistance in pancreatic cancer cells. <i>International Journal of Oncology</i> , 2018, 52, 621-629.	1.4	231
6340	RNA sequencing uncovers the key microRNAs potentially contributing to sudden sensorineural hearing loss. <i>Medicine (United States)</i> , 2017, 96, e8837.	0.4	21
6341	An RNA-Seq Bioinformatics Pipeline for Data Processing of Arabidopsis Thaliana Datasets. , 2017, , .		0
6342	Network-based visualization tool for analyzing gene expression data. , 2017, , .		0
6343	Rapid Communication: MicroRNA co-expression network reveals apoptosis in the reproductive tract during molting in laying hens <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2017, 95, 5100-5104.	0.2	2
6344	Learning reference-enriched approach towards large scale active ontology alignment and integration. , 2017, , .		1
6345	Identification of candidate genes that may contribute to the metastasis of prostate cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2018, 15, 1220-1228.	0.8	8
6346	Identify Biological Modules and Hub MiRNAs for Oral Squamous Cell Carcinomas. , 2017, , .		0
6347	A New Way of Visualizing Curricula Using Competencies: Cosine Similarity, Multidimensional Scaling Methods, and Scatter Plotting. , 2017, , .		12
6348	Analysis of expression profile data identifies key genes and pathways in hepatocellular carcinoma. <i>Oncology Letters</i> , 2018, 15, 2625-2630.	0.8	6
6349	Functional and evolutionary analysis of Korean bob-tailed native dog using whole-genome sequencing data. <i>Scientific Reports</i> , 2017, 7, 17303.	1.6	4
6350	Bio-Docklets: virtualization containers for single-step execution of NGS pipelines. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	12
6351	Genome expression profiling predicts the molecular mechanism of peripheral myelination. <i>International Journal of Molecular Medicine</i> , 2017, 41, 1500-1508.	1.8	8

#	ARTICLE	IF	CITATIONS
6352	WRKY transcription factors and regulation of the stilbene biosynthetic pathway in grapevine: new insights and perspectives. <i>Acta Horticulturae</i> , 2017, , 1-8.	0.1	0
6353	A Global Interactome Map of the Dengue Virus NS1 Identifies Virus Restriction and Dependency Host Factors. <i>Cell Reports</i> , 2017, 21, 3900-3913.	2.9	90
6354	Identification of regulatory role of DNA methylation in colon cancer gene expression via systematic bioinformatics analysis. <i>Medicine (United States)</i> , 2017, 96, e8487.	0.4	18
6355	A novel correlation between ATP5A1 gene expression and progression of human clear cell renal cell carcinoma identified by co-expression analysis. <i>Oncology Reports</i> , 2018, 39, 525-536.	1.2	20
6356	Analyzing the Effect of V66M Mutation in BDNF in Causing Mood Disorders. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017, 108, 85-103.	1.0	6
6357	Genetic Architecture and Candidate Genes Identified for Follicle Number in Chicken. <i>Scientific Reports</i> , 2017, 7, 16412.	1.6	18
6358	Temporal dynamics of bacterial communities and predicted nitrogen metabolism genes in a full-scale wastewater treatment plant. <i>RSC Advances</i> , 2017, 7, 56317-56327.	1.7	68
6359	Robust method for identification of prognostic gene signatures from gene expression profiles. <i>Scientific Reports</i> , 2017, 7, 16926.	1.6	7
6360	Improved detection of synthetic lethal interactions in <i>Drosophila</i> cells using variable dose analysis (VDA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10755-E10762.	3.3	8
6361	Identification of key pathways and genes in Barrett's esophagus using integrated bioinformatics methods. <i>Molecular Medicine Reports</i> , 2017, 17, 3069-3077.	1.1	2
6362	RNA sequencing provides insights into the evolution of lettuce and the regulation of flavonoid biosynthesis. <i>Nature Communications</i> , 2017, 8, 2264.	5.8	133
6363	Enhancement mechanisms of short-time aerobic digestion for waste activated sludge in the presence of cocoamidopropyl betaine. <i>Scientific Reports</i> , 2017, 7, 13491.	1.6	27
6364	Metabolomic investigation into molecular mechanisms of a clinical herb prescription against metabolic syndrome by a systematic approach. <i>RSC Advances</i> , 2017, 7, 55389-55399.	1.7	3
6365	Multiscale dynamic visualization of signal transduction processes with detailing of target-genes activation in three-dimensional genome structure. <i>Procedia Computer Science</i> , 2017, 119, 182-189.	1.2	0
6366	Ras/MAPK Modifier Loci Revealed by eQTL in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3185-3193.	0.8	38
6367	LncRNA profiling of skeletal muscles in Large White pigs and Mashen pigs during development <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2017, 95, 4239-4250.	0.2	47
6368	Microbiota Diversification and Crash Induced by Dietary Oxalate in the Mammalian Herbivore <i>Neotoma albigula</i> . <i>MSphere</i> , 2017, 2, .	1.3	22
6369	Phosphoproteomics of cAMP signaling of Bordetella adenylate cyclase toxin in mouse dendritic cells. <i>Scientific Reports</i> , 2017, 7, 16298.	1.6	7

#	ARTICLE	IF	CITATIONS
6370	Conserved Transcription Factors Steer Growth-Related Genomic Programs in Daphnia. <i>Genome Biology and Evolution</i> , 2017, 9, 1821-1842.	1.1	13
6371	A METHYLATION-TO-EXPRESSION FEATURE MODEL FOR GENERATING ACCURATE PROGNOSTIC RISK SCORES AND IDENTIFYING DISEASE TARGETS IN CLEAR CELL KIDNEY CANCER. , 2017, 22, 509-520.		4
6372	Bioinformatics analysis of gene expression profiles to identify causal genes in luminal B2 breast cancer. <i>Oncology Letters</i> , 2017, 14, 7880-7888.	0.8	10
6373	The JASMONATE ZIM-Domain Gene Family Mediates JA Signaling and Stress Response in Cotton. <i>Plant and Cell Physiology</i> , 2017, 58, 2139-2154.	1.5	70
6374	Ash leaf metabolomes reveal differences between trees tolerant and susceptible to ash dieback disease. <i>Scientific Data</i> , 2017, 4, 170190.	2.4	13
6375	Integration of miRNA and gene expression profiles suggest a role for miRNAs in the pathobiological processes of acute <i>Trypanosoma cruzi</i> infection. <i>Scientific Reports</i> , 2017, 7, 17990.	1.6	46
6376	Organoids model distinct Vitamin E effects at different stages of prostate cancer evolution. <i>Scientific Reports</i> , 2017, 7, 16285.	1.6	19
6377	Profiles of differentially expressed genes and overexpression of NEBL indicates a positive prognosis in patients with colorectal cancer. <i>Molecular Medicine Reports</i> , 2018, 17, 3028-3034.	1.1	8
6378	Fibroblasts play a potential role in bone destruction via osteopontin related caldesmon expression and polymerization in human non-functioning pituitary adenomas. <i>Scientific Reports</i> , 2017, 7, 17523.	1.6	7
6379	Sex differences in microRNA-mRNA networks: examination of novel epigenetic programming mechanisms in the sexually dimorphic neonatal hypothalamus. <i>Biology of Sex Differences</i> , 2017, 8, 27.	1.8	27
6380	Whole metagenome profiles of particulates collected from the International Space Station. <i>Microbiome</i> , 2017, 5, 81.	4.9	54
6382	Exploring Online Ad Images Using a Deep Convolutional Neural Network Approach. , 2017, , .		6
6383	Modelling Multimedia Social Networks Using Semantically Labelled Graphs. , 2017, , .		7
6384	An integrated framework for verifying multiple care pathways. , 2017, , .		6
6385	Connectivity development for binary classifier using neuron cultures. , 2017, , .		0
6386	A combinatorial approach to construct core and generic gene co-expression networks of colon cancer. , 2017, , .		1
6387	Proteomic and bioinformatics analysis of human saliva for the dental-risk assessment. <i>Open Life Sciences</i> , 2017, 12, 248-265.	0.6	2
6388	Transcriptome analysis reveals differences in mechanisms regulating cessation of luteal function in pregnant and non-pregnant dogs. <i>BMC Genomics</i> , 2017, 18, 757.	1.2	26



#	ARTICLE	IF	CITATIONS
6389	Genome variation and conserved regulation identify genomic regions responsible for strain specific phenotypes in rat. BMC Genomics, 2017, 18, 986.	1.2	3
6390	Genome-wide computational analysis of potential long noncoding RNA mediated DNA:DNA:RNA triplexes in the human genome. Journal of Translational Medicine, 2017, 15, 186.	1.8	30
6391	Deciphering the genetic regulation of peripheral blood transcriptome in pigs through expression genome-wide association study and allele-specific expression analysis. BMC Genomics, 2017, 18, 967.	1.2	22
6392	Iterative Design and Evaluation of Regulatory Network Visualisation at Scale. , 2017, , .		1
6393	NDlib: Studying Network Diffusion Dynamics. , 2017, , .		8
6394	Functional protein networks underlying the comorbidity of gout and hyperuricemia. , 2017, , .		0
6395	Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , .		0
6396	Functional protein-protein interaction networks regulated by 6-gingerol targeting stomach and small intestine. , 2017, , .		1
6397	A mutational co-occurrence network of a stomach adenocarcinoma using an association index. , 2017, , .		1
6398	OSG-KINC: High-throughput gene co-expression network construction using the open science grid. , 2017, , .		6
6399	Evaluation of the oral microbiome as a biomarker for early detection of human oral carcinomas. , 2017, , .		2
6400	The ontology reference model for visual selectivity analysis in drug-target interactions. , 2017, , .		1
6401	A network-based approach to mine temporal genes exhibiting significant expression variation in Caenorhabditis elegans. , 2017, , .		0
6402	Digestive functions regulated by 6-shogaol towards stomach and small intestine. , 2017, , .		0
6403	GUIdock-VNC: Using a graphical desktop sharing system to provide a browser-based interface for containerized software. GigaScience, 2017, 6, 1-6.	3.3	6
6404	Bioinformatic analysis of gene expression profiles of pituitary gonadotroph adenomas. Oncology Letters, 2017, 15, 1655-1663.	0.8	10
6405	Co-expression networks between protein encoding mitochondrial genes and all the remaining genes in human tissues. , 2017, , .		0
6406	Bioinformatical analysis of gene expression signatures of different glioma subtypes. Oncology Letters, 2017, 15, 2807-2814.	0.8	7

#	ARTICLE	IF	CITATIONS
6407	Graphical Modeling Meets Systems Pharmacology. <i>Gene Regulation and Systems Biology</i> , 2017, 11, 117762501769193.	2.3	4
6408	Multiple network-constrained regressions expand insights into influenza vaccination responses. <i>Bioinformatics</i> , 2017, 33, i208-i216.	1.8	9
6409	How new tertiary cardiac centers influence care provider network. , 2017, , .		0
6410	Network analysis of inter-organizational success factor relationships. , 2017, , .		0
6411	Uncovering the relationship and mechanisms of Tartary buckwheat ( <i>Fagopyrum tataricum</i> ) and Type II diabetes, hypertension, and hyperlipidemia using a network pharmacology approach. <i>PeerJ</i> , 2017, 5, e4042.	0.9	19
6412	Network analysis of the genomic basis of the placebo effect. <i>JCI Insight</i> , 2017, 2, .	2.3	37
6413	Er:YAG Laser and Cyclosporin A Effect on Cell Cycle Regulation of Human Gingival Fibroblast Cells. <i>Journal of Lasers in Medical Sciences</i> , 2017, 8, 143-149.	0.4	32
6414	Identification of laryngeal cancer prognostic biomarkers using an inflammatory gene-related, competitive endogenous RNA network. <i>Oncotarget</i> , 2017, 8, 9525-9534.	0.8	19
6415	Identifying prognostic biomarkers based on aberrant DNA methylation in kidney renal clear cell carcinoma. <i>Oncotarget</i> , 2017, 8, 5268-5280.	0.8	19
6416	Identification of potential prognostic ceRNA module biomarkers in patients with pancreatic adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 94493-94504.	0.8	15
6417	Node Formation. , 2017, , .		2
6418	Network Analysis of Obesity Expression Data. , 2017, , .		0
6419	Comprehensive Network Analysis of Cancer Stem Cell Signalling through Systematic Integration of Post-Translational Modification Dynamics. , 0, , .		0
6420	Computational Modeling of Complex Protein Activity Networks. , 0, , .		1
6421	Computational Identification of Indispensable Virulence Proteins of Salmonella Typhi CT18. , 0, , .		9
6422	Gene correction of HAX1 reversed Kostmann disease phenotype in patient-specific induced pluripotent stem cells. <i>Blood Advances</i> , 2017, 1, 903-914.	2.5	18
6423	Macrophages and osteoclasts stem from a bipotent progenitor downstream of a macrophage/osteoclast/dendritic cell progenitor. <i>Blood Advances</i> , 2017, 1, 1993-2006.	2.5	36
6424	Incorporating interaction networks into the determination of functionally related hit genes in genomic experiments with Markov random fields. <i>Bioinformatics</i> , 2017, 33, i170-i179.	1.8	13

#	ARTICLE	IF	CITATIONS
6425	Bioinformatic Analysis Of Coronary Disease Associated SNPs And Genes To Identify Proteins Potentially Involved In The Pathogenesis Of Atherosclerosis. <i>Journal of Proteomics and Genomics Research</i> , 2017, 2, 1-12.	0.7	10
6426	Dammarane Sapogenins Ameliorates Neurocognitive Functional Impairment Induced by Simulated Long-Duration Spaceflight. <i>Frontiers in Pharmacology</i> , 2017, 8, 315.	1.6	42
6427	Global Metabolomics Reveals the Metabolic Dysfunction in Ox-LDL Induced Macrophage-Derived Foam Cells. <i>Frontiers in Pharmacology</i> , 2017, 8, 586.	1.6	15
6428	Multi-Level Integration of Environmentally Perturbed Internal Phenotypes Reveals Key Points of Connectivity between Them. <i>Frontiers in Physiology</i> , 2017, 8, 388.	1.3	4
6429	Formal Modeling of mTOR Associated Biological Regulatory Network Reveals Novel Therapeutic Strategy for the Treatment of Cancer. <i>Frontiers in Physiology</i> , 2017, 8, 416.	1.3	4
6430	Identification of Biomarkers Correlated with the TNM Staging and Overall Survival of Patients with Bladder Cancer. <i>Frontiers in Physiology</i> , 2017, 8, 947.	1.3	104
6431	Co-expression Network Approach Reveals Functional Similarities among Diseases Affecting Human Skeletal Muscle. <i>Frontiers in Physiology</i> , 2017, 8, 980.	1.3	19
6432	Time-Series Analyses of Transcriptomes and Proteomes Reveal Molecular Networks Underlying Oil Accumulation in Canola. <i>Frontiers in Plant Science</i> , 2016, 07, 2007.	1.7	30
6433	Metabolite Profiling of adh1 Mutant Response to Cold Stress in Arabidopsis. <i>Frontiers in Plant Science</i> , 2016, 7, 2072.	1.7	42
6434	Community Structure, Species Variation, and Potential Functions of Rhizosphere-Associated Bacteria of Different Winter Wheat ( <i>Triticum aestivum</i> ) Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 132.	1.7	137
6435	Comprehensive Analysis of the CDPK-SnRK Superfamily Genes in Chinese Cabbage and Its Evolutionary Implications in Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 162.	1.7	41
6436	Mass Spectrometry Based Molecular 3D-Cartography of Plant Metabolites. <i>Frontiers in Plant Science</i> , 2017, 8, 429.	1.7	24
6437	Identification of Candidate Genes and Biosynthesis Pathways Related to Fertility Conversion by Wheat KTM3315A Transcriptome Profiling. <i>Frontiers in Plant Science</i> , 2017, 8, 449.	1.7	31
6438	A Quantitative Proteomic Analysis of Brassinosteroid-induced Protein Phosphorylation in Rice ( <i>Oryza</i> ) Tj ETQq1 1 0,784314 rgBT /Overlo	1.7	24
6439	Light-induced Variation in Phenolic Compounds in Cabernet Sauvignon Grapes ( <i>Vitis vinifera</i> L.) Involves Extensive Transcriptome Reprogramming of Biosynthetic Enzymes, Transcription Factors, and Phytohormonal Regulators. <i>Frontiers in Plant Science</i> , 2017, 8, 547.	1.7	98
6440	OsPhyB-Mediating Novel Regulatory Pathway for Drought Tolerance in Rice Root Identified by a Global RNA-Seq Transcriptome Analysis of Rice Genes in Response to Water Deficiencies. <i>Frontiers in Plant Science</i> , 2017, 8, 580.	1.7	56
6441	Differences in Flower Transcriptome between Grapevine Clones Are Related to Their Cluster Compactness, Fruitfulness, and Berry Size. <i>Frontiers in Plant Science</i> , 2017, 8, 632.	1.7	37
6442	Transcriptome Analyses Reveal Candidate Pod Shattering-Associated Genes Involved in the Pod Ventral Sutures of Common Vetch ( <i>Vicia sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 649.	1.7	53

#	ARTICLE	IF	CITATIONS
6443	Transcriptomic Identification of Drought-Related Genes and SSR Markers in Sudan Grass Based on RNA-Seq. <i>Frontiers in Plant Science</i> , 2017, 8, 687.	1.7	14
6444	Discovery of Putative Herbicide Resistance Genes and Its Regulatory Network in Chickpea Using Transcriptome Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 958.	1.7	21
6445	Identification of Two New Mechanisms That Regulate Fruit Growth by Cell Expansion in Tomato. <i>Frontiers in Plant Science</i> , 2017, 8, 988.	1.7	25
6446	Co-overexpression of the Constitutively Active Form of OsZIP46 and ABA-Activated Protein Kinase SAPK6 Improves Drought and Temperature Stress Resistance in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1102.	1.7	68
6447	<i>Neofusicoccum parvum</i> Colonization of the Grapevine Woody Stem Triggers Asynchronous Host Responses at the Site of Infection and in the Leaves. <i>Frontiers in Plant Science</i> , 2017, 8, 1117.	1.7	37
6448	Multi-Omics and Integrated Network Analyses Reveal New Insights into the Systems Relationships between Metabolites, Structural Genes, and Transcriptional Regulators in Developing Grape Berries ( <i>Vitis vinifera</i> L.) Exposed to Water Deficit. <i>Frontiers in Plant Science</i> , 2017, 8, 1124.	1.7	108
6449	QTL Mapping for Pest and Disease Resistance in Cassava and Coincidence of Some QTL with Introgression Regions Derived from <i>Manihot glaziovii</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1168.	1.7	51
6450	Unraveling Key Metabolomic Alterations in Wheat Embryos Derived from Freshly Harvested and Water-Imbibed Seeds of Two Wheat Cultivars with Contrasting Dormancy Status. <i>Frontiers in Plant Science</i> , 2017, 8, 1203.	1.7	23
6451	Evolution of Daily Gene Co-expression Patterns from Algae to Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1217.	1.7	26
6452	Tissue-Specific Floral Transcriptome Analysis of the Sexually Deceptive Orchid <i>Chiloglottis trapeziformis</i> Provides Insights into the Biosynthesis and Regulation of Its Unique UV-B Dependent Floral Volatile, Chiloglottone 1. <i>Frontiers in Plant Science</i> , 2017, 8, 1260.	1.7	18
6453	Potassium in the Grape ( <i>Vitis vinifera</i> L.) Berry: Transport and Function. <i>Frontiers in Plant Science</i> , 2017, 8, 1629.	1.7	107
6454	Assembly and Annotation of Transcriptome Provided Evidence of miRNA Mobility between Wheat and Wheat Stem Sawfly. <i>Frontiers in Plant Science</i> , 2017, 8, 1653.	1.7	18
6455	Comparative UAV and Field Phenotyping to Assess Yield and Nitrogen Use Efficiency in Hybrid and Conventional Barley. <i>Frontiers in Plant Science</i> , 2017, 8, 1733.	1.7	136
6456	Abiotic Stress Responsive miRNA-Target Network and Related Markers (SNP, SSR) in <i>Brassica juncea</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1943.	1.7	39
6457	Unravelling Protein-Protein Interaction Networks Linked to Aliphatic and Indole Glucosinolate Biosynthetic Pathways in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2028.	1.7	21
6458	Integrative View of the Diversity and Evolution of SWEET and SemiSWEET Sugar Transporters. <i>Frontiers in Plant Science</i> , 2017, 8, 2178.	1.7	54
6459	Salicylic Acid Perturbs sRNA-Gibberellin Regulatory Network in Immune Response of Potato to Potato virus Y Infection. <i>Frontiers in Plant Science</i> , 2017, 8, 2192.	1.7	41
6460	Application of Proteomics to Medical Diagnostics. , 2017, , 233-248.		0

#	ARTICLE	IF	CITATIONS
6461	iTRAQ-Based Proteomics Analysis and Network Integration for Kernel Tissue Development in Maize. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1840.	1.8	12
6462	Metabolomics Identifies Metabolic Markers of Maturation in Human Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Theranostics</i> , 2017, 7, 2078-2091.	4.6	31
6463	Biological networks in Parkinson's disease: an insight into the epigenetic mechanisms associated with this disease. <i>BMC Genomics</i> , 2017, 18, 721.	1.2	31
6464	Identification of DNA methylation associated gene signatures in endometrial cancer via integrated analysis of DNA methylation and gene expression systematically. <i>Journal of Gynecologic Oncology</i> , 2017, 28, e83.	1.0	65
6465	Genome-wide characterization of the aldehyde dehydrogenase gene superfamily in soybean and its potential role in drought stress response. <i>BMC Genomics</i> , 2017, 18, 518.	1.2	59
6466	Type 1 Diabetes: Urinary Proteomics and Protein Network Analysis Support Perturbation of Lysosomal Function. <i>Theranostics</i> , 2017, 7, 2704-2717.	4.6	30
6467	Weighted gene co-expression network analysis in identification of metastasis-related genes of lung squamous cell carcinoma based on the Cancer Genome Atlas database. <i>Journal of Thoracic Disease</i> , 2017, 9, 42-53.	0.6	48
6468	Sunflower Leaf Senescence: A Complex Genetic Process with Economic Impact on Crop Production. , 0, , .		2
6469	Clinical significance and prospective molecular mechanism of MALAT1 in pancreatic cancer exploration: a comprehensive study based on the GeneChip, GEO, Oncomine, and TCGA databases. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3991-4005.	1.0	31
6470	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017, 18, 723.	1.2	51
6471	The landscape of DNA methylation-mediated regulation of long non-coding RNAs in breast cancer. <i>Oncotarget</i> , 2017, 8, 51134-51150.	0.8	12
6472	Synteny analysis of genes and distribution of loci controlling oil content and fatty acid profile based on QTL alignment map in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2017, 18, 776.	1.2	34
6473	<i>Mycobacterium tuberculosis</i> Transmission among Elderly Persons, Yamagata Prefecture, Japan, 2009-2015. <i>Emerging Infectious Diseases</i> , 2017, 23, 448-455.	2.0	29
6474	Identification of microRNAs associated with medullary thyroid carcinoma by bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2017, 15, 4266-4272.	1.1	4
6475	Systematic module approach identifies altered genes and pathways in four types of ovarian cancer. <i>Molecular Medicine Reports</i> , 2017, 16, 7907-7914.	1.1	2
6476	Comparative muscle transcriptome associated with carcass traits of Nellore cattle. <i>BMC Genomics</i> , 2017, 18, 506.	1.2	51
6477	Exploration of the molecular mechanism of prostate cancer based on mRNA and miRNA expression profiles. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3225-3232.	1.0	11
6478	Genome-scale analysis to identify prognostic markers in patients with early-stage pancreatic ductal adenocarcinoma after pancreaticoduodenectomy. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 4493-4506.	1.0	82

#	ARTICLE	IF	CITATIONS
6479	Genome-Wide Identification and Characterization of the GmSnRK2 Family in Soybean. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1834.	1.8	30
6480	Discovering the Deregulated Molecular Functions Involved in Malignant Transformation of Endometriosis to Endometriosis-Associated Ovarian Carcinoma Using a Data-Driven, Function-Based Analysis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2345.	1.8	20
6481	Nitric Oxide Mediates Crosstalk between Interleukin 1 $\beta$ and WNT Signaling in Primary Human Chondrocytes by Reducing DKK1 and FRZB Expression. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2491.	1.8	28
6482	Laucysteinamide A, a Hybrid PKS/NRPS Metabolite from a Saipan Cyanobacterium, cf. <i>Caldora penicillata</i> . <i>Marine Drugs</i> , 2017, 15, 121.	2.2	18
6483	Upregulation and Identification of Antibiotic Activity of a Marine-Derived <i>Streptomyces</i> sp. via Co-Cultures with Human Pathogens. <i>Marine Drugs</i> , 2017, 15, 250.	2.2	55
6484	Metabolomic Modularity Analysis (MMA) to Quantify Human Liver Perfusion Dynamics. <i>Metabolites</i> , 2017, 7, 58.	1.3	6
6485	GC-MS Metabolomic Analysis to Reveal the Metabolites and Biological Pathways Involved in the Developmental Stages and Tissue Response of <i>Panax ginseng</i> . <i>Molecules</i> , 2017, 22, 496.	1.7	28
6486	Biochemical and Comparative Transcriptomic Analyses Identify Candidate Genes Related to Variegation Formation in <i>Paeonia rockii</i> . <i>Molecules</i> , 2017, 22, 1364.	1.7	18
6487	Synergic Anti-Pruritus Mechanisms of Action for the Radix <i>Sophorae Flavescentis</i> and Fructus <i>Cnidii</i> Herbal Pair. <i>Molecules</i> , 2017, 22, 1465.	1.7	25
6488	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , 2017, 22, 1599.	1.7	9
6489	Exploring the Impact of Food on the Gut Ecosystem Based on the Combination of Machine Learning and Network Visualization. <i>Nutrients</i> , 2017, 9, 1307.	1.7	15
6490	Metabolomic Profiling of Soybeans ( <i>Glycine max</i> L.) Reveals the Importance of Sugar and Nitrogen Metabolism under Drought and Heat Stress. <i>Plants</i> , 2017, 6, 21.	1.6	154
6491	Different Metabolic Pathways Are Involved in Response of <i>Saccharomyces cerevisiae</i> to L-A and M Viruses. <i>Toxins</i> , 2017, 9, 233.	1.5	20
6492	Identification of HIV-1 Tat-Associated Proteins Contributing to HIV-1 Transcription and Latency. <i>Viruses</i> , 2017, 9, 67.	1.5	18
6493	Inference of a Geminivirus $\leftrightarrow$ Host Protein $\leftrightarrow$ Protein Interaction Network through Affinity Purification and Mass Spectrometry Analysis. <i>Viruses</i> , 2017, 9, 275.	1.5	35
6494	A transcriptome-based protein network that identifies new therapeutic targets in colorectal cancer. <i>BMC Genomics</i> , 2017, 18, 758.	1.2	5
6495	Handling Big Data in Precision Medicine. , 2017, , 251-268.		3
6496	Integrated analysis of coding genes and non-coding RNAs during hair follicle cycle of cashmere goat ( <i>Capra hircus</i> ). <i>BMC Genomics</i> , 2017, 18, 767.	1.2	119

#	ARTICLE	IF	CITATIONS
6497	Transcriptional Analysis of <i>Acinetobacter</i> sp. neg1 Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , 2016, 7, 2162.	1.5	48
6498	Melatonin Suppresses Neuropathic Pain via MT2-Dependent and -Independent Pathways in Dorsal Root Ganglia Neurons of Mice. <i>Theranostics</i> , 2017, 7, 2015-2032.	4.6	40
6499	MicroRNA Profiling in Cartilage Ageing. <i>International Journal of Genomics</i> , 2017, 2017, 1-11.	0.8	21
6500	Genome-wide analysis of basic helix-loop-helix (bHLH) transcription factors in <i>Brachypodium distachyon</i> . <i>BMC Genomics</i> , 2017, 18, 619.	1.2	74
6501	Identification of Candidate Casein Kinase 2 Substrates in Mitosis by Quantitative Phosphoproteomics. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 97.	1.8	63
6502	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 680.	1.2	193
6503	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1880.	1.8	90
6504	Integrated proteomic and N-glycoproteomic analyses of doxorubicin sensitive and resistant ovarian cancer cells reveal glycoprotein alteration in protein abundance and glycosylation. <i>Oncotarget</i> , 2017, 8, 13413-13427.	0.8	18
6505	DegoViz: An Interactive Visualization Tool for a Differentially Expressed Genes Heatmap and Gene Ontology Graph. <i>Applied Sciences (Switzerland)</i> , 2017, 7, 543.	1.3	4
6506	Expression Profiling in <i>Pinus pinaster</i> in Response to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2017, 8, 279.	0.9	22
6507	Integrative miRNA-Gene Expression Analysis Enables Refinement of Associated Biology and Prediction of Response to Cetuximab in Head and Neck Squamous Cell Cancer. <i>Genes</i> , 2017, 8, 35.	1.0	27
6508	Auxin Response Factor Genes Repertoire in Mulberry: Identification, and Structural, Functional and Evolutionary Analyses. <i>Genes</i> , 2017, 8, 202.	1.0	16
6509	The Plasticizer Bisphenol A Perturbs the Hepatic Epigenome: A Systems Level Analysis of the miRNome. <i>Genes</i> , 2017, 8, 269.	1.0	28
6510	Gene Regulatory Network Rewiring in the Immune Cells Associated with Cancer. <i>Genes</i> , 2017, 8, 308.	1.0	12
6511	Immunoinformatics Features Linked to Leishmania Vaccine Development: Data Integration of Experimental and In Silico Studies. <i>International Journal of Molecular Sciences</i> , 2017, 18, 371.	1.8	22
6512	Tumor Cell-Derived Microvesicles Induced Not Epithelial-Mesenchymal Transition but Apoptosis in Human Proximal Tubular (HK-2) Cells: Implications for Renal Impairment in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2017, 18, 513.	1.8	6
6513	Identification of Key Candidate Genes and Pathways in Colorectal Cancer by Integrated Bioinformatical Analysis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 722.	1.8	132
6514	Identification of Differentially Expressed Micromas Associate with Glucose Metabolism in Different Organs of Blunt Snout Bream ( <i>Megalobrama amblycephala</i> ). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1161.	1.8	42



#	ARTICLE	IF	CITATIONS
6515	Semi-Quantitative Mass Spectrometry in AML Cells Identifies New Non-Genomic Targets of the EZH2 Methyltransferase. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1440.	1.8	7
6516	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. <i>Advances in Bioinformatics</i> , 2017, 2017, 1-8.	5.7	44
6517	Persistent Exposure to <i>Porphyromonas gingivalis</i> Promotes Proliferative and Invasion Capabilities, and Tumorigenic Properties of Human Immortalized Oral Epithelial Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 57.	1.8	84
6518	Computational Analysis of Host-Pathogen Protein Interactions between Humans and Different Strains of Enterohemorrhagic <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 128.	1.8	14
6519	Quantitative Proteomic Analysis Reveals Changes in the Benchmark <i>Corynebacterium pseudotuberculosis</i> Biovar <i>Equi</i> Exoproteome after Passage in a Murine Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 325.	1.8	12
6520	An Integrative Analysis Reveals a Central Role of P53 Activation via MDM2 in Zika Virus Infection Induced Cell Death. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 327.	1.8	23
6521	Alterations of the Gut Microbiome in Hypertension. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 381.	1.8	313
6522	A Comprehensive View of the $\beta^2$ -Arrestinome. <i>Frontiers in Endocrinology</i> , 2017, 8, 32.	1.5	29
6523	Leptin Induces Mitosis and Activates the Canonical Wnt/ $\beta^2$ -Catenin Signaling Pathway in Neurogenic Regions of <i>Xenopus</i> Tadpole Brain. <i>Frontiers in Endocrinology</i> , 2017, 8, 99.	1.5	14
6524	Modeling the Attractor Landscape of Disease Progression: a Network-Based Approach. <i>Frontiers in Genetics</i> , 2017, 8, 48.	1.1	24
6525	The MicroRNA Interaction Network of Lipid Diseases. <i>Frontiers in Genetics</i> , 2017, 8, 116.	1.1	15
6526	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. <i>Frontiers in Genetics</i> , 2017, 8, 171.	1.1	63
6527	Wnt/ $\beta^2$ -catenin Signaling Pathway Regulates Specific lncRNAs That Impact Dermal Fibroblasts and Skin Fibrosis. <i>Frontiers in Genetics</i> , 2017, 8, 183.	1.1	27
6528	Transcriptomic Analysis of Intestinal Tissues from Two 90-Day Feeding Studies in Rats Using Genetically Modified MON810 Maize Varieties. <i>Frontiers in Genetics</i> , 2017, 8, 222.	1.1	6
6529	A Comprehensive Gene Expression Meta-analysis Identifies Novel Immune Signatures in Rheumatoid Arthritis Patients. <i>Frontiers in Immunology</i> , 2017, 8, 74.	2.2	35
6530	Anaphylatoxin C5a Regulates 6-Sulfo-LacNAc Dendritic Cell Function in Human through Crosstalk with Toll-Like Receptor-Induced CREB Signaling. <i>Frontiers in Immunology</i> , 2017, 8, 818.	2.2	12
6531	Investigation of the Cross-talk Mechanism in Caco-2 Cells during <i>Clostridium difficile</i> Infection through Genetic-and-Epigenetic Interspecies Networks: Big Data Mining and Genome-Wide Identification. <i>Frontiers in Immunology</i> , 2017, 8, 901.	2.2	5
6532	Induction of Cell Cycle and NK Cell Responses by Live-Attenuated Oral Vaccines against Typhoid Fever. <i>Frontiers in Immunology</i> , 2017, 8, 1276.	2.2	10

#	ARTICLE	IF	CITATIONS
6533	<i>Helicobacter pylori</i> Affects the Antigen Presentation Activity of Macrophages Modulating the Expression of the Immune Receptor CD300E through miR-4270. <i>Frontiers in Immunology</i> , 2017, 8, 1288.	2.2	45
6534	Regulation of Fn14 Receptor and NF- $\kappa$ B Underlies Inflammation in Meniere's Disease. <i>Frontiers in Immunology</i> , 2017, 8, 1739.	2.2	48
6535	Seasonal and Interannual Changes in Ciliate and Dinoflagellate Species Assemblages in the Arctic Ocean (Amundsen Gulf, Beaufort Sea, Canada). <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	35
6536	Changes in Eukaryotic and Bacterial Communities along a 120 m Transect Associated with a Shallow Marine Hydrothermal Vent. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	1
6537	High-Resolution Liquid Chromatography Tandem Mass Spectrometry Enables Large Scale Molecular Characterization of Dissolved Organic Matter. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	94
6538	Bacterial Community Structure after Long-term Organic and Inorganic Fertilization Reveals Important Associations between Soil Nutrients and Specific Taxa Involved in Nutrient Transformations. <i>Frontiers in Microbiology</i> , 2017, 8, 187.	1.5	212
6539	Gut Microbial Diversity Assessment of Indian Type-2-Diabetics Reveals Alterations in Eubacteria, Archaea, and Eukaryotes. <i>Frontiers in Microbiology</i> , 2017, 8, 214.	1.5	81
6540	Serpentinization-Influenced Groundwater Harbors Extremely Low Diversity Microbial Communities Adapted to High pH. <i>Frontiers in Microbiology</i> , 2017, 8, 308.	1.5	76
6541	Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions. <i>Frontiers in Microbiology</i> , 2017, 08, 358.	1.5	45
6542	Core Microbiota and Metabolome of <i>Vitis vinifera</i> L. cv. Corvina Grapes and Musts. <i>Frontiers in Microbiology</i> , 2017, 8, 457.	1.5	24
6543	Comparative Proteomic Analysis of <i>Mycobacterium tuberculosis</i> Lineage 7 and Lineage 4 Strains Reveals Differentially Abundant Proteins Linked to Slow Growth and Virulence. <i>Frontiers in Microbiology</i> , 2017, 8, 795.	1.5	34
6544	Temporal Dynamics of Soil Microbial Communities below the Seedbed under Two Contrasting Tillage Regimes. <i>Frontiers in Microbiology</i> , 2017, 8, 1127.	1.5	124
6545	Modulation of Host miRNAs Transcriptome in Lung and Spleen of Peste des Petits Ruminants Virus Infected Sheep and Goats. <i>Frontiers in Microbiology</i> , 2017, 8, 1146.	1.5	44
6546	Distinct Network Interactions in Particle-Associated and Free-Living Bacterial Communities during a <i>Microcystis aeruginosa</i> Bloom in a Plateau Lake. <i>Frontiers in Microbiology</i> , 2017, 8, 1202.	1.5	125
6547	Eelgrass Leaf Surface Microbiomes Are Locally Variable and Highly Correlated with Epibiotic Eukaryotes. <i>Frontiers in Microbiology</i> , 2017, 8, 1312.	1.5	72
6548	Microbial Communities and Their Predicted Metabolic Functions in Growth Laminae of a Unique Large Conical Mat from Lake Untersee, East Antarctica. <i>Frontiers in Microbiology</i> , 2017, 8, 1347.	1.5	51
6549	Genome-Wide Mapping of Transcriptional Regulation and Metabolism Describes Information-Processing Units in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1466.	1.5	17
6550	Identification of Secondary Metabolite Gene Clusters in the <i>Pseudovibrio</i> Genus Reveals Encouraging Biosynthetic Potential toward the Production of Novel Bioactive Compounds. <i>Frontiers in Microbiology</i> , 2017, 8, 1494.	1.5	54

#	ARTICLE	IF	CITATIONS
6551	Long-term Fertilization Structures Bacterial and Archaeal Communities along Soil Depth Gradient in a Paddy Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 1516.	1.5	72
6552	Succession and Fermentation Products of Grass Carp ( <i>Ctenopharyngodon idellus</i> ) Hindgut Microbiota in Response to an Extreme Dietary Shift. <i>Frontiers in Microbiology</i> , 2017, 8, 1585.	1.5	77
6553	Analysis of Microbial Functions in the Rhizosphere Using a Metabolic-Network Based Framework for Metagenomics Interpretation. <i>Frontiers in Microbiology</i> , 2017, 8, 1606.	1.5	59
6554	Identification of Novel Long Non-coding and Circular RNAs in Human Papillomavirus-Mediated Cervical Cancer. <i>Frontiers in Microbiology</i> , 2017, 8, 1720.	1.5	44
6555	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. <i>Frontiers in Microbiology</i> , 2017, 8, 1772.	1.5	31
6556	Protective Effect of <i>Akkermansia muciniphila</i> against Immune-Mediated Liver Injury in a Mouse Model. <i>Frontiers in Microbiology</i> , 2017, 8, 1804.	1.5	209
6557	Basin Scale Variation on the Composition and Diversity of Archaea in the Pacific Ocean. <i>Frontiers in Microbiology</i> , 2017, 8, 2057.	1.5	21
6558	Cyanobacteria and Alphaproteobacteria May Facilitate Cooperative Interactions in Niche Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 2099.	1.5	36
6559	Seasonal Shifts in Bacterial Community Responses to Phytoplankton-Derived Dissolved Organic Matter in the Western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2017, 8, 2117.	1.5	35
6560	Evolutionary Analysis of HIV-1 Pol Proteins Reveals Representative Residues for Viral Subtype Differentiation. <i>Frontiers in Microbiology</i> , 2017, 8, 2151.	1.5	13
6561	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 2306.	1.5	103
6562	Enhancing the Resolution of Rumen Microbial Classification from Metatranscriptomic Data Using Kraken and Mothur. <i>Frontiers in Microbiology</i> , 2017, 8, 2445.	1.5	47
6563	Oxygenation of Hypoxic Coastal Baltic Sea Sediments Impacts on Chemistry, Microbial Community Composition, and Metabolism. <i>Frontiers in Microbiology</i> , 2017, 8, 2453.	1.5	29
6564	Blood Transcriptomic Meta-analysis Identifies Dysregulation of Hemoglobin and Iron Metabolism in Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 73.	1.7	31
6565	Biosystems Study of the Molecular Networks Underlying Hippocampal Aging Progression and Anti-aging Treatment in Mice. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 393.	1.7	3
6566	Screening the Molecular Framework Underlying Local Dendritic mRNA Translation. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 45.	1.4	6
6567	Integrative Analysis of Brain Region-specific Shank3 Interactomes for Understanding the Heterogeneity of Neuronal Pathophysiology Related to SHANK3 Mutations. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 110.	1.4	32
6568	Striatal Transcriptome and Interactome Analysis of Shank3-overexpressing Mice Reveals the Connectivity between Shank3 and mTORC1 Signaling. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 201.	1.4	48

#	ARTICLE	IF	CITATIONS
6569	Expression and Regulatory Network Analysis of miR-140-3p, a New Potential Serum Biomarker for Autism Spectrum Disorder. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 250.	1.4	33
6570	Co-expression Patterns between ATN1 and ATXN2 Coincide with Brain Regions Affected in Huntingtonâ€™s Disease. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 399.	1.4	9
6571	MicroRNA Mediating Networks in Granulosa Cells Associated with Ovarian Follicular Development. <i>BioMed Research International</i> , 2017, 2017, 1-18.	0.9	11
6572	Layer-specific chromatin accessibility landscapes reveal regulatory networks in adult mouse visual cortex. <i>ELife</i> , 2017, 6, .	2.8	73
6573	Prediction and Validation of Hub Genes Associated with Colorectal Cancer by Integrating PPI Network and Gene Expression Data. <i>BioMed Research International</i> , 2017, 2017, 1-12.	0.9	30
6574	Transcriptomic and proteomic landscape of mitochondrial dysfunction reveals secondary coenzyme Q deficiency in mammals. <i>ELife</i> , 2017, 6, .	2.8	169
6575	Network Pharmacology-Based Approach to Investigate the Analgesic Efficacy and Molecular Targets of Xuangui Dropping Pill for Treating Primary Dysmenorrhea. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-12.	0.5	27
6576	Screening for Key Pathways Associated with the Development of Osteoporosis by Bioinformatics Analysis. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	2
6577	Negative Correlation between miR-200c and Decorin Plays an Important Role in the Pathogenesis of Colorectal Carcinoma. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	8
6578	The Impact of GFP Reporter Gene Transduction and Expression on Metabolomics of Placental Mesenchymal Stem Cells Determined by UHPLC-Q/TOF-MS. <i>Stem Cells International</i> , 2017, 2017, 1-12.	1.2	7
6579	Microarray Analysis and Detection of MicroRNAs Associated with Chronic Thromboembolic Pulmonary Hypertension. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	17
6580	Identification of Pharmacologically Tractable Protein Complexes in Cancer Using the R-Based Network Clustering and Visualization Program MCODER. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	4
6581	New Targets for Zika Virus Determined by Human-Viral Interactomic: A Bioinformatics Approach. <i>BioMed Research International</i> , 2017, 2017, 1-15.	0.9	16
6582	Preventive Effect and Safety of a Follicle Stimulating Hormone Inhibitory Formulation Containing a Mixture of Coicis Semen and <i>Artemisia capillaris</i> for Precocious Puberty: A Preliminary Experimental Study Using Female Rats. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-8.	0.5	7
6583	Identification of Significant Pathways Induced by PAX5 Haploinsufficiency Based on Protein-Protein Interaction Networks and Cluster Analysis in Raji Cell Line. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	5
6584	Identification of Transcriptional Modules and Key Genes in Chickens Infected with <i>Salmonella enterica</i> Serovar Pullorum Using Integrated Coexpression Analyses. <i>BioMed Research International</i> , 2017, 2017, 1-12.	0.9	8
6585	Correlation Clustering of Stable Angina Clinical Care Patterns for 506 Thousand Patients. <i>Journal of Healthcare Engineering</i> , 2017, 2017, 1-10.	1.1	2
6586	Efficacy of Î²-lactam/Î²-lactamase inhibitor combination is linked to WhiB4-mediated changes in redox physiology of <i>Mycobacterium tuberculosis</i> . <i>ELife</i> , 2017, 6, .	2.8	50

#	ARTICLE	IF	CITATIONS
6587	Native KCC2 interactome reveals PACSIN1 as a critical regulator of synaptic inhibition. <i>ELife</i> , 2017, 6, .	2.8	44
6588	RNA Sequencing Analysis Reveals Interactions between Breast Cancer or Melanoma Cells and the Tissue Microenvironment during Brain Metastasis. <i>BioMed Research International</i> , 2017, 2017, 1-10.	0.9	28
6589	Cyclin A/Cdk1 modulates Plk1 activity in prometaphase to regulate kinetochore-microtubule attachment stability. <i>ELife</i> , 2017, 6, .	2.8	42
6590	Identification of differentially expressed genes in flower, leaf and bulb scale of <i>Lilium oriental hybrid 'Sorbonne'</i> ™ and putative control network for scent genes. <i>BMC Genomics</i> , 2017, 18, 899.	1.2	18
6591	Identification of potential biomarkers and analysis of prognostic values in head and neck squamous cell carcinoma by bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 2315-2321.	1.0	26
6592	Genes uniquely expressed in human growth plate chondrocytes uncover a distinct regulatory network. <i>BMC Genomics</i> , 2017, 18, 983.	1.2	17
6593	Mapping the microRNA Expression Profiles in Glyoxalase Overexpressing Salinity Tolerant Rice. <i>Current Genomics</i> , 2017, 19, 21-35.	0.7	9
6594	Retinal Pigment Epithelial Cells are a Potential Reservoir for Ebola Virus in the Human Eye. <i>Translational Vision Science and Technology</i> , 2017, 6, 12.	1.1	53
6595	The transcription factor Maf-S regulates metabolic resistance to insecticides in the malaria vector <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2017, 18, 669.	1.2	65
6596	Identification of Linkages between EDCs in Personal Care Products and Breast Cancer through Data Integration Combined with Gene Network Analysis. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 1158.	1.2	6
6597	Computational Studies and Biosynthesis of Natural Products with Promising Anticancer Properties. , 2017, , .		5
6598	Network Biomarkers Constructed from Gene Expression and Protein-Protein Interaction Data for Accurate Prediction of Leukemia. <i>Journal of Cancer</i> , 2017, 8, 278-286.	1.2	15
6599	Bioactive Nutrients and Nutrigenomics in Age-Related Diseases. <i>Molecules</i> , 2017, 22, 105.	1.7	61
6600	Nutrient supply affects the mRNA expression profile of the porcine skeletal muscle. <i>BMC Genomics</i> , 2017, 18, 603.	1.2	21
6601	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. <i>BMC Genomics</i> , 2017, 18, 679.	1.2	4
6602	Identification of Key Transcription Factors Associated with Lung Squamous Cell Carcinoma. <i>Medical Science Monitor</i> , 2017, 23, 172-206.	0.5	25
6603	Identification of lncRNAs involved in biological regulation in early age-related macular degeneration. <i>International Journal of Nanomedicine</i> , 2017, Volume 12, 7589-7602.	3.3	30
6604	3,4-Dihydroxyphenylacetate 2,3-dioxygenase from <i>Pseudomonas aeruginosa</i> : An Fe(II)-containing enzyme with fast turnover. <i>PLoS ONE</i> , 2017, 12, e0171135.	1.1	8

#	ARTICLE	IF	CITATIONS
6605	Sm-p80-based schistosomiasis vaccine mediated epistatic interactions identified potential immune signatures for vaccine efficacy in mice and baboons. PLoS ONE, 2017, 12, e0171677.	1.1	15
6606	Exploration of inhibitory mechanisms of curcumin in lung cancer metastasis using a miRNA-transcription factor-target gene network. PLoS ONE, 2017, 12, e0172470.	1.1	20
6607	The amyloid interactome: Exploring protein aggregation. PLoS ONE, 2017, 12, e0173163.	1.1	25
6608	Abnormal expression of mRNA, microRNA alteration and aberrant DNA methylation patterns in rectal adenocarcinoma. PLoS ONE, 2017, 12, e0174461.	1.1	21
6609	Crude oil impairs immune function and increases susceptibility to pathogenic bacteria in southern flounder. PLoS ONE, 2017, 12, e0176559.	1.1	38
6610	Stratification of clear cell renal cell carcinoma (ccRCC) genomes by gene-directed copy number alteration (CNA) analysis. PLoS ONE, 2017, 12, e0176659.	1.1	17
6611	SIGNet: A signaling network data simulator to enable signaling network inference. PLoS ONE, 2017, 12, e0177701.	1.1	7
6612	WetA bridges cellular and chemical development in <i>Aspergillus flavus</i> . PLoS ONE, 2017, 12, e0179571.	1.1	48
6613	Prediction of novel target genes and pathways involved in irinotecan-resistant colorectal cancer. PLoS ONE, 2017, 12, e0180616.	1.1	22
6614	Compartmentalized metabolic network reconstruction of microbial communities to determine the effect of agricultural intervention on soils. PLoS ONE, 2017, 12, e0181826.	1.1	6
6615	Uncovering robust patterns of microRNA co-expression across cancers using Bayesian Relevance Networks. PLoS ONE, 2017, 12, e0183103.	1.1	6
6616	Mapping the STK4/Hippo signaling network in prostate cancer cell. PLoS ONE, 2017, 12, e0184590.	1.1	22
6617	CytoGTA: A cytoscape plugin for identifying discriminative subnetwork markers using a game theoretic approach. PLoS ONE, 2017, 12, e0185016.	1.1	5
6618	Species-specific signatures of the microbiome from <i>Camponotus</i> and <i>Colobopsis</i> ants across developmental stages. PLoS ONE, 2017, 12, e0187461.	1.1	36
6619	Scientometric study of the effects of exposure to non-ionizing electromagnetic fields on fertility: A contribution to understanding the reasons of partial failure. PLoS ONE, 2017, 12, e0187890.	1.1	9
6620	Dietary protein sources differentially affect microbiota, mTOR activity and transcription of mTOR signaling pathways in the small intestine. PLoS ONE, 2017, 12, e0188282.	1.1	25
6621	A transcriptomics approach uncovers novel roles for poly(ADP-ribosyl)ation in the basal defense response in <i>Arabidopsis thaliana</i> . PLoS ONE, 2017, 12, e0190268.	1.1	16
6622	The yeast form of the fungus <i>Candida albicans</i> promotes persistence in the gut of gnotobiotic mice. PLoS Pathogens, 2017, 13, e1006699.	2.1	74



#	ARTICLE	IF	CITATIONS
6623	Characterization of host proteins interacting with the lymphocytic choriomeningitis virus L protein. <i>PLoS Pathogens</i> , 2017, 13, e1006758.	2.1	19
6624	The Ink4a/Arf locus operates as a regulator of the circadian clock modulating RAS activity. <i>PLoS Biology</i> , 2017, 15, e2002940.	2.6	47
6625	Network analysis based on TCGA reveals hub genes in colon cancer. <i>Wspolczesna Onkologia</i> , 2017, 2, 136-144.	0.7	11
6626	Proteomics and Host-Pathogen Interactions. , 2017, , 227-255.		1
6627	An integrated overview of the midgut bacterial flora composition of <i>Phlebotomus perniciosus</i> , a vector of zoonotic visceral leishmaniasis in the Western Mediterranean Basin. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005484.	1.3	38
6628	Integrated systems biology analysis of KSHV latent infection reveals viral induction and reliance on peroxisome mediated lipid metabolism. <i>PLoS Pathogens</i> , 2017, 13, e1006256.	2.1	53
6629	Chronically dysregulated NOTCH1 interactome in the dentate gyrus after traumatic brain injury. <i>PLoS ONE</i> , 2017, 12, e0172521.	1.1	22
6630	Interactions between the tumor and the blood systemic response of breast cancer patients. <i>PLoS Computational Biology</i> , 2017, 13, e1005680.	1.5	22
6631	A composite network of conserved and tissue specific gene interactions reveals possible genetic interactions in glioma. <i>PLoS Computational Biology</i> , 2017, 13, e1005739.	1.5	15
6632	Rfx2 Stabilizes Foxj1 Binding at Chromatin Loops to Enable Multiciliated Cell Gene Expression. <i>PLoS Genetics</i> , 2017, 13, e1006538.	1.5	68
6633	Formation of a TBX20-CASZ1 protein complex is protective against dilated cardiomyopathy and critical for cardiac homeostasis. <i>PLoS Genetics</i> , 2017, 13, e1007011.	1.5	24
6634	Shared genetic regulatory networks for cardiovascular disease and type 2 diabetes in multiple populations of diverse ethnicities in the United States. <i>PLoS Genetics</i> , 2017, 13, e1007040.	1.5	82
6635	DenvInt: A database of protein-protein interactions between dengue virus and its hosts. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005879.	1.3	34
6636	A tissue-based approach to selection of reference genes for quantitative real-time PCR in a sheep osteoporosis model. <i>BMC Genomics</i> , 2017, 18, 975.	1.2	22
6637	JunB promotes Th17 cell identity and restrains alternative CD4+ T-cell programs during inflammation. <i>Nature Communications</i> , 2017, 8, 301.	5.8	93
6638	Bioinformatics resources for deciphering the biogenesis and action pathways of plant small RNAs. <i>Rice</i> , 2017, 10, 38.	1.7	18
6639	Maize network analysis revealed gene modules involved in development, nutrients utilization, metabolism, and stress response. <i>BMC Plant Biology</i> , 2017, 17, 131.	1.6	24
6640	Seed maturation associated transcriptional programs and regulatory networks underlying genotypic difference in seed dormancy and size/weight in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 154.	1.6	22



#	ARTICLE	IF	CITATIONS
6641	Global analysis of the MATE gene family of metabolite transporters in tomato. <i>BMC Plant Biology</i> , 2017, 17, 185.	1.6	64
6642	A post-gene silencing bioinformatics protocol for plant-defence gene validation and underlying process identification: case study of the <i>Arabidopsis thaliana</i> NPR1. <i>BMC Plant Biology</i> , 2017, 17, 218.	1.6	5
6643	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	1.7	238
6644	A widespread family of polymorphic toxins encoded by temperate phages. <i>BMC Biology</i> , 2017, 15, 75.	1.7	33
6645	Incorporating genomic, transcriptomic and clinical data: a prognostic and stem cell-like MYC and PRC imbalance in high-risk neuroblastoma. <i>BMC Systems Biology</i> , 2017, 11, 92.	3.0	7
6646	Network pharmacological mechanisms of <i>Vernonia anthelmintica</i> (L.) in the treatment of vitiligo: Isorhamnetin induction of melanogenesis via up-regulation of melanin-biosynthetic genes. <i>BMC Systems Biology</i> , 2017, 11, 103.	3.0	32
6647	Consensus strategy in genes prioritization and combined bioinformatics analysis for preeclampsia pathogenesis. <i>BMC Medical Genomics</i> , 2017, 10, 50.	0.7	18
6648	Special role of JUN in papillary thyroid carcinoma based on bioinformatics analysis. <i>World Journal of Surgical Oncology</i> , 2017, 15, 119.	0.8	10
6649	Statistically controlled identification of differentially expressed genes in one-to-one cell line comparisons of the CMAP database for drug repositioning. <i>Journal of Translational Medicine</i> , 2017, 15, 198.	1.8	14
6650	Identification of potential transcriptomic markers in developing pediatric sepsis: a weighted gene co-expression network analysis and a case-control validation study. <i>Journal of Translational Medicine</i> , 2017, 15, 254.	1.8	19
6651	Differential expression of porcine microRNAs in African swine fever virus infected pigs: a proof-of-concept study. <i>Virology Journal</i> , 2017, 14, 198.	1.4	22
6652	Arete candidate gene prioritization using biological network topology with additional evidence types. <i>BioData Mining</i> , 2017, 10, 22.	2.2	10
6653	Phosphoproteomics reveals network rewiring to a pro-adhesion state in annexin-1-deficient mammary epithelial cells. <i>Breast Cancer Research</i> , 2017, 19, 132.	2.2	13
6654	Knowledge-guided gene prioritization reveals new insights into the mechanisms of chemoresistance. <i>Genome Biology</i> , 2017, 18, 153.	3.8	33
6655	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	3.8	363
6656	The nuclear receptor ER $\beta$ engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. <i>Genome Biology</i> , 2017, 18, 189.	3.8	63
6657	Quantitative in vivo phosphoproteomics reveals reversible signaling processes during nitrogen starvation and recovery in the biofuel model organism <i>Chlamydomonas reinhardtii</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 280.	6.2	60
6658	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. <i>BMC Research Notes</i> , 2017, 10, 278.	0.6	31

#	ARTICLE	IF	CITATIONS
6659	Towards a more molecular taxonomy of disease. <i>Journal of Biomedical Semantics</i> , 2017, 8, 25.	0.9	11
6660	The structure of the <i>Brassica napus</i> seed microbiome is cultivar-dependent and affects the interactions of symbionts and pathogens. <i>Microbiome</i> , 2017, 5, 104.	4.9	144
6661	Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017, 5, 117.	4.9	17
6662	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. <i>Microbiome</i> , 2017, 5, 123.	4.9	74
6663	Individual signatures and environmental factors shape skin microbiota in healthy dogs. <i>Microbiome</i> , 2017, 5, 139.	4.9	38
6664	Microbial biodiversity assessment of the European Space Agency's ExoMars 2016 mission. <i>Microbiome</i> , 2017, 5, 143.	4.9	27
6665	Mapreduce model for finding closely knit communities in large scale networks. , 2017, , .		5
6666	Genome-wide identification and expression analysis of calmodulin-like (CML) genes in Chinese cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> ). <i>BMC Genomics</i> , 2017, 18, 842.	1.2	36
6667	A new method to study the change of miRNA-mRNA interactions due to environmental exposures. <i>Bioinformatics</i> , 2017, 33, i199-i207.	1.8	4
6668	CellNetVis: a web tool for visualization of biological networks using force-directed layout constrained by cellular components. <i>BMC Bioinformatics</i> , 2017, 18, 395.	1.2	20
6669	Functional analysis of <i>Plasmodium falciparum</i> subpopulations associated with artemisinin resistance in Cambodia. <i>Malaria Journal</i> , 2017, 16, 493.	0.8	17
6670	Multiple-trait genomewide mapping and gene network analysis for scrotal circumference growth curves in Brahman cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2017, 95, 3331-3345.	0.2	16
6671	BioLinker: Bottom-up exploration of protein interaction networks. , 2017, , .		3
6672	Theoretical Studies of Intracellular Concentration of Micro-organisms's Metabolites. <i>Scientific Reports</i> , 2017, 7, 9048.	1.6	5
6673	Chemokines protect vascular smooth muscle cells from cell death induced by cyclic mechanical stretch. <i>Scientific Reports</i> , 2017, 7, 16128.	1.6	19
6674	Network design and analysis for multi-enzyme biocatalysis. <i>BMC Bioinformatics</i> , 2017, 18, 366.	1.2	7
6675	CAMSA: a tool for comparative analysis and merging of scaffold assemblies. <i>BMC Bioinformatics</i> , 2017, 18, 496.	1.2	11
6676	A proximity-based graph clustering method for the identification and application of transcription factor clusters. <i>BMC Bioinformatics</i> , 2017, 18, 530.	1.2	1

#	ARTICLE	IF	CITATIONS
6677	Cellulosic fibres of flax recruit both primary and secondary cell wall cellulose synthases during deposition of thick tertiary cell walls and in the course of graviresponse. <i>Functional Plant Biology</i> , 2017, 44, 820.	1.1	45
6678	Changes in Neuronal Signaling and Cell Stress Response Pathways are Associated with a Multigenic Response of <i>Drosophila melanogaster</i> to DDT Selection. <i>Genome Biology and Evolution</i> , 2017, 9, 3356-3372.	1.1	24
6679	Maternal chromium restriction induces insulin resistance in adult mice offspring through miRNA. <i>International Journal of Molecular Medicine</i> , 2018, 41, 1547-1559.	1.8	15
6680	Transcriptional and Functional Plasticity Induced by Chronic Insulin Exposure in a Mast Cell-Like Basophilic Leukemia Cell Model. <i>Journal of Immunobiology</i> , 2017, 02, .	0.3	2
6681	CancerLinker: Explorations of Cancer Study Network. , 2017, , .		2
6682	DECIPHERING THE ACTION MECHANISM OF INDONESIA HERBAL DECOCTION IN THE TREATMENT OF TYPE II DIABETES USING A NETWORK PHARMACOLOGY APPROACH. <i>International Journal of Pharmacy and Pharmaceutical Sciences</i> , 2017, 9, 243.	0.3	2
6683	Machine learning for predicting lifespan-extending chemical compounds. <i>Aging</i> , 2017, 9, 1721-1737.	1.4	34
6684	The Saliva Exposome for Monitoring of Individuals' Health Trajectories. <i>Environmental Health Perspectives</i> , 2017, 125, 077014.	2.8	44
6685	miR-9a mediates the role of Lethal giant larvae as an epithelial growth inhibitor in <i>Drosophila</i> . <i>Biology Open</i> , 2018, 7, .	0.6	6
6686	Long non-coding RNA associated-competing endogenous RNAs are induced by clusterin in retinal pigment epithelial cells. <i>Molecular Medicine Reports</i> , 2017, 16, 8399-8405.	1.1	10
6687	A mutation in the viral sensor 2'5'-oligoadenylate synthetase 2 causes failure of lactation. <i>PLoS Genetics</i> , 2017, 13, e1007072.	1.5	21
6688	Valorizing omics visualization for discovery. <i>Data Science</i> , 2017, 1, 131-137.	0.7	0
6689	DanHong injection targets endothelin receptor type B and angiotensin II receptor type 1 in protection against cardiac hypertrophy. <i>Oncotarget</i> , 2017, 8, 103393-103409.	0.8	7
6690	Integrated analysis reveals candidate genes and transcription factors in lung adenocarcinoma. <i>Molecular Medicine Reports</i> , 2017, 16, 8371-8379.	1.1	4
6691	Insights from Systems Biology in Physiological Studies: Learning from Context. <i>Cellular Physiology and Biochemistry</i> , 2017, 42, 939-951.	1.1	3
6692	Screening and validation of differentially expressed extracellular miRNAs in acute pancreatitis. <i>Molecular Medicine Reports</i> , 2017, 16, 6412-6418.	1.1	11
6693	Comprehensive Analysis of the Cork Oak ( <i>Quercus suber</i> ) Transcriptome Involved in the Regulation of Bud Sprouting. <i>Forests</i> , 2017, 8, 486.	0.9	6
6694	Single-cell profiling reveals GPCR heterogeneity and functional patterning during neuroinflammation. <i>JCI Insight</i> , 2017, 2, .	2.3	19

#	ARTICLE	IF	CITATIONS
6695	Computational Challenges and -omics Approaches for the Identification of microRNAs and Targets. , 2017, , 39-59.		1
6696	Diabetic Retinopathy and Laser Therapy in Rats: A Protein-Protein Interaction Network Analysis. Journal of Lasers in Medical Sciences, 2017, 8, S20-S21.	0.4	20
6697	Comparison of miRNA and gene expression profiles between metastatic and primary prostate cancer. Oncology Letters, 2017, 14, 6085-6090.	0.8	9
6698	Multiplexed Nucleic Acid Programmable Protein Arrays. Theranostics, 2017, 7, 4057-4070.	4.6	25
6699	BRENDA in 2017: new perspectives and new tools in BRENDA. Nucleic Acids Research, 2017, 45, D380-D388.	6.5	251
6700	Identification of the anticancer effects of a novel proteasome inhibitor, ixazomib, on colorectal cancer using a combined method of microarray and bioinformatics analysis. OncoTargets and Therapy, 2017, Volume 10, 3591-3606.	1.0	13
6701	Cross-Kingdom Regulation of Putative miRNAs Derived from Happy Tree in Cancer Pathway: A Systems Biology Approach. International Journal of Molecular Sciences, 2017, 18, 1191.	1.8	38
6702	MicroRNA profiling of platelets from immune thrombocytopenia and target gene prediction. Molecular Medicine Reports, 2017, 16, 2835-2843.	1.1	20
6703	Identification of microRNAs in acute respiratory distress syndrome based on microRNA expression profile in rats. Molecular Medicine Reports, 2017, 16, 3357-3362.	1.1	7
6704	A Network Pharmacology Approach to Determine the Active Components and Potential Targets of Curculigo Orchioides in the Treatment of Osteoporosis. Medical Science Monitor, 2017, 23, 5113-5122.	0.5	44
6705	A Quantitative Acetylotomic Analysis of Early Seed Development in Rice (Oryza sativa L.). International Journal of Molecular Sciences, 2017, 18, 1376.	1.8	20
6706	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers1. Journal of Animal Science, 2017, 95, 599-615.	0.2	27
6707	Bioinformatics analysis of key genes and signaling pathways associated with myocardial infarction following telomerase activation. Molecular Medicine Reports, 2017, 16, 2915-2924.	1.1	2
6708	Big Tumorigenesis Mechanisms in Systems Cancer Biology via Big Database Mining and Network Modeling. , 2017, , 431-526.		1
6709	Identification of key genes and molecular mechanisms associated with dedifferentiated liposarcoma based on bioinformatic methods. OncoTargets and Therapy, 2017, Volume 10, 3017-3027.	1.0	9
6710	Identification of hub miRNA biomarkers for bladder cancer by weighted gene coexpression network analysis. OncoTargets and Therapy, 2017, Volume 10, 5551-5559.	1.0	13
6711	Drosophila. , 2017, , 345-358.		11
6712	PiiL: visualization of DNA methylation and gene expression data in gene pathways. BMC Genomics, 2017, 18, 571.	1.2	3

#	ARTICLE	IF	CITATIONS
6713	Integrative testis transcriptome analysis reveals differentially expressed miRNAs and their mRNA targets during early puberty in Atlantic salmon. <i>BMC Genomics</i> , 2017, 18, 801.	1.2	34
6714	Identification of miRNA-mRNA crosstalk in laryngeal squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2017, 16, 4179-4186.	1.1	7
6715	Genome-wide identification of miRNAs and lncRNAs in <i>Cajanus cajan</i> . <i>BMC Genomics</i> , 2017, 18, 878.	1.2	40
6716	Gut microbiome in ADHD and its relation to neural reward anticipation. <i>PLoS ONE</i> , 2017, 12, e0183509.	1.1	215
6717	Identification of genes and pathways in nasopharyngeal carcinoma by bioinformatics analysis. <i>Oncotarget</i> , 2017, 8, 63738-63749.	0.8	22
6718	Identification of Key Genes Affecting Results of Hyperthermia in Osteosarcoma Based on Integrative ChIP-Seq/TargetScan Analysis. <i>Medical Science Monitor</i> , 2017, 23, 2042-2048.	0.5	47
6719	MicroRNA expression in esophageal squamous cell carcinoma: Novel diagnostic and prognostic biomarkers. <i>Molecular Medicine Reports</i> , 2017, 15, 3833-3839.	1.1	6
6720	Big Mechanisms of Information Flow in Cellular Systems in Response to Environmental Stress Signals via System Identification and Data Mining. , 2017, , 155-248.		0
6721	Identification of key mRNAs and microRNAs in the pathogenesis and progression of osteoarthritis using microarray analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 5659-5666.	1.1	6
6722	Integrated analysis of competing endogenous RNA network revealing lncRNAs as potential prognostic biomarkers in human lung squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 65997-66018.	0.8	39
6723	On the (im)possibility of reconstructing plasmids from whole-genome short-read sequencing data. <i>Microbial Genomics</i> , 2017, 3, e000128.	1.0	198
6724	High-resolution microbiome profiling uncovers <i>Fusobacterium nucleatum</i> , <i>Lactobacillus gasseri/johnsonii</i> , and <i>Lactobacillus vaginalis</i> associated to oral and oropharyngeal cancer in saliva from HPV positive and HPV negative patients treated with surgery and chemo-radiation. <i>Oncotarget</i> , 2017, 8, 110931-110948.	0.8	79
6725	Identification of Key Genes and Pathways in Tongue Squamous Cell Carcinoma Using Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2017, 23, 5924-5932.	0.5	40
6726	CTD2 Dashboard: a searchable web interface to connect validated results from the Cancer Target Discovery and Development Network. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	23
6727	Systematic Analysis of GWAS Data Reveals Genomic Hotspots for Shared Mechanisms between Neurodegenerative Diseases. , 2017, 7, .		1
6728	Speciation Genomics of Protein-Coding Genes Common to Mycoplasmatales. <i>Journal of Phylogenetics &amp; Evolutionary Biology</i> , 2017, 05, .	0.2	0
6729	Overview of Drug Polypharmacology and Multitargeted Molecular Design. , 2017, , 259-275.		4
6730	Toxicogenomics of Bisphenol A and Neurodevelopmental Disorders. , 0, , .		1

#	ARTICLE	IF	CITATIONS
6731	Tianfoshen oral liquid: a CFDA approved clinical traditional Chinese medicine, normalizes major cellular pathways disordered during colorectal carcinogenesis. <i>Oncotarget</i> , 2017, 8, 14549-14569.	0.8	88
6732	Specialized plant biochemistry drives gene clustering in fungi. <i>ISME Journal</i> , 2018, 12, 1694-1705.	4.4	20
6733	HEPES activates a MiT/TFE-dependent lysosomal-autophagic gene network in cultured cells: A call for caution. <i>Autophagy</i> , 2018, 14, 437-449.	4.3	18
6734	<i>Yersinia pestis</i> Targets the Host Endosome Recycling Pathway during the Biogenesis of the <i>Yersinia</i> -Containing Vacuole To Avoid Killing by Macrophages. <i>MBio</i> , 2018, 9, .	1.8	29
6735	GNCâ€‘app: A new Cytoscape app to rate gene networks biological coherence using geneâ€‘gene indirect relationships. <i>BioSystems</i> , 2018, 166, 61-65.	0.9	14
6736	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	13.5	1,068
6737	A Model for Manganese interaction with <i>Deinococcus radiodurans</i> proteome network involved in ROS response and defense. <i>Journal of Trace Elements in Medicine and Biology</i> , 2018, 50, 465-473.	1.5	23
6738	Bipartite graphs in systems biology and medicine: a survey of methods and applications. <i>GigaScience</i> , 2018, 7, 1-31.	3.3	117
6739	Differential Expression of MiR-106b-5p and MiR-200c-3p in Newly Diagnosed Versus Chronic Primary Immune Thrombocytopenia Patients Based on Systematic Analysis. <i>Cellular Physiology and Biochemistry</i> , 2018, 45, 301-318.	1.1	19
6740	Synthesis, antimycobacterial evaluation, and QSAR analysis of meso-dihydroguaiaretic acid derivatives. <i>Medicinal Chemistry Research</i> , 2018, 27, 1026-1042.	1.1	3
6741	From correlation to causation: analysis of metabolomics data using systems biology approaches. <i>Metabolomics</i> , 2018, 14, 37.	1.4	151
6742	Genome-wide strategies identify downstream target genes of connective tissue-associated transcription factors. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	20
6743	Insights into the ubiquitin-proteasome system of human embryonic stem cells. <i>Scientific Reports</i> , 2018, 8, 4092.	1.6	44
6744	Comparative Protein Interaction Network Analysis Identifies Shared and Distinct Functions for the Human ROCO Proteins. <i>Proteomics</i> , 2018, 18, e1700444.	1.3	34
6745	Integrating molecular and ecological approaches to identify potential polymicrobial pathogens over a shrimp disease progression. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3755-3764.	1.7	44
6746	Collective transcriptomic deregulation of hypertrophic and dilated cardiomyopathy â€‘ Importance of fibrotic mechanism in heart failure. <i>Computational Biology and Chemistry</i> , 2018, 73, 85-94.	1.1	7
6747	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018, 8, 3434.	1.6	43
6748	Machine learning for the meta-analyses of microbial pathogensâ€™ volatile signatures. <i>Scientific Reports</i> , 2018, 8, 3360.	1.6	40

#	ARTICLE	IF	CITATIONS
6749	ADAM17 is required for EGF-Rα-induced intestinal tumors via IL-6 trans-signaling. <i>Journal of Experimental Medicine</i> , 2018, 215, 1205-1225.	4.2	63
6750	The MYO6 interactome reveals adaptor complexes coordinating early endosome and cytoskeletal dynamics. <i>EMBO Reports</i> , 2018, 19, .	2.0	49
6751	Toward an integrated map of genetic interactions in cancer cells. <i>Molecular Systems Biology</i> , 2018, 14, e7656.	3.2	64
6752	Crosstalk between prognostic long noncoding RNAs and messenger RNAs as transcriptional hallmarks in gastric cancer. <i>Epigenomics</i> , 2018, 10, 433-443.	1.0	15
6753	Identification of key microRNAs, transcription factors and genes associated with congenital obstructive nephropathy in a mouse model of megabladder. <i>Gene</i> , 2018, 650, 77-85.	1.0	4
6754	Identification of potential target genes for ankylosing spondylitis treatment. <i>Medicine (United States)</i> , 2018, 97, e9760.	0.4	6
6755	Differentially expressed proteins associated with drought tolerance in bananas ( <i>Musa spp.</i> ). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	12
6756	Comparative Study of Withanolide Biosynthesis-Related miRNAs in Root and Leaf Tissues of <i>Withania somnifera</i> . <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 1145-1159.	1.4	25
6757	CXCL12/CXCR4-Mediated Procollagen Secretion Is Coupled To Cullin-RING Ubiquitin Ligase Activation. <i>Scientific Reports</i> , 2018, 8, 3499.	1.6	13

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6767	Transcriptional Roadmap to Seasonal Variation in Wood Formation of Norway Spruce. <i>Plant Physiology</i> , 2018, 176, 2851-2870.	2.3	40
6768	Large Blooms of <i>Bacillales</i> ( <i>Firmicutes</i> ) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. <i>MBio</i> , 2018, 9, .	1.8	28
6769	Protein network module-based identification of key pharmacological pathways of <i>Curcuma phaeocaulis</i> Val. acting on hepatitis. <i>Journal of Ethnopharmacology</i> , 2018, 221, 10-19.	2.0	9
6770	An Augmented Pocketome: Detection and Analysis of Small-Molecule Binding Pockets in Proteins of Known 3D Structure. <i>Structure</i> , 2018, 26, 499-512.e2.	1.6	38
6771	Comparative Transcriptome Analysis Revealing the Effect of Light on Anthocyanin Biosynthesis in Purple Grains of Wheat. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 3465-3476.	2.4	19
6772	Prediction and characterization of human ageing-related proteins by using machine learning. <i>Scientific Reports</i> , 2018, 8, 4094.	1.6	44
6773	A VCP inhibitor substrate trapping approach (VISTA) enables proteomic profiling of endogenous ERAD substrates. <i>Molecular Biology of the Cell</i> , 2018, 29, 1021-1030.	0.9	31
6774	Extracellular vesicle <i>scRNA</i> s reflect placenta dysfunction and are a biomarker source for preterm labour. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2760-2773.	1.6	62
6775	A <i>Vitis vinifera</i> basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. <i>Plant Biotechnology Journal</i> , 2018, 16, 1595-1615.	4.1	39
6776	From systems biology to P4 medicine: applications in respiratory medicine. <i>European Respiratory Review</i> , 2018, 27, 170110.	3.0	35
6777	The SMAD2/3 interactome reveals that TGF $\beta$ 2 controls m6A mRNA methylation in pluripotency. <i>Nature</i> , 2018, 555, 256-259.	13.7	283
6778	Comparative <i>iTRAQ</i> analysis of protein abundance in the human sinoatrial node and working cardiomyocytes. <i>Journal of Anatomy</i> , 2018, 232, 956-964.	0.9	4
6779	Quantitative prediction of shrimp disease incidence via the profiles of gut eukaryotic microbiota. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3315-3326.	1.7	40
6780	VDJdb: a curated database of T-cell receptor sequences with known antigen specificity. <i>Nucleic Acids Research</i> , 2018, 46, D419-D427.	6.5	391
6781	Dissociable meta-analytic brain networks contribute to coordinated emotional processing. <i>Human Brain Mapping</i> , 2018, 39, 2514-2531.	1.9	35
6782	Bacteria That Make a Meal of Sulfonamide Antibiotics: Blind Spots and Emerging Opportunities. <i>Environmental Science &amp; Technology</i> , 2018, 52, 3854-3868.	4.6	97
6783	Bioactivity-Based Molecular Networking for the Discovery of Drug Leads in Natural Product Bioassay-Guided Fractionation. <i>Journal of Natural Products</i> , 2018, 81, 758-767.	1.5	237
6784	Gene expression models based on a reference laboratory strain are poor predictors of <i>Mycobacterium tuberculosis</i> complex transcriptional diversity. <i>Scientific Reports</i> , 2018, 8, 3813.	1.6	14

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6785	A cross-omics approach to investigate temporal gene expression regulation by 5-hydroxymethylcytosine via TBH-derived oxidative stress showed involvement of different regulatory kinases. <i>Toxicology in Vitro</i> , 2018, 48, 318-328.	1.1	4
6786	In-silico study of toxicokinetics and disease association of chemicals present in smokeless tobacco products. <i>Regulatory Toxicology and Pharmacology</i> , 2018, 95, 8-16.	1.3	7
6787	A web platform for the network analysis of high-throughput data in melanoma and its use to investigate mechanisms of resistance to anti-PD1 immunotherapy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2315-2328.	1.8	18
6788	High-throughput profiling of seasonal variations of antibiotic resistance gene transport in a peri-urban river. <i>Environment International</i> , 2018, 114, 87-94.	4.8	150
6789	Bioinformatic identification of key genes and pathways that may be involved in the pathogenesis of HBV-associated acute liver failure. <i>Genes and Diseases</i> , 2018, 5, 349-357.	1.5	12
6790	ATP-dependent substrate reduction at an [Fe <sup>8</sup> S <sup>9</sup> ] double-cubane cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2994-2999.	3.3	30
6791	Systematic analysis of complex genetic interactions. <i>Science</i> , 2018, 360, .	6.0	201
6792	Gene expression profiles of ion channels and receptors in mouse resistance arteries: Effects of cell type, vascular bed, and age. <i>Microcirculation</i> , 2018, 25, e12452.	1.0	7
6793	Exploring the Genetic Landscape of Metabolic Phenotypes with MetaboSignal. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 14.14.1-14.14.13.	25.8	6
6794	Transcriptome analysis for identifying possible gene regulations during maize root emergence and formation at the initial growth stage. <i>Genes and Genomics</i> , 2018, 40, 755-766.	0.5	12
6795	Validation and bioinformatic analysis of propofol-induced differentially expressed microRNAs in primary cultured neural stem cells. <i>Gene</i> , 2018, 664, 90-100.	1.0	16
6796	Metagenomic binning reveals the functional roles of core abundant microorganisms in twelve full-scale biogas plants. <i>Water Research</i> , 2018, 140, 123-134.	5.3	122
6797	<i>Vibrio</i> Ecology in the Neuse River Estuary, North Carolina, Characterized by Next-Generation Amplicon Sequencing of the Gene Encoding Heat Shock Protein 60 ( <i>hsp60</i> ). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	48
6798	Characterization of the cork formation and production transcriptome in <i>Quercus cerris</i> — <i>Q. suber</i> hybrids. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 535-549.	1.4	9
6799	Discovery of a Kojibiose Phosphorylase in <i>Escherichia coli</i> K-12. <i>Biochemistry</i> , 2018, 57, 2857-2867.	1.2	23
6800	A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , 2018, 9, 1604.	5.8	130
6801	Ataxia-telangiectasia. <i>Neurology: Genetics</i> , 2018, 4, e228.	0.9	11
6802	mTORC1 Is Transiently Reactivated in Injured Nerves to Promote c-Jun Elevation and Schwann Cell Dedifferentiation. <i>Journal of Neuroscience</i> , 2018, 38, 4811-4828.	1.7	48

#	ARTICLE	IF	CITATIONS
6803	Molecular activities and ligand-binding specificities of StAR-related lipid transfer domains: exploring integrated in silico methods and ensemble-docking approaches. SAR and QSAR in Environmental Research, 2018, 29, 483-501.	1.0	8
6804	Diversity of herbaceous plants and bacterial communities regulates soil resistome across forest biomes. Environmental Microbiology, 2018, 20, 3186-3200.	1.8	55
6805	Revealing the Inhibitory Effect of Ginseng on Mitochondrial Respiration through Synaptosomal Proteomics. Proteomics, 2018, 18, 1700354.	1.3	8
6806	Gene expression profiles reveal key genes for early diagnosis and treatment of adamantinomatous craniopharyngioma. Cancer Gene Therapy, 2018, 25, 227-239.	2.2	22
6807	A comparative analysis of rod bipolar cell transcriptomes identifies novel genes implicated in night vision. Scientific Reports, 2018, 8, 5506.	1.6	12
6808	Alternative polyadenylation drives genome-to-phenome information detours in the AMPK $\pm$ 1 and AMPK $\pm$ 2 knockout mice. Scientific Reports, 2018, 8, 6462.	1.6	10
6809	PathwaySplice: an R package for unbiased pathway analysis of alternative splicing in RNA-Seq data. Bioinformatics, 2018, 34, 3220-3222.	1.8	3
6810	Effects of PSII Manganese-Stabilizing Protein Succinylation on Photosynthesis in the Model Cyanobacterium Synechococcus sp. PCC 7002. Plant and Cell Physiology, 2018, 59, 1466-1482.	1.5	8
6811	RAPTOR Controls Developmental Growth Transitions by Altering the Hormonal and Metabolic Balance. Plant Physiology, 2018, 177, 565-593.	2.3	66
6812	Gut microbial functional maturation and succession during human early life. Environmental Microbiology, 2018, 20, 2160-2177.	1.8	30
6813	Redundancy in Anaerobic Digestion Microbiomes during Disturbances by the Antibiotic Monensin. Applied and Environmental Microbiology, 2018, 84, .	1.4	28
6814	Modulation of Protein-Interaction States through the Cell Cycle. Cell, 2018, 173, 1481-1494.e13.	13.5	116
6815	RBind: computational network method to predict RNA binding sites. Bioinformatics, 2018, 34, 3131-3136.	1.8	31
6816	Microbial <i>rRNA</i> gene expression and co-occurrence profiles associate with biokinetics and elemental composition in full-scale anaerobic digesters. Microbial Biotechnology, 2018, 11, 694-709.	2.0	42
6817	Scrutinizing key steps for reliable metabarcoding of environmental samples. Methods in Ecology and Evolution, 2018, 9, 134-147.	2.2	425
6818	Tissue Multiplatform-Based Metabolomics/Metabonomics for Enhanced Metabolome Coverage. Methods in Molecular Biology, 2018, 1738, 239-260.	0.4	8
6819	Application of pathways activity profiling to urine metabolomics for screening Qi-tonifying biomarkers and metabolic pathways of honey-processed <i>Astragalus</i> . Journal of Separation Science, 2018, 41, 2661-2671.	1.3	19
6820	Pan-cancer analysis of somatic mutations and transcriptomes reveals common functional gene clusters shared by multiple cancer types. Scientific Reports, 2018, 8, 6041.	1.6	46

#	ARTICLE	IF	CITATIONS
6821	Conservation of a domestic metapopulation structured into related and partly admixed strains. <i>Molecular Ecology</i> , 2018, 27, 1633-1650.	2.0	23
6822	Integrated Transcriptomic and Proteomic Analyses Suggest the Participation of Endogenous Protease Inhibitors in the Regulation of Protease Gene Expression in <i>Helicoverpa armigera</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1324-1336.	2.5	14
6823	Tracing of the fecal microbiota of commercial pigs at five growth stages from birth to shipment. <i>Scientific Reports</i> , 2018, 8, 6012.	1.6	100
6824	A comprehensive analysis of Wnt/ $\beta$ -catenin signaling pathway-related genes and crosstalk pathways in the treatment of As2O3 in renal cancer. <i>Renal Failure</i> , 2018, 40, 331-339.	0.8	3
6825	Mapping the tumour human leukocyte antigen (HLA) ligandome by mass spectrometry. <i>Immunology</i> , 2018, 154, 331-345.	2.0	101
6826	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	13.5	102
6827	The Evolutionary Landscape of Localized Prostate Cancers Drives Clinical Aggression. <i>Cell</i> , 2018, 173, 1003-1013.e15.	13.5	176
6828	Volatile metabolites in breath strongly correlate with gut microbiome in CD patients. <i>Analytica Chimica Acta</i> , 2018, 1025, 1-11.	2.6	64
6829	Yoink: An interaction-based partitioning API. <i>Journal of Computational Chemistry</i> , 2018, 39, 799-806.	1.5	13
6830	GKAP Acts as a Genetic Modulator of NMDAR Signaling to Govern Invasive Tumor Growth. <i>Cancer Cell</i> , 2018, 33, 736-751.e5.	7.7	53
6831	Identification of Hub Genes and Pathways in Zika Virus Infection Using RNA-Seq Data: A Network-Based Computational Approach. <i>Viral Immunology</i> , 2018, 31, 321-332.	0.6	10
6832	Integrative exploration of large high-dimensional datasets. <i>Annals of Applied Statistics</i> , 2018, 12, .	0.5	4
6833	Integrated transcriptomes throughout swine oestrous cycle reveal dynamic changes in reproductive tissues interacting networks. <i>Scientific Reports</i> , 2018, 8, 5436.	1.6	32
6834	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
6835	Understanding antidepressant discontinuation syndrome (ADS) through preclinical experimental models. <i>European Journal of Pharmacology</i> , 2018, 829, 129-140.	1.7	12
6836	Network-based meta-analysis in the identification of biomarkers for papillary thyroid cancer. <i>Gene</i> , 2018, 661, 160-168.	1.0	20
6837	saRNAdb: Resource of Small Activating RNAs for Up-regulating the Gene Expression. <i>Journal of Molecular Biology</i> , 2018, 430, 2212-2218.	2.0	5
6838	Genome-Wide Association Studies of Image Traits Reveal Genetic Architecture of Drought Resistance in Rice. <i>Molecular Plant</i> , 2018, 11, 789-805.	3.9	151

#	ARTICLE	IF	CITATIONS
6839	Network approach of the conformational change of c-Src, a tyrosine kinase, by molecular dynamics simulation. <i>Scientific Reports</i> , 2018, 8, 5673.	1.6	10
6840	Identification of biomarkers of venous thromboembolism by bioinformatics analyses. <i>Medicine (United States)</i> , 2018, 97, 10784314.	0.4	16
6841	Novel functions of the Arabidopsis transcription factor <i>TCP5</i> in petal development and ethylene biosynthesis. <i>Plant Journal</i> , 2018, 94, 867-879.	2.8	46
6842	Immune Gene Expression Profile in Hepatocellular Carcinoma and Surrounding Tissue Predicts Time to Tumor Recurrence. <i>Liver Cancer</i> , 2018, 7, 277-294.	4.2	21
6843	High-resolution definition of humoral immune response correlates of effective immunity against HIV. <i>Molecular Systems Biology</i> , 2018, 14, e7881.	3.2	37
6844	A comprehensive analysis of the predicted targets of miR-642b-3p associated with the long non-coding RNA HOXA11-AS in NSCLC cells. <i>Oncology Letters</i> , 2018, 15, 6147-6160.	0.8	17
6845	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
6846	eDNA-based bioassessment of coastal sediments impacted by an oil spill. <i>Environmental Pollution</i> , 2018, 238, 739-748.	3.7	47
6847	JAMI: fast computation of conditional mutual information for ceRNA network analysis. <i>Bioinformatics</i> , 2018, 34, 3050-3051.	1.8	13
6848	Identification of <i>ST3AGL4</i> , <i>MFHAS1</i> , <i>CSNK2A2</i> and <i>CD226</i> as loci associated with systemic lupus erythematosus (SLE) and evaluation of SLE genetics in drug repositioning. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1078-1084.	0.5	34
6849	Identification of Prognostic Biomarkers by Combined mRNA and miRNA Expression Microarray Analysis in Pancreatic Cancer. <i>Translational Oncology</i> , 2018, 11, 700-714.	1.7	40
6850	Identification of new disease genes from protein-protein interaction network. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 0, , 1.	3.3	3
6851	Profiling expression of coding genes, long noncoding RNA, and circular RNA in lung adenocarcinoma by ribosomal RNA-depleted RNA sequencing. <i>FEBS Open Bio</i> , 2018, 8, 544-555.	1.0	54
6852	Functional Genome-wide Screen Identifies Pathways Restricting Central Nervous System Axonal Regeneration. <i>Cell Reports</i> , 2018, 23, 415-428.	2.9	43
6853	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018, 6, 424-443.e7.	2.9	68
6854	PyPathway: Python Package for Biological Network Analysis and Visualization. <i>Journal of Computational Biology</i> , 2018, 25, 499-504.	0.8	3
6855	SUMO1 conjugation is altered during normal aging but not by increased amyloid burden. <i>Aging Cell</i> , 2018, 17, e12760.	3.0	15
6856	Clinical significance of high expression of miR-452-5p in lung squamous cell carcinoma. <i>Oncology Letters</i> , 2018, 15, 6418-6430.	0.8	37

#	ARTICLE	IF	CITATIONS
6857	DNA Repair Network Analysis Reveals Shieldin as a Key Regulator of NHEJ and PARP Inhibitor Sensitivity. <i>Cell</i> , 2018, 173, 972-988.e23.	13.5	349
6858	Deciphering the Combined Effects of Environmental Stressors on Gene Transcription: A Conceptual Approach. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5479-5489.	4.6	20
6859	The Pharmacophore Network: A Computational Method for Exploring Structure-Activity Relationships from a Large Chemical Data Set. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 3551-3564.	2.9	19
6860	Coupled Mutations-Enabled Glycerol Transportation in an Aquaporin Z Mutant. <i>ACS Omega</i> , 2018, 3, 4113-4122.	1.6	3
6861	Broad-Spectrum Regulation of Nonreceptor Tyrosine Kinases by the Bacterial ADP-Ribosyltransferase EspJ. <i>MBio</i> , 2018, 9, .	1.8	21
6862	Curcumin may serve an anticancer role in human osteosarcoma cell line U-2 OS by targeting ITPR1. <i>Oncology Letters</i> , 2018, 15, 5593-5601.	0.8	9
6863	Bioinformatic analysis reveals the key pathways and genes in early-onset breast cancer. <i>Medical Oncology</i> , 2018, 35, 67.	1.2	5
6864	Widespread changes in transcriptome profile of human mesenchymal stem cells induced by two-dimensional nanosilicates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3905-E3913.	3.3	119
6865	Alcohol Metabolic Inefficiency: Structural Characterization of Polymorphism-Induced ALDH2 Dysfunctionality and Allosteric Site Identification for Design of Potential Wildtype Reactivators. <i>Protein Journal</i> , 2018, 37, 216-222.	0.7	12
6866	Investigation of miR-136-5p key target genes and pathways in lung squamous cell cancer based on TCGA database and bioinformatics analysis. <i>Pathology Research and Practice</i> , 2018, 214, 644-654.	1.0	36
6867	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <i>Scientific Reports</i> , 2018, 8, 5875.	1.6	123
6868	Synergistic regulation mechanism of iperoxo and LY2119620 for muscarinic acetylcholine M2 receptor. <i>RSC Advances</i> , 2018, 8, 13067-13074.	1.7	3
6869	Coordination of meristem and boundary functions by transcription factors in the SHOOT MERISTEMLESS regulatory network. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	41
6870	Gastric cancer biomarkers; A systems biology approach. <i>Biochemistry and Biophysics Reports</i> , 2018, 13, 141-146.	0.7	20
6871	Comparative phosphoproteomic analysis reveals signaling networks regulating monopolar and bipolar cytokinesis. <i>Scientific Reports</i> , 2018, 8, 2269.	1.6	9
6872	Reconstruction of the sialylation pathway in the ancestor of eukaryotes. <i>Scientific Reports</i> , 2018, 8, 2946.	1.6	20
6873	AOP-DB: A database resource for the exploration of Adverse Outcome Pathways through integrated association networks. <i>Toxicology and Applied Pharmacology</i> , 2018, 343, 71-83.	1.3	59
6874	A Gene Regulatory Network for Cellular Reprogramming in Plant Regeneration. <i>Plant and Cell Physiology</i> , 2018, 59, 770-782.	1.5	81



#	ARTICLE	IF	CITATIONS
6875	Identification of cancer-related potential biomarkers based on lncRNA-pseudogene-mRNA competitive networks. <i>FEBS Letters</i> , 2018, 592, 973-986.	1.3	9
6876	Genome-wide gene expression analysis of 45-days pregnant fetal cotyledons vis-a-vis non-pregnant caruncles in buffalo ( <i>Bubalus bubalis</i> ). <i>Gene</i> , 2018, 654, 127-137.	1.0	12
6877	Aggregation-prone Regions in HYPK Help It to Form Sequestration Complex for Toxic Protein Aggregates. <i>Journal of Molecular Biology</i> , 2018, 430, 963-986.	2.0	17
6878	Target and untargeted GC-MS based metabolomic study of mouse optic nerve and its potential in the study of neurological visual diseases. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 153, 44-56.	1.4	13
6879	Delayed gut microbiota development in high-risk for asthma infants is temporarily modifiable by <i>Lactobacillus</i> supplementation. <i>Nature Communications</i> , 2018, 9, 707.	5.8	158
6880	Roles of Birth Mode and Infant Gut Microbiota in Intergenerational Transmission of Overweight and Obesity From Mother to Offspring. <i>JAMA Pediatrics</i> , 2018, 172, 368.	3.3	235
6881	Characterization of the nasopharyngeal and middle ear microbiota in gastroesophageal reflux-prone versus gastroesophageal reflux non-prone children. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 851-857.	1.3	17
6882	Aldolase A overexpression is associated with poor prognosis and promotes tumor progression by the epithelial-mesenchymal transition in colon cancer. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 639-645.	1.0	28
6883	Co-expression network analysis and cis-regulatory element enrichment determine putative functions and regulatory mechanisms of grapevine ATL E3 ubiquitin ligases. <i>Scientific Reports</i> , 2018, 8, 3151.	1.6	6
6884	The Mechanisms of Bushen-Yizhi Formula as a Therapeutic Agent against Alzheimer's Disease. <i>Scientific Reports</i> , 2018, 8, 3104.	1.6	46
6885	The genome sequence and transcriptome of <i>Potentilla micrantha</i> and their comparison to <i>Fragaria vesca</i> (the woodland strawberry). <i>GigaScience</i> , 2018, 7, 1-14.	3.3	37
6886	An integrated method for direct interrogation of sphingolipid homeostasis in the heart and brain tissues of mice through postnatal development up to reproductive senescence. <i>Analytica Chimica Acta</i> , 2018, 1037, 152-158.	2.6	20
6887	Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules. <i>Cell</i> , 2018, 172, 590-604.e13.	13.5	672
6888	Acclimation-induced metabolic reprogramming contributes to rapid desiccation tolerance acquisition in <i>Boea hygrometrica</i> . <i>Environmental and Experimental Botany</i> , 2018, 148, 70-84.	2.0	23
6889	High-Density Proximity Mapping Reveals the Subcellular Organization of mRNA-Associated Granules and Bodies. <i>Molecular Cell</i> , 2018, 69, 517-532.e11.	4.5	583
6890	rSNPBase 3.0: an updated database of SNP-related regulatory elements, element-gene pairs and SNP-based gene regulatory networks. <i>Nucleic Acids Research</i> , 2018, 46, D1111-D1116.	6.5	26
6891	Comprehensive analysis of the lysine acetylome and its potential regulatory roles in the virulence of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2018, 176, 46-55.	1.2	37
6892	Asymmetric dimethylarginine (ADMA) is identified as a potential biomarker of insulin resistance in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 2133.	1.6	29



#	ARTICLE	IF	CITATIONS
6893	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2455-2464.	1.7	47
6894	Combined analysis of DNA methylation and gene expression profiles of osteosarcoma identified several prognosis signatures. <i>Gene</i> , 2018, 650, 7-14.	1.0	53
6899	Combined Analysis of Stress- and ECM-Related Genes in Their Effect on Weight Regain. <i>Obesity</i> , 2018, 26, 492-498.	1.5	11
6900	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018, 430, 1024-1050.	2.0	32
6901	A computationally driven analysis of the polyphenol-protein interactome. <i>Scientific Reports</i> , 2018, 8, 2232.	1.6	59
6902	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , 2018, 34, 2150-2152.	1.8	109
6903	Network Analysis to Risk Stratify Patients With Exercise Intolerance. <i>Circulation Research</i> , 2018, 122, 864-876.	2.0	42
6904	Initiating Events in Direct Cardiomyocyte Reprogramming. <i>Cell Reports</i> , 2018, 22, 1913-1922.	2.9	23
6905	Inhibition of hepatocellular carcinoma tumorigenesis by curcumin may be associated with CDKN1A and CTGF. <i>Gene</i> , 2018, 651, 183-193.	1.0	20
6906	A citation network analysis of lithic microwear research. <i>Journal of Archaeological Science</i> , 2018, 91, 33-42.	1.2	7
6907	Metabolomic response of a marine bacterium to 3,6-anhydro- $\alpha$ -D-galactose, the rare sugar from red macroalgae, as the sole carbon source. <i>Journal of Biotechnology</i> , 2018, 270, 12-20.	1.9	2
6908	Improving water quality using settleable microalga <i>Ettlia</i> sp. and the bacterial community in freshwater recirculating aquaculture system of <i>Danio rerio</i> . <i>Water Research</i> , 2018, 135, 112-121.	5.3	32
6909	Fragment-Based Screening of a Natural Product Library against 62 Potential Malaria Drug Targets Employing Native Mass Spectrometry. <i>ACS Infectious Diseases</i> , 2018, 4, 431-444.	1.8	50
6910	Metabolomics-based chemotaxonomy of root endophytic fungi for natural products discovery. <i>Environmental Microbiology</i> , 2018, 20, 1253-1270.	1.8	24
6911	Exploration of the platelet proteome in patients with early-stage cancer. <i>Journal of Proteomics</i> , 2018, 177, 65-74.	1.2	65
6912	Unraveling the transcriptional complexity of compactness in sistan grape cluster. <i>Plant Science</i> , 2018, 270, 198-208.	1.7	10
6913	Clinical and Genomic Correlates of Neutrophil Reactive Oxygen Species Production in Pediatric Patients With Crohn's Disease. <i>Gastroenterology</i> , 2018, 154, 2097-2110.	0.6	63
6914	Comprehensive Analysis of DNA Methylation and Gene Expression Datasets Identified MMP9 and TWIST1 as Important Pathogenic Genes of Lung Adenocarcinoma. <i>DNA and Cell Biology</i> , 2018, 37, 336-346.	0.9	5

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6915	A system view and analysis of essential hypertension. <i>Journal of Hypertension</i> , 2018, 36, 1094-1103.	0.3	13
6916	Discovering Putative Peptides Encoded from Noncoding RNAs in Ribosome Profiling Data of <i>Arabidopsis thaliana</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 655-663.	1.9	6
6917	The Biotrophic Development of <i>Ustilago maydis</i> Studied by RNA-Seq Analysis. <i>Plant Cell</i> , 2018, 30, 300-323.	3.1	186
6918	Specific plasmid patterns and high rates of bacterial occurrence within the coral holobiont. <i>Ecology and Evolution</i> , 2018, 8, 1818-1832.	0.8	27
6919	The regulatory network analysis of long noncoding RNAs in human colorectal cancer. <i>Functional and Integrative Genomics</i> , 2018, 18, 261-275.	1.4	22
6920	NGS-based methylation profiling differentiates TCF3-HLF and TCF3-PBX1 positive B-cell acute lymphoblastic leukemia. <i>Epigenomics</i> , 2018, 10, 133-147.	1.0	10
6921	Plant Response to Metal-Containing Engineered Nanomaterials: An Omics-Based Perspective. <i>Environmental Science &amp; Technology</i> , 2018, 52, 2451-2467.	4.6	106
6922	Changes in bacterioplankton community structure during early lake ontogeny resulting from the retreat of the Greenland Ice Sheet. <i>ISME Journal</i> , 2018, 12, 544-555.	4.4	16
6923	<i>WRKY1</i> acts as a key component improving resistance against <i>Alternaria solani</i> in wild tomato, <i>Solanum arcanum</i> Peralta. <i>Plant Biotechnology Journal</i> , 2018, 16, 1502-1513.	4.1	31
6924	Identification of Novel Potentially Pleiotropic Variants Associated With Osteoporosis and Obesity Using the cFDR Method. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 125-138.	1.8	39
6925	A quantitative and temporal map of proteostasis during heat shock in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2018, 14, 37-52.	1.4	17
6926	Genome-wide analysis of AP2/ERF transcription factors in zoysiagrass, <i>Zoysia japonica</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 303-308.	0.5	27
6927	Cell-type-resolved alternative splicing patterns in mouse liver. <i>DNA Research</i> , 2018, 25, 265-275.	1.5	14
6928	Integrated analysis of the genetic basis of suicidal behavior. <i>Psychiatric Genetics</i> , 2018, 28, 31-37.	0.6	10
6929	Metabolomic response to coffee consumption: application to a three-stage clinical trial. <i>Journal of Internal Medicine</i> , 2018, 283, 544-557.	2.7	39
6930	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	2.8	133
6931	Discrete roles and bifurcation of PTEN signaling and mTORC1-mediated anabolic metabolism underlie IL-7-driven B lymphopoiesis. <i>Science Advances</i> , 2018, 4, eaar5701.	4.7	35
6932	Ancient Diversification of Three-Finger Toxins in <i>Micrurus</i> Coral Snakes. <i>Journal of Molecular Evolution</i> , 2018, 86, 58-67.	0.8	30

#	ARTICLE	IF	CITATIONS
6933	The GARP/MYB-related grape transcription factor AQUILO improves cold tolerance and promotes the accumulation of raffinose family oligosaccharides. <i>Journal of Experimental Botany</i> , 2018, 69, 1749-1764.	2.4	74
6934	Combined analysis of gene expression and genome binding profiles identified potential therapeutic targets of ciclopirox in Ewing sarcoma. <i>Molecular Medicine Reports</i> , 2018, 17, 4291-4298.	1.1	7
6935	Systematical analysis of lncRNA-mRNA competing endogenous RNA network in breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2018, 169, 267-275.	1.1	47
6936	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 826-834.	2.5	36
6937	GEMMER: GENome-wide tool for Multi-scale Modeling data Extraction and Representation for <i>Saccharomyces cerevisiae</i> . <i>Bioinformatics</i> , 2018, 34, 2147-2149.	1.8	6
6938	Anterior Pituitary Transcriptome Suggests Differences in ACTH Release in Tame and Aggressive Foxes. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 859-873.	0.8	26
6939	Construction and investigation of lncRNA-associated ceRNA regulatory network in papillary thyroid cancer. <i>Oncology Reports</i> , 2018, 39, 1197-1206.	1.2	71
6940	Bioinformatics Support for Farm Animal Proteomics. , 2018, , 361-386.		0
6941	The Genotype-Phenotype Relationships in the Light of Natural Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 525-542.	3.5	16
6943	3D-Chem: Structural Cheminformatics Workflows for Computer-Aided Drug Discovery. <i>ChemMedChem</i> , 2018, 13, 614-626.	1.6	17
6944	Mapping an Entrepreneurial, Innovative and Sustainable Ecosystem Using Social Network Analysis: An Exploratory Approach of Publicly Funded Innovative Project Data. <i>Applying Quality of Life Research</i> , 2018, , 237-254.	0.3	0
6945	Cross-regulatory network in <i>Pseudomonas aeruginosa</i> biofilm genes and TiO <sub>2</sub> anatase induced molecular perturbations in key proteins unraveled by a systems biology approach. <i>Gene</i> , 2018, 647, 289-296.	1.0	15
6946	Information Diffusion on Social Media During Natural Disasters. <i>IEEE Transactions on Computational Social Systems</i> , 2018, 5, 265-276.	3.2	59
6947	Corallivory and the microbial debacle in two branching scleractinians. <i>ISME Journal</i> , 2018, 12, 1109-1126.	4.4	18
6948	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. <i>Bioinformatics</i> , 2018, 34, 1428-1430.	1.8	17
6949	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.	6.5	197
6950	Unification of Protein Abundance Datasets Yields a Quantitative <i>Saccharomyces cerevisiae</i> Proteome. <i>Cell Systems</i> , 2018, 6, 192-205.e3.	2.9	349
6951	Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. <i>ISME Journal</i> , 2018, 12, 1210-1224.	4.4	188

#	ARTICLE	IF	CITATIONS
6952	Integration of GWAS, pathway and network analyses reveals novel mechanistic insights into the synthesis of milk proteins in dairy cows. <i>Scientific Reports</i> , 2018, 8, 566.	1.6	39
6953	Interactive network visualization in Jupyter notebooks: visJS2jupyter. <i>Bioinformatics</i> , 2018, 34, 126-128.	1.8	14
6954	High Expression of TET1 Predicts Poor Survival in Cytogenetically Normal Acute Myeloid Leukemia From Two Cohorts. <i>EBioMedicine</i> , 2018, 28, 90-96.	2.7	33
6955	Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. <i>Scientific Reports</i> , 2018, 8, 1413.	1.6	58
6956	A Useful Guide of Main Indices and Software Used for Ecological Networks Studies. , 2018, , 185-196.		10
6957	A metabolomic map of Zellweger spectrum disorders reveals novel disease biomarkers. <i>Genetics in Medicine</i> , 2018, 20, 1274-1283.	1.1	40
6958	Differentiated surface fungal communities at point of harvest on apple fruits from rural and peri-urban orchards. <i>Scientific Reports</i> , 2018, 8, 2165.	1.6	31
6959	Social status shapes the bacterial and fungal gut communities of the honey bee. <i>Scientific Reports</i> , 2018, 8, 2019.	1.6	64
6960	Bioinformatic analyses of microRNA-targeted genes and microarray-identified genes correlated with Barrett's esophagus. <i>Cell Cycle</i> , 2018, 17, 792-800.	1.3	9
6961	A Regulatory Circuitry Between Gria2, miR-409, and miR-495 Is Affected by ALS FUS Mutation in ESC-Derived Motor Neurons. <i>Molecular Neurobiology</i> , 2018, 55, 7635-7651.	1.9	32
6962	miR-145 overexpression triggers alteration of the whole transcriptome and inhibits breast cancer development. <i>Biomedicine and Pharmacotherapy</i> , 2018, 100, 72-82.	2.5	34
6963	Identification of metabolic pathway disturbances using multimodal metabolomics in autistic disorders in a Middle Eastern population. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 152, 57-65.	1.4	49
6964	Three-step transcriptional priming that drives the commitment of multipotent progenitors toward B cells. <i>Genes and Development</i> , 2018, 32, 112-126.	2.7	24
6965	Microarray analysis reveals Tmub1 as a cell cycle-associated protein in rat hepatocytes. <i>Molecular Medicine Reports</i> , 2018, 17, 4337-4344.	1.1	7
6966	Pathways. , 2018, , 95-123.		0
6967	Network pharmacology-based analysis of Chinese herbal Naodesheng formula for application to Alzheimer's disease. <i>Chinese Journal of Natural Medicines</i> , 2018, 16, 53-62.	0.7	37
6968	Alanine mutation of the catalytic sites of Pantothenate Synthetase causes distinct conformational changes in the ATP binding region. <i>Scientific Reports</i> , 2018, 8, 903.	1.6	18
6969	Integrated miRNA-mRNA spatial signature for oral squamous cell carcinoma: a prospective profiling study of Narrow Band Imaging guided resection. <i>Scientific Reports</i> , 2018, 8, 823.	1.6	22

#	ARTICLE	IF	CITATIONS
6970	Characterization of moso bamboo ( <i>Phyllostachys edulis</i> ) Dof transcription factors in floral development and abiotic stress responses. <i>Genome</i> , 2018, 61, 151-156.	0.9	16
6971	Neuroimaging meta-analysis of cannabis use studies reveals convergent functional alterations in brain regions supporting cognitive control and reward processing. <i>Journal of Psychopharmacology</i> , 2018, 32, 283-295.	2.0	54
6972	Integrated analysis of single-cell embryo data yields a unified transcriptome signature for the human preimplantation epiblast. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	155
6973	Preoperative anemia in colorectal cancer: relationships with tumor characteristics, systemic inflammation, and survival. <i>Scientific Reports</i> , 2018, 8, 1126.	1.6	90
6974	Identification of CDK2 as a novel target in treatment of prostate cancer. <i>Future Oncology</i> , 2018, 14, 709-718.	1.1	37
6975	Discovering Altered Regulation and Signaling Through Network-based Integration of Transcriptomic, Epigenomic, and Proteomic Tumor Data. <i>Methods in Molecular Biology</i> , 2018, 1711, 13-26.	0.4	11
6976	Modular origins of biological electron transfer chains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1280-1285.	3.3	29
6977	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018, 220, 1161-1171.	3.5	206
6978	Detection of Combinatorial Mutational Patterns in Human Cancer Genomes by Exclusivity Analysis. <i>Methods in Molecular Biology</i> , 2018, 1711, 3-11.	0.4	1
6979	The PEG-responding desiccome of the alder microsymbiont <i>Frankia alni</i> . <i>Scientific Reports</i> , 2018, 8, 759.	1.6	14
6980	Comparative analysis of mouse and human placentae across gestation reveals species-specific regulators of placental development. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	120
6981	Community Diff. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2018, 12, 1-34.	2.5	5
6982	Prebiotic Chemistry of HCN Tetramerization by Automated Reaction Search. <i>Chemistry - A European Journal</i> , 2018, 24, 4885-4894.	1.7	28
6983	Network analysis of SRC-1 reveals a novel transcription factor hub which regulates endocrine resistant breast cancer. <i>Oncogene</i> , 2018, 37, 2008-2021.	2.6	23
6984	MWASTools: an R/bioconductor package for metabolome-wide association studies. <i>Bioinformatics</i> , 2018, 34, 890-892.	1.8	18
6985	A network-based meta-analysis for characterizing the genetic landscape of human aging. <i>Biogerontology</i> , 2018, 19, 81-94.	2.0	16
6986	Microbiome Influences Prenatal and Adult Microglia in a Sex-Specific Manner. <i>Cell</i> , 2018, 172, 500-516.e16.	13.5	563
6987	Identification of the potential targets for keloid and hypertrophic scar prevention. <i>Journal of Dermatological Treatment</i> , 2018, 29, 600-605.	1.1	15

#	ARTICLE	IF	CITATIONS
6988	Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. <i>Anaerobe</i> , 2018, 49, 121-131.	1.0	249
6989	Unravelling the differences: comparative proteomic analysis of a clonal virulent and an attenuated <i>Histomonas meleagridis</i> strain. <i>International Journal for Parasitology</i> , 2018, 48, 145-157.	1.3	24
6990	Contributions of ryegrass, lignin and rhamnolipid to polycyclic aromatic hydrocarbon dissipation in an arable soil. <i>Soil Biology and Biochemistry</i> , 2018, 118, 27-34.	4.2	39
6991	MiR-184 expression is regulated by AMPK in pancreatic islets. <i>FASEB Journal</i> , 2018, 32, 2587-2600.	0.2	39
6992	Dysbiosis Signatures of Gut Microbiota Along the Sequence from Healthy, Young Patients to Those with Overweight and Obesity. <i>Obesity</i> , 2018, 26, 351-361.	1.5	155
6993	Bacterial rather than fungal community composition is associated with microbial activities and nutrient-use efficiencies in a paddy soil with short-term organic amendments. <i>Plant and Soil</i> , 2018, 424, 335-349.	1.8	88
6994	A Proximity Labeling Strategy Provides Insights into the Composition and Dynamics of Lipid Droplet Proteomes. <i>Developmental Cell</i> , 2018, 44, 97-112.e7.	3.1	240
6995	Rewiring of the Fruit Metabolome in Tomato Breeding. <i>Cell</i> , 2018, 172, 249-261.e12.	13.5	606
6996	Autochthonous facility-specific microbiota dominates washed-rind Austrian hard cheese surfaces and its production environment. <i>International Journal of Food Microbiology</i> , 2018, 267, 54-61.	2.1	31
6997	Proteomic analysis reveals the important roles of alpha-5-collagen and ATP5 <sup>Î²</sup> during skin ulceration syndrome progression of sea cucumber <i>Apostichopus japonicus</i> . <i>Journal of Proteomics</i> , 2018, 175, 136-143.	1.2	14
6998	Proteomics and Metabolomics for AKI Diagnosis. <i>Seminars in Nephrology</i> , 2018, 38, 63-87.	0.6	59
6999	Gestational diabetes exacerbates maternal immune activation effects in the developing brain. <i>Molecular Psychiatry</i> , 2018, 23, 1920-1928.	4.1	51
7000	Metabolomics and Precision Medicine in Trauma: The State of the Field. <i>Shock</i> , 2018, 50, 5-13.	1.0	18
7001	Proliferation genes in lung development associated with the prognosis of lung adenocarcinoma but not squamous cell carcinoma. <i>Cancer Science</i> , 2018, 109, 308-316.	1.7	9
7002	Glycosphingolipid metabolic reprogramming drives neural differentiation. <i>EMBO Journal</i> , 2018, 37, .	3.5	56
7003	Role of mTOR in autophagic and lysosomal reactions to environmental stressors in molluscs. <i>Aquatic Toxicology</i> , 2018, 195, 114-128.	1.9	37
7004	In vitro genotoxic effect of secondary minerals crystallized in rocks from coal mine drainage. <i>Journal of Hazardous Materials</i> , 2018, 346, 263-272.	6.5	75
7005	Co-occurrence patterns of soybean rhizosphere microbiome at a continental scale. <i>Soil Biology and Biochemistry</i> , 2018, 118, 178-186.	4.2	258

#	ARTICLE	IF	CITATIONS
7006	A candidate tolerance gene identified in a natural population of field voles ( <i>Microtus agrestis</i> ). <i>Molecular Ecology</i> , 2018, 27, 1044-1052.	2.0	13
7007	Transcriptome comparison of meniscus from patients with and without osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2018, 26, 422-432.	0.6	50
7008	Pilot investigation on formation of 2,4,6-trichloroanisole via microbial O-methylation of 2,4,6-trichlorophenol in drinking water distribution system: An insight into microbial mechanism. <i>Water Research</i> , 2018, 131, 11-21.	5.3	44
7009	The effect of electron competition on chromate reduction using methane as electron donor. <i>Environmental Science and Pollution Research</i> , 2018, 25, 6609-6618.	2.7	20
7010	Gene Network Analysis of Interstitial Macrophages After Treatment with Induced Pluripotent Stem Cells Secretome (iPSC-cm) in the Bleomycin Injured Rat Lung. <i>Stem Cell Reviews and Reports</i> , 2018, 14, 412-424.	5.6	14
7011	Various cellular stress components change as the rat ages: An insight into the putative overall age-related cellular stress network. <i>Experimental Gerontology</i> , 2018, 102, 36-42.	1.2	5
7012	Dynamic miRNA-mRNA regulations are essential for maintaining <i>Drosophila</i> immune homeostasis during <i>Micrococcus luteus</i> infection. <i>Developmental and Comparative Immunology</i> , 2018, 81, 210-224.	1.0	19
7013	Proteomic analysis of <i>Bombyx mori</i> molting fluid: Insights into the molting process. <i>Journal of Proteomics</i> , 2018, 173, 115-125.	1.2	28
7014	Coelacanth-specific adaptive genes give insights into primitive evolution for water-to-land transition of tetrapods. <i>Marine Genomics</i> , 2018, 38, 89-95.	0.4	1
7015	Field study reveals core plant microbiota and relative importance of their drivers. <i>Environmental Microbiology</i> , 2018, 20, 124-140.	1.8	255
7016	Comparative transcriptomic analysis of human placentae at term and preterm delivery. <i>Biology of Reproduction</i> , 2018, 98, 89-101.	1.2	23
7017	Genomic islands of differentiation in two songbird species reveal candidate genes for hybrid female sterility. <i>Molecular Ecology</i> , 2018, 27, 949-958.	2.0	25
7018	Contrasting Network Features between Free-Living and Particle-Attached Bacterial Communities in Taihu Lake. <i>Microbial Ecology</i> , 2018, 76, 303-313.	1.4	46
7019	Integrated microRNA and mRNA signatures in peripheral blood lymphocytes of familial epithelial ovarian cancer. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 191-198.	1.0	5
7020	funRiceGenes dataset for comprehensive understanding and application of rice functional genes. <i>GigaScience</i> , 2018, 7, 1-9.	3.3	86
7021	What do the genetic association data say about the high risk of suicide in people with depression? A novel network-based approach to find common molecular basis for depression and suicidal behavior and related therapeutic targets. <i>Journal of Affective Disorders</i> , 2018, 229, 463-468.	2.0	12
7022	Immunomodulatory effect of CD200-positive human placenta-derived stem cells in the early phase of stroke. <i>Experimental and Molecular Medicine</i> , 2018, 50, e425-e425.	3.2	29
7023	The eukaryotic linear motif resource – 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	6.5	183



#	ARTICLE	IF	CITATIONS
7024	Application of Weighted Gene Co-expression Network Analysis for Data from Paired Design. <i>Scientific Reports</i> , 2018, 8, 622.	1.6	120
7025	Dual gene activation and knockout screen reveals directional dependencies in genetic networks. <i>Nature Biotechnology</i> , 2018, 36, 170-178.	9.4	120
7026	Visualization and analysis of non-covalent contacts using the Protein Contacts Atlas. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 185-194.	3.6	103
7027	Protistan parasites along oxygen gradients in a seasonally anoxic fjord: A network approach to assessing potential host-parasite interactions. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 156, 97-110.	0.6	28
7028	RINspecter: a Cytoscape app for centrality analyses and DynaMine flexibility prediction. <i>Bioinformatics</i> , 2018, 34, 294-296.	1.8	23
7029	The planarian TCF/LEF factor <i>Smed-tcf1</i> is required for the regeneration of dorsal-lateral neuronal subtypes. <i>Developmental Biology</i> , 2018, 433, 374-383.	0.9	20
7030	TDP-43 pathology disrupts nuclear pore complexes and nucleocytoplasmic transport in ALS/FTD. <i>Nature Neuroscience</i> , 2018, 21, 228-239.	7.1	404
7031	Parasitological and immunological evaluation of cattle experimentally infected with <i>Trypanosoma vivax</i> . <i>Experimental Parasitology</i> , 2018, 185, 98-106.	0.5	5
7032	Network-Guided Discovery of Extensive Epistasis between Transcription Factors Involved in Aliphatic Glucosinolate Biosynthesis. <i>Plant Cell</i> , 2018, 30, 178-195.	3.1	40
7033	Bacterial community assembly from cow teat skin to ripened cheeses is influenced by grazing systems. <i>Scientific Reports</i> , 2018, 8, 200.	1.6	71
7034	aBiofilm: a resource of anti-biofilm agents and their potential implications in targeting antibiotic drug resistance. <i>Nucleic Acids Research</i> , 2018, 46, D894-D900.	6.5	98
7035	Comparative analysis of gene expression in maternal peripheral blood and monocytes during spontaneous preterm labor. <i>American Journal of Obstetrics and Gynecology</i> , 2018, 218, 345.e1-345.e30.	0.7	47
7036	Physiological effects caused by microcystin-producing and non-microcystin producing <i>Microcystis aeruginosa</i> on medaka fish: A proteomic and metabolomic study on liver. <i>Environmental Pollution</i> , 2018, 234, 523-537.	3.7	51
7037	Adaptation to high zinc depends on distinct mechanisms in metal-tolerant populations of <i>Arabidopsis halleri</i> . <i>New Phytologist</i> , 2018, 218, 269-282.	3.5	90
7038	GeneDive: A gene interaction search and visualization tool to facilitate precision medicine. , 2018, , .		3
7039	Circadian clock genes are differentially modulated during the daily cycles and chronological age in the social honeybee ( <i>Apis mellifera</i> ). <i>Apidologie</i> , 2018, 49, 71-83.	0.9	3
7040	Sirtuin 1-Chromatin-Binding Dynamics Points to a Common Mechanism Regulating Inflammatory Targets in SIV Infection and in the Aging Brain. <i>Journal of NeuroImmune Pharmacology</i> , 2018, 13, 163-178.	2.1	15
7041	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. <i>American Journal of Human Genetics</i> , 2018, 102, 58-68.	2.6	32

#	ARTICLE	IF	CITATIONS
7042	Drug-Driven Phenotypic Convergence Supports Rational Treatment Strategies of Chronic Infections. <i>Cell</i> , 2018, 172, 121-134.e14.	13.5	131
7043	motifStack for the analysis of transcription factor binding site evolution. <i>Nature Methods</i> , 2018, 15, 8-9.	9.0	74
7044	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , 2018, 46, e33-e33.	6.5	104
7045	Systematic identification of mitochondrial lysine succinylome in silkworm ( <i>Bombyx mori</i> ) midgut during the larval gluttonous stage. <i>Journal of Proteomics</i> , 2018, 174, 61-70.	1.2	12
7046	Lysine Succinylation Contributes to Aflatoxin Production and Pathogenicity in <i>Aspergillus flavus</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 457-471.	2.5	59
7047	Sequential feature selection and inference using multi-variate random forests. <i>Bioinformatics</i> , 2018, 34, 1336-1344.	1.8	7
7048	Document co-citation analysis to enhance transdisciplinary research. <i>Science Advances</i> , 2018, 4, e1701130.	4.7	181
7049	A network-based analysis of the human TET Gene Family. <i>Biologia (Poland)</i> , 2018, 73, 415-423.	0.8	0
7050	Genome-wide association study for milking speed in French Holstein cows. <i>Journal of Dairy Science</i> , 2018, 101, 6205-6219.	1.4	39
7051	Identification of differential expression lncRNAs in gastric cancer using transcriptome sequencing and bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 8189-8195.	1.1	11
7052	Low-level laser irradiation induces a transcriptional myotube-like profile in C2C12 myoblasts. <i>Lasers in Medical Science</i> , 2018, 33, 1673-1683.	1.0	6
7053	Molecular aspect of silver nanoparticles regulated embryonic development in Zebrafish ( <i>Danio rerio</i> ) by Oct-4 expression. <i>Chemosphere</i> , 2018, 206, 560-567.	4.2	26
7054	Text mining and network analysis to find functional associations of genes in high altitude diseases. <i>Computational Biology and Chemistry</i> , 2018, 75, 101-110.	1.1	17
7055	New insights into the phylogeny of the TMBIM superfamily across the tree of life: Comparative genomics and synteny networks reveal independent evolution of the BI and LFG families in plants. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 266-278.	1.2	15
7056	Transcriptional analysis and histochemistry reveal that hypersensitive cell death and H <sub>2</sub> O <sub>2</sub> have crucial roles in the resistance of tea plant ( <i>Camellia sinensis</i> (L.) O. Kuntze) to anthracnose. <i>Horticulture Research</i> , 2018, 5, 18.	2.9	46
7057	Discriminate the response of Acute Myeloid Leukemia patients to treatment by using proteomics data and Answer Set Programming. <i>BMC Bioinformatics</i> , 2018, 19, 59.	1.2	10
7058	An integrated approach to infer cross-talks between intracellular protein transport and signaling pathways. <i>BMC Bioinformatics</i> , 2018, 19, 58.	1.2	5
7059	Genexpi: a toolset for identifying regulons and validating gene regulatory networks using time-course expression data. <i>BMC Bioinformatics</i> , 2018, 19, 137.	1.2	9

#	ARTICLE	IF	CITATIONS
7060	Systematic analysis of the lysine malonylome in common wheat. <i>BMC Genomics</i> , 2018, 19, 209.	1.2	30
7061	A comparative genomics study of carbohydrate/glucose metabolic genes: from fish to mammals. <i>BMC Genomics</i> , 2018, 19, 246.	1.2	40
7062	miR-148b-3p functions as a tumor suppressor in GISTs by directly targeting KIT. <i>Cell Communication and Signaling</i> , 2018, 16, 16.	2.7	29
7063	Characterization and potential role of microRNA in the Chinese dominant malaria mosquito <i>Anopheles sinensis</i> (Diptera: Culicidae) throughout four different life stages. <i>Cell and Bioscience</i> , 2018, 8, 29.	2.1	9
7064	VIM-positive <i>Pseudomonas aeruginosa</i> in a large tertiary care hospital: matched case-control studies and a network analysis. <i>Antimicrobial Resistance and Infection Control</i> , 2018, 7, 32.	1.5	18
7065	Grapevine rootstocks shape underground bacterial microbiome and networking but not potential functionality. <i>Microbiome</i> , 2018, 6, 3.	4.9	194
7066	A comparison of methods used to unveil the genetic and metabolic pool in the built environment. <i>Microbiome</i> , 2018, 6, 71.	4.9	19
7067	Exploring Biological Networks in 3D, Stereoscopic 3D, and Immersive 3D with iCAVE. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.27.1-8.27.26.	25.8	6
7068	Genome-wide expression analysis suggests a role for jasmonates in the resistance to blue mold in apple. <i>Plant Growth Regulation</i> , 2018, 85, 375-387.	1.8	8
7069	Screening and analysis of key active constituents in Guanxinshutong capsule using mass spectrum and integrative network pharmacology. <i>Chinese Journal of Natural Medicines</i> , 2018, 16, 302-312.	0.7	9
7070	Transcriptional profiling of human bronchial epithelial cell BEAS-2B exposed to diesel and biomass ultrafine particles. <i>BMC Genomics</i> , 2018, 19, 302.	1.2	43
7071	Identification of novel drug targets for diamond-blackfan anemia based on RPS19 gene mutation using protein-protein interaction network. <i>BMC Systems Biology</i> , 2018, 12, 39.	3.0	15
7072	Plasma proteomic analysis reveals altered protein abundances in cardiovascular disease. <i>Journal of Translational Medicine</i> , 2018, 16, 104.	1.8	48
7073	Transcription factors <i>Tp73</i> , <i>Cebpd</i> , <i>Pax6</i> , and <i>Spi1</i> rather than DNA methylation regulate chronic transcriptomics changes after experimental traumatic brain injury. <i>Acta Neuropathologica Communications</i> , 2018, 6, 17.	2.4	28
7074	Preliminary exploration of co-functional gene networks for wireless sensor networks. , 2018, , .		1
7075	Assessment of Embryo-Induced Transcriptomic Changes in Hamster Uterus Using RNA-Seq. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 1868-1878.	1.1	11
7076	Transcriptome analysis reveals enrichment of genes associated with auditory system in swimbladder of channel catfish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 27, 30-39.	0.4	8
7077	Bronchiolitis obliterans syndrome susceptibility and the pulmonary microbiome. <i>Journal of Heart and Lung Transplantation</i> , 2018, 37, 1131-1140.	0.3	23

#	ARTICLE	IF	CITATIONS
7078	Sauchinone controls hepatic cholesterol homeostasis by the negative regulation of PCSK9 transcriptional network. <i>Scientific Reports</i> , 2018, 8, 6737.	1.6	26
7079	Genome-wide Identification and characterization of circular RNAs in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2018, 8, 6757.	1.6	13
7080	Transcriptome analysis reveals hybridization-induced genome shock in an interspecific <i>F<sub>1</sub></i> hybrid from <i>Camellia</i> . <i>Genome</i> , 2018, 61, 477-485.	0.9	7
7081	Inflammatory genes are novel prognostic biomarkers for colorectal cancer. <i>International Journal of Molecular Medicine</i> , 2018, 42, 368-380.	1.8	24
7082	Whole-exome sequencing and microRNA profiling reveal PI3K/AKT pathway's involvement in juvenile myelomonocytic leukemia. <i>Quantitative Biology</i> , 2018, 6, 85-97.	0.3	1
7083	Shortening the list of essential genes in the human genome by network analysis. <i>Meta Gene</i> , 2018, 17, 68-77.	0.3	3
7084	An RNAi-mediated screen identifies novel targets for next-generation antiepileptic drugs based on increased expression of the homeostatic regulator pumilio. <i>Journal of Neurogenetics</i> , 2018, 32, 106-117.	0.6	3
7085	Micromanaging freeze tolerance: the biogenesis and regulation of neuroprotective microRNAs in frozen brains. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 3635-3647.	2.4	33
7086	Understanding the structural and energetic basis of PD-1 and monoclonal antibodies bound to PD-L1: A molecular modeling perspective. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 576-588.	1.1	21
7087	Fasting and refeeding induces changes in the mouse hepatic lipid droplet proteome. <i>Journal of Proteomics</i> , 2018, 181, 213-224.	1.2	33
7088	Characterization of the Small Intestinal Lesion in Celiac Disease by Label-Free Quantitative Mass Spectrometry. <i>American Journal of Pathology</i> , 2018, 188, 1563-1579.	1.9	12
7089	Ethanol Induced Disordering of Pancreatic Acinar Cell Endoplasmic Reticulum: An ER Stress/Defective Unfolded Protein Response Model. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 5, 479-497.	2.3	19
7090	The Correlation Between the Immune and Epithelial-Mesenchymal Transition Signatures Suggests Potential Therapeutic Targets and Prognosis Prediction Approaches in Kidney Cancer. <i>Scientific Reports</i> , 2018, 8, 6570.	1.6	20
7091	Contrasting beneficial and pathogenic microbial communities across consecutive cropping fields of greenhouse strawberry. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5717-5729.	1.7	54
7092	The abundance and diversity of antibiotic resistance genes in the atmospheric environment of composting plants. <i>Environment International</i> , 2018, 116, 229-238.	4.8	92
7093	Biomedical Informatics on the Cloud. <i>Circulation Research</i> , 2018, 122, 1290-1301.	2.0	22
7095	Relationships between digestive efficiency and metabolomic profiles of serum and intestinal contents in chickens. <i>Scientific Reports</i> , 2018, 8, 6678.	1.6	20
7096	Screening potential biomarkers for colorectal cancer based on circular RNA chips. <i>Oncology Reports</i> , 2018, 39, 2499-2512.	1.2	46

#	ARTICLE	IF	CITATIONS
7097	Arabidopsis HEAT SHOCK TRANSCRIPTION FACTOR1b regulates multiple developmental genes under benign and stress conditions. <i>Journal of Experimental Botany</i> , 2018, 69, 2847-2862.	2.4	56
7098	A survey on Protein Protein Interactions (PPI) methods, databases, challenges and future directions. , 2018, , .		3
7099	EClerize: A customized force-directed graph drawing algorithm for biological graphs with EC attributes. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1850007.	0.3	1
7100	Redox Regulation, Rather than Stress-Induced Phosphorylation, of a Hog1 Mitogen-Activated Protein Kinase Modulates Its Nitrosative-Stress-Specific Outputs. <i>MBio</i> , 2018, 9, .	1.8	23
7101	Alterations of circular RNAs in hyperglycemic human endothelial cells. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 551-555.	1.0	27
7102	Gene expression profiling of human bronchial epithelial cells exposed to fine particulate matter (PM) Tj ETQq1 1 0.784314 rgBT /Over bo	1.3	9
7103	Methylation-to-Expression Feature Models of Breast Cancer Accurately Predict Overall Survival, Distant-Recurrence Free Survival, and Pathologic Complete Response in Multiple Cohorts. <i>Scientific Reports</i> , 2018, 8, 5190.	1.6	9
7104	Identification of key genes and miRNAs associated with carotid atherosclerosis based on mRNA-seq data. <i>Medicine (United States)</i> , 2018, 97, e9832.	0.4	21
7105	Fertilizer N application rate impacts plant-soil feedback in a sanqi production system. <i>Science of the Total Environment</i> , 2018, 633, 796-807.	3.9	113
7106	MicroRNA Expression Levels Are Altered in the Cerebrospinal Fluid of Patients with Young-Onset Alzheimer's Disease. <i>Molecular Neurobiology</i> , 2018, 55, 8826-8841.	1.9	111
7107	Proteomic Profiling of Integrin Adhesion Complex Assembly. <i>Methods in Molecular Biology</i> , 2018, 1764, 193-236.	0.4	10
7108	Automated Computational Inference of Multi-protein Assemblies from Biochemical Co-purification Data. <i>Methods in Molecular Biology</i> , 2018, 1764, 391-399.	0.4	1
7109	Deciphering the proteinâ€DNA code of bacterial winged helixâ€turnâ€helix transcription factors. <i>Quantitative Biology</i> , 2018, 6, 68-84.	0.3	2
7110	Identification of candidate genes for necrotizing enterocolitis based on microarray data. <i>Gene</i> , 2018, 661, 152-159.	1.0	11
7111	The Warburg Effect in Diabetic Kidney Disease. <i>Seminars in Nephrology</i> , 2018, 38, 111-120.	0.6	75
7112	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. <i>Nature Genetics</i> , 2018, 50, 613-620.	9.4	116
7113	Constructing lightweight and flexible pipelines using Plugin-Based Microbiome Analysis (PluMA). <i>Bioinformatics</i> , 2018, 34, 2881-2888.	1.8	5
7114	miR-130a and miR-212 Disrupt the Intestinal Epithelial Barrier through Modulation of PPARÎ³ and Occludin Expression in Chronic Simian Immunodeficiency Virusâ€Infected Rhesus Macaques. <i>Journal of Immunology</i> , 2018, 200, 2677-2689.	0.4	39

#	ARTICLE	IF	CITATIONS
7115	Transcriptomics analysis revealing candidate networks and genes for the body size sexual dimorphism of Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Functional and Integrative Genomics</i> , 2018, 18, 327-339.	1.4	61
7116	Philadelphia-negative myeloproliferative neoplasms as disorders marked by cytokine modulation. <i>Hematology, Transfusion and Cell Therapy</i> , 2018, 40, 120-131.	0.1	30
7117	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. <i>Journal of Proteomics</i> , 2018, 179, 30-41.	1.2	53
7118	Promyelocytic Leukemia Protein (PML) Requirement for Interferon-induced Global Cellular SUMOylation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1196-1208.	2.5	22
7119	Network Analysis of Protein Adaptation: Modeling the Functional Impact of Multiple Mutations. <i>Molecular Biology and Evolution</i> , 2018, 35, 1507-1519.	3.5	8
7120	Integration of multi-omics datasets enables molecular classification of COPD. <i>European Respiratory Journal</i> , 2018, 51, 1701930.	3.1	83
7121	Predominant gut <i>Lactobacillus murinus</i> strain mediates anti-inflammaging effects in calorie-restricted mice. <i>Microbiome</i> , 2018, 6, 54.	4.9	141
7122	Nutrient enrichment during shrimp cultivation alters bacterioplankton assemblies and destroys community stability. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 366-374.	2.9	30
7123	Glycan affinity magnetic nanoplateforms for urinary glycomarkers discovery in bladder cancer. <i>Talanta</i> , 2018, 184, 347-355.	2.9	29
7124	Cytidine Diphosphoramidate Kinase: An Enzyme Required for the Biosynthesis of the <i>O</i> -Methyl Phosphoramidate Modification in the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2018, 57, 2238-2244.	1.2	18
7125	Double agents: genes with both oncogenic and tumor-suppressor functions. <i>Oncogenesis</i> , 2018, 7, 25.	2.1	88
7126	Gene Co-occurrence Networks Reflect Bacteriophage Ecology and Evolution. <i>MBio</i> , 2018, 9, .	1.8	41
7127	Insight into Genes Regulating Postharvest Aflatoxin Contamination of Tetraploid Peanut from Transcriptional Profiling. <i>Genetics</i> , 2018, 209, 143-156.	1.2	23
7128	Loss of TDP43 inhibits progression of triple-negative breast cancer in coordination with SRSF3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3426-E3435.	3.3	74
7129	SUMOylome Profiling Reveals a Diverse Array of Nuclear Targets Modified by the SUMO Ligase Siz1 during Heat Stress. <i>Plant Cell</i> , 2018, 30, 1077-1099.	3.1	120
7130	Screening for key lncRNAs in the progression of gallbladder cancer using bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 6449-6455.	1.1	8
7131	Type I Immune Response Induces Keratinocyte Necroptosis and Is Associated with Interface Dermatitis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1785-1794.	0.3	52
7132	Short-term dynamics and interactions of marine protist communities during the spring-summer transition. <i>ISME Journal</i> , 2018, 12, 1907-1917.	4.4	84

#	ARTICLE	IF	CITATIONS
7133	Lifelong calorie restriction affects indicators of colonic health in aging C57Bl/6J mice. <i>Journal of Nutritional Biochemistry</i> , 2018, 56, 152-164.	1.9	24
7134	Phenotype-driven identification of epithelial signalling clusters. <i>Scientific Reports</i> , 2018, 8, 4034.	1.6	1
7135	The primary biological network of Bifidobacterium in the gut. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	26
7136	Identification of lncRNAs by microarray analysis reveals the potential role of lncRNAs in cervical cancer pathogenesis. <i>Oncology Letters</i> , 2018, 15, 5584-5592.	0.8	18
7137	Network analytics approach towards identifying potential antivirulence drug targets within the <i>Staphylococcus aureus</i> staphyloxanthin biosynthetic network. <i>Archives of Biochemistry and Biophysics</i> , 2018, 645, 81-86.	1.4	9
7138	Deciphering synergistic regulatory networks of microRNAs in hESCs and fibroblasts. <i>International Journal of Biological Macromolecules</i> , 2018, 113, 1279-1286.	3.6	13
7139	Application of kernel principal component analysis and computational machine learning to exploration of metabolites strongly associated with diet. <i>Scientific Reports</i> , 2018, 8, 3426.	1.6	33
7140	Analysis of microRNA and Gene Expression Profiles in Alzheimer's Disease: A Meta-Analysis Approach. <i>Scientific Reports</i> , 2018, 8, 4767.	1.6	119
7141	Interleukin-1 $\beta$ Signaling in Dendritic Cells Induces Antiviral Interferon Responses. <i>MBio</i> , 2018, 9, .	1.8	45
7142	Integrated analysis of mRNA-seq and miRNA-seq for host susceptibilities to influenza A (H7N9) infection in inbred mouse lines. <i>Functional and Integrative Genomics</i> , 2018, 18, 411-424.	1.4	6
7143	IRF8 Regulates Transcription of Naips for NLRC4 Inflammasome Activation. <i>Cell</i> , 2018, 173, 920-933.e13.	13.5	142
7144	Integrated analysis of miRNA and mRNA expression data identifies multiple miRNAs regulatory networks for the tumorigenesis of colorectal cancer. <i>Gene</i> , 2018, 659, 44-51.	1.0	23
7145	An AP-MS- and BioID-compatible MAC-tag enables comprehensive mapping of protein interactions and subcellular localizations. <i>Nature Communications</i> , 2018, 9, 1188.	5.8	191
7146	Small molecules capable of activating DNA methylation-repressed genes targeted by the p38 mitogen-activated protein kinase pathway. <i>Journal of Biological Chemistry</i> , 2018, 293, 7423-7436.	1.6	10
7147	A Data Fusion Pipeline for Generating and Enriching Adverse Outcome Pathway Descriptions. <i>Toxicological Sciences</i> , 2018, 162, 264-275.	1.4	51
7148	The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.	6.0	101
7149	<i>Caenorhabditis elegans</i> sperm membrane protein interactome. <i>Biology of Reproduction</i> , 2018, 98, 776-783.	1.2	10
7150	An LaeA- and BrlA-Dependent Cellular Network Governs Tissue-Specific Secondary Metabolism in the Human Pathogen <i>Aspergillus fumigatus</i> . <i>MSphere</i> , 2018, 3, .	1.3	58



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7151	The mRNA, miRNA and lncRNA networks in hepatocellular carcinoma: An integrative transcriptomic analysis from Gene Expression Omnibus. <i>Molecular Medicine Reports</i> , 2018, 17, 6472-6482.	1.1	21
7152	Identification of key differentially expressed genes associated with non-small cell lung cancer by bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 6379-6386.	1.1	22
7153	Mapping <i>Anopheles stephensi</i> midgut proteome using high-resolution mass spectrometry. <i>Data in Brief</i> , 2018, 17, 1295-1303.	0.5	4
7154	Integration of Biochemometrics and Molecular Networking to Identify Antimicrobials in <i>Angelica keiskei</i> . <i>Planta Medica</i> , 2018, 84, 721-728.	0.7	36
7155	Comparative characterization of aluminum responsive transcriptome in <i>Arabidopsis</i> roots: comparison with other rhizotoxic ions at different stress intensities. <i>Soil Science and Plant Nutrition</i> , 2018, 64, 469-481.	0.8	6
7156	Allergen-induced activation of natural killer cells represents an early-life immune response in the development of allergic asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1856-1866.	1.5	26
7157	Thyroid Dysfunction, Neurological Disorder and Immunosuppression as the Consequences of Long-term Combined Stress. <i>Scientific Reports</i> , 2018, 8, 4552.	1.6	8
7158	Network of proteins, enzymes and genes linked to biomass degradation shared by <i>Trichoderma</i> species. <i>Scientific Reports</i> , 2018, 8, 1341.	1.6	48
7159	Deciphering metabonomics biomarkers-targets interactions for psoriasis vulgaris by network pharmacology. <i>Annals of Medicine</i> , 2018, 50, 323-332.	1.5	10
7160	Adductomic signatures of benzene exposure provide insights into cancer induction. <i>Carcinogenesis</i> , 2018, 39, 661-668.	1.3	42
7161	Obese rats supplemented with bitter melon display marked shifts in the expression of genes controlling inflammatory response and lipid metabolism by RNA-Seq analysis of colonic mucosa. <i>Genes and Genomics</i> , 2018, 40, 561-567.	0.5	7
7162	Alpha-oxoglutarate inhibits the proliferation of immortalized normal bladder epithelial cells via an epigenetic switch involving ARID1A. <i>Scientific Reports</i> , 2018, 8, 4505.	1.6	13
7163	Differences in microbial community structure and nitrogen cycling in natural and drained tropical peatland soils. <i>Scientific Reports</i> , 2018, 8, 4742.	1.6	70
7164	Comprehensive analysis of differential expression profiles reveals potential biomarkers associated with the cell cycle and regulated by p53 in human small cell lung cancer. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 3273-3282.	0.8	13
7165	Horizontal Gene Transfer Building Prokaryote Genomes: Genes Related to Exchange Between Cell and Environment are Frequently Transferred. <i>Journal of Molecular Evolution</i> , 2018, 86, 190-203.	0.8	20
7166	FERTILIZATION-INDEPENDENT SEED-Polycomb Repressive Complex 2 Plays a Dual Role in Regulating Type I MADS-Box Genes in Early Endosperm Development. <i>Plant Physiology</i> , 2018, 177, 285-299.	2.3	60
7167	Darkened Leaves Use Different Metabolic Strategies for Senescence and Survival. <i>Plant Physiology</i> , 2018, 177, 132-150.	2.3	62
7168	Exploring the oncoproteomic response of human prostate cancer to therapeutic radiation using data-independent acquisition (DIA) mass spectrometry. <i>Prostate</i> , 2018, 78, 563-575.	1.2	23

#	ARTICLE	IF	CITATIONS
7169	Step-by-Step Construction of Gene Co-expression Networks from High-Throughput Arabidopsis RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1761, 275-301.	0.4	42
7170	Bacterial community changes in response to oil contamination and perennial crop cultivation. <i>Environmental Science and Pollution Research</i> , 2018, 25, 14575-14584.	2.7	13
7171	Single-gene prognostic signatures for advanced stage serous ovarian cancer based on 1257 patient samples. <i>Molecular Omics</i> , 2018, 14, 103-108.	1.4	0
7172	Bioinformatics Analysis of Microarray Data to Reveal Novel Genes Related to Cold-Resistance of Maize. <i>Russian Journal of Plant Physiology</i> , 2018, 65, 278-285.	0.5	4
7173	Metabolomic strategies for aquaculture research: a primer. <i>Reviews in Aquaculture</i> , 2018, 10, 26-56.	4.6	50
7174	The structures and flows of a large tourist itinerancy network. <i>Current Issues in Tourism</i> , 2018, 21, 103-122.	4.6	14
7175	LPRP: A Gene-Genome Interaction Network Construction Algorithm and Its Application in Breast Cancer Data Analysis. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 131-142.	2.2	5
7176	Condition-dependent coregulation of genomic clusters of virulence factors in the grapevine trunk pathogen <i>Neofusicoccum parvum</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 21-34.	2.0	55
7177	A Novel Metric to Quantify and Enable Resilient Distribution System Using Graph Theory and Choquet Integral. <i>IEEE Transactions on Smart Grid</i> , 2018, 9, 2918-2929.	6.2	107
7178	Systems genetics analysis of pharmacogenomics variation during antidepressant treatment. <i>Pharmacogenomics Journal</i> , 2018, 18, 144-152.	0.9	6
7179	Querying of Disparate Association and Interaction Data in Biomedical Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1052-1065.	1.9	2
7180	Analyzing Differential Regulatory Networks Modulated by Continuous-State Genomic Features in Glioblastoma Multiforme. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1754-1764.	1.9	3
7181	Network Analysis Identifies Disease-Specific Pathways for Parkinson's Disease. <i>Molecular Neurobiology</i> , 2018, 55, 370-381.	1.9	23
7182	Circulating microRNAs signature correlates with positive [18F]fluorodeoxyglucose-positron emission tomography in patients with abdominal aortic aneurysm. <i>Journal of Vascular Surgery</i> , 2018, 67, 585-595.e3.	0.6	10
7183	The Cucurbita pepo seed microbiome: genotype-specific composition and implications for breeding. <i>Plant and Soil</i> , 2018, 422, 35-49.	1.8	131
7184	A review of metabolomics approaches and their application in identifying causal pathways of childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1191-1201.	1.5	67
7185	IGF2 mRNA binding protein 3 (IMP3) mediated regulation of transcriptome and translome in glioma cells. <i>Cancer Biology and Therapy</i> , 2018, 19, 42-52.	1.5	14
7186	Dynamic modeling and network approaches for omics time course data: overview of computational approaches and applications. <i>Briefings in Bioinformatics</i> , 2018, 19, 1051-1068.	3.2	25

#	ARTICLE	IF	CITATIONS
7187	Exogenous transforming growth factor- $\beta$ 1 enhances smooth muscle differentiation in embryonic mouse jejunal explants. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2018, 12, 252-264.	1.3	6
7188	Characterization of Dysregulated miRNA in Peripheral Blood Mononuclear Cells from Ischemic Stroke Patients. <i>Molecular Neurobiology</i> , 2018, 55, 1419-1429.	1.9	35
7189	A Combined PLS and Negative Binomial Regression Model for Inferring Association Networks from Next-Generation Sequencing Count Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 760-773.	1.9	3
7190	Covariation and phenotypic integration in chemical communication displays: biosynthetic constraints and eco-evolutionary implications. <i>New Phytologist</i> , 2018, 220, 739-749.	3.5	101
7191	CommViz: Visualization of semantic patterns in large social communication networks. <i>Information Visualization</i> , 2018, 17, 66-88.	1.2	3
7192	Unveiling antimicrobial peptide-generating human proteases using PROTEASIX. <i>Journal of Proteomics</i> , 2018, 171, 53-62.	1.2	11
7193	A sociogram is worth a thousand words: proposing a method for the visual analysis of narrative data. <i>Qualitative Research</i> , 2018, 18, 70-87.	2.2	11
7194	Transcriptional network analysis in frontal cortex in <i>scp</i> body diseases with focus on dementia with <i>scp</i> bodies. <i>Brain Pathology</i> , 2018, 28, 315-333.	2.1	35
7195	How to use and integrate bioinformatics tools to compare proteomic data from distinct conditions? A tutorial using the pathological similarities between Aortic Valve Stenosis and Coronary Artery Disease as a case-study. <i>Journal of Proteomics</i> , 2018, 171, 37-52.	1.2	8
7196	Comprehensive functional analysis of large lists of genes and proteins. <i>Journal of Proteomics</i> , 2018, 171, 2-10.	1.2	80
7197	Comparison of the general co-expression landscapes between human and mouse. <i>Briefings in Bioinformatics</i> , 2018, 19, 811-820.	3.2	3
7198	The Effects of Graded Levels of Calorie Restriction: X. Transcriptomic Responses of Epididymal Adipose Tissue. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 279-288.	1.7	18
7199	Base excision repair proteins couple activation-induced cytidine deaminase and endonuclease G during replication stress-induced MLL destabilization. <i>Leukemia</i> , 2018, 32, 159-167.	3.3	8
7200	Finding the Maximal Day-Time Dependent Component of a Subway System. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 562-572.	0.5	0
7201	Exploring the molecular pathogenesis and biomarkers of high risk oral premalignant lesions on the basis of long noncoding RNA expression profiling by serial analysis of gene expression. <i>European Journal of Cancer Prevention</i> , 2018, 27, 370-378.	0.6	16
7202	SEGtool: a specifically expressed gene detection tool and applications in human tissue and single-cell sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, 1325-1336.	3.2	20
7203	The Stress-Responding miR-132-3p Shows Evolutionarily Conserved Pathway Interactions. <i>Cellular and Molecular Neurobiology</i> , 2018, 38, 141-153.	1.7	12
7204	A simple in silico strategy identifies candidate biomarkers for the diagnosis of liver fibrosis in morbidly obese subjects. <i>Liver International</i> , 2018, 38, 155-163.	1.9	5

#	ARTICLE	IF	CITATIONS
7205	VEGFA Involves in the Use of Fluvastatin and Zoledronate Against Breast Cancer. <i>Pathology and Oncology Research</i> , 2018, 24, 557-565.	0.9	5
7206	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. <i>Protein Science</i> , 2018, 27, 14-25.	3.1	3,377
7207	Ginseng seed oil ameliorates hepatic lipid accumulation in vitro and in vivo. <i>Journal of Ginseng Research</i> , 2018, 42, 419-428.	3.0	19
7208	Global proteome and phosphoproteome dynamics indicate novel mechanisms of vitamin C induced dormancy in <i>Mycobacterium smegmatis</i> . <i>Journal of Proteomics</i> , 2018, 180, 1-10.	1.2	16
7209	Transcriptomic discovery and comparative analysis of neuropeptide precursors in sea cucumbers (Holothuroidea). <i>Peptides</i> , 2018, 99, 231-240.	1.2	53
7210	From vineyard to winery: a source map of microbial diversity driving wine fermentation. <i>Environmental Microbiology</i> , 2018, 20, 75-84.	1.8	102
7211	Identification of new protein-protein and protein-DNA interactions linked with wood formation in <i>Populus trichocarpa</i> . <i>Tree Physiology</i> , 2018, 38, 362-377.	1.4	17
7212	Co-Expression Network Approach to Studying the Effects of Botulinum Neurotoxin-A. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 2009-2016.	1.9	3
7213	Drug repurposing: An approach to tackle drug resistance in <i>S. typhimurium</i> . <i>Journal of Cellular Biochemistry</i> , 2018, 119, 2818-2831.	1.2	3
7214	Integrated analysis supports ATXN1 as a schizophrenia risk gene. <i>Schizophrenia Research</i> , 2018, 195, 298-305.	1.1	5
7215	A CRISPR-Cas9-based gene drive platform for genetic interaction analysis in <i>Candida albicans</i> . <i>Nature Microbiology</i> , 2018, 3, 73-82.	5.9	135
7216	Rapid Novel Facile Biosynthesized Silver Nanoparticles From Bacterial Release Induce Biogenicity and Concentration Dependent In Vivo Cytotoxicity With Embryonic Zebrafish: A Mechanistic Insight. <i>Toxicological Sciences</i> , 2018, 161, 125-138.	1.4	50
7217	The SSU processome interactome in <i>Saccharomyces cerevisiae</i> reveals novel protein subcomplexes. <i>Rna</i> , 2018, 24, 77-89.	1.6	18
7218	Pluripotent Stem Cell-Derived Hematopoietic Progenitors Are Unable to Downregulate Key Epithelial-Mesenchymal Transition-Associated miRNAs. <i>Stem Cells</i> , 2018, 36, 55-64.	1.4	3
7219	Acetylation and methylation of sperm histone 3 lysine 27 (H3K27ac and H3K27me3) are associated with bull fertility. <i>Andrologia</i> , 2018, 50, e12915.	1.0	34
7220	Meta-expression analysis of unannotated genes in rice and approaches for network construction to suggest the probable roles. <i>Plant Molecular Biology</i> , 2018, 96, 17-34.	2.0	4
7221	Microarray analysis to identify the similarities and differences of pathogenesis between aortic occlusive disease and abdominal aortic aneurysm. <i>Vascular</i> , 2018, 26, 301-314.	0.4	6
7222	Identification of breast cancer hub genes and analysis of prognostic values using integrated bioinformatics analysis. <i>Cancer Biomarkers</i> , 2018, 21, 373-381.	0.8	37

#	ARTICLE	IF	CITATIONS
7223	The V279F polymorphism might change protein character and immunogenicity in Lp-PLA2 protein. Egyptian Journal of Medical Human Genetics, 2018, 19, 107-112.	0.5	3
7224	Gut Microbiota Perturbations in Reactive Arthritis and Postinfectious Spondyloarthritis. Arthritis and Rheumatology, 2018, 70, 242-254.	2.9	88
7225	TGF- $\beta$ 1 targets a microRNA network that regulates cellular adhesion and migration in renal cancer. Cancer Letters, 2018, 412, 155-169.	3.2	47
7226	Integrated Proteomic and Transcriptomic Analysis Reveals Long Noncoding RNA HOX Transcript Antisense Intergenic RNA (HOTAIR) Promotes Hepatocellular Carcinoma Cell Proliferation by Regulating Opioid Growth Factor Receptor (OGFr). Molecular and Cellular Proteomics, 2018, 17, 146-159.	2.5	33
7227	The nuclear DEK interactome supports multi-functionality. Proteins: Structure, Function and Bioinformatics, 2018, 86, 88-97.	1.5	19
7228	Substitution impact of highly conserved arginine residue at position 75 in GJB1 gene in association with X-linked Charcot-Marie-tooth disease: A computational study. Journal of Theoretical Biology, 2018, 437, 305-317.	0.8	32
7229	The Transcriptional Landscape of Radiation-Treated Human Prostate Cancer: Analysis of a Prospective Tissue Cohort. International Journal of Radiation Oncology Biology Physics, 2018, 100, 188-198.	0.4	24
7230	Gene expression signatures of mating system evolution. Genome, 2018, 61, 287-297.	0.9	13
7231	Computational Approaches for Therapeutic Application of Natural Products in Alzheimer's Disease. Neuromethods, 2018, , 483-511.	0.2	6
7232	Proteomic Analysis of Extracellular HMGB1 Identifies Binding Partners and Exposes Its Potential Role in Airway Epithelial Cell Homeostasis. Journal of Proteome Research, 2018, 17, 33-45.	1.8	14
7233	H/D exchange mass spectrometry and statistical coupling analysis reveal a role for allostery in a ferredoxin-dependent bifurcating transhydrogenase catalytic cycle. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 9-17.	1.1	38
7234	Recent Advances in the Systems Biology of Aging. Antioxidants and Redox Signaling, 2018, 29, 973-984.	2.5	15
7235	Antimicrobial metabolites from Saraca asoca impairs the membrane transport system and quorum-sensing system in Pseudomonas aeruginosa. Archives of Microbiology, 2018, 200, 237-253.	1.0	6
7236	Annotation: A Computational Solution for Streamlining Metabolomics Analysis. Analytical Chemistry, 2018, 90, 480-489.	3.2	126
7237	MicroRNA profiling reveals dysregulated microRNAs and their target gene regulatory networks in cementossifying fibroma. Journal of Oral Pathology and Medicine, 2018, 47, 78-85.	1.4	19
7238	Fibromodulin and regulation of the intricate balance between myoblast differentiation to myocytes or adipocyte-like cells. FASEB Journal, 2018, 32, 768-781.	0.2	41
7239	Neurodevelopmental disease mechanisms, primary cilia, and endosomes converge on the BLOC1 and BORG complexes. Developmental Neurobiology, 2018, 78, 311-330.	1.5	21
7240	Differential gene regulatory networks in development and disease. Cellular and Molecular Life Sciences, 2018, 75, 1013-1025.	2.4	78

#	ARTICLE	IF	CITATIONS
7241	The P/N (Positive-to-Negative Links) Ratio in Complex Networksâ€”A Promising In Silico Biomarker for Detecting Changes Occurring in the Human Microbiome. <i>Microbial Ecology</i> , 2018, 75, 1063-1073.	1.4	20
7242	Expression of miRNAâ€”p and its target TRPS 1 is associated with radiation exposure in postâ€”C hernobyl breast cancer. <i>International Journal of Cancer</i> , 2018, 142, 573-583.	2.3	29
7243	Deciphering structural stability and binding mechanisms of potential antagonists with smoothed protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2917-2937.	2.0	6
7244	Temporal variations in a phytoplankton community in a subtropical reservoir: An interplay of extrinsic and intrinsic community effects. <i>Science of the Total Environment</i> , 2018, 612, 720-727.	3.9	37
7245	Intelligent mining of large-scale bio-data: Bioinformatics applications. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 10-29.	0.5	29
7246	The diversity and biogeography of abundant and rare intertidal marine microeukaryotes explained by environment and dispersal limitation. <i>Environmental Microbiology</i> , 2018, 20, 462-476.	1.8	112
7247	Short overview on metabolomics approach to study pathophysiology of oxidative stress in cancer. <i>Redox Biology</i> , 2018, 14, 47-58.	3.9	102
7248	Analyzing the LncRNA, miRNA, and mRNA Regulatory Network in Prostate Cancer with Bioinformatics Software. <i>Journal of Computational Biology</i> , 2018, 25, 146-157.	0.8	55
7249	Quantitative phosphoproteomic analysis of acquired cancer drug resistance to pazopanib and dasatinib. <i>Journal of Proteomics</i> , 2018, 170, 130-140.	1.2	27
7250	All-atom molecular dynamics comparison of disease-associated zinc fingers. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2581-2594.	2.0	3
7251	New insights into the impacts of elevated CO2, nitrogen, and temperature levels on the regulation of C and N metabolism in durum wheat using network analysis. <i>New Biotechnology</i> , 2018, 40, 192-199.	2.4	24
7252	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. <i>Hepatology</i> , 2018, 67, 1270-1283.	3.6	388
7253	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. <i>ISME Journal</i> , 2018, 12, 124-135.	4.4	14
7254	<i>Streptococcus pneumoniae</i> colonization of the nasopharynx is associated with increased severity during respiratory syncytial virus infection in young children. <i>Respirology</i> , 2018, 23, 220-227.	1.3	48
7255	A systematic integrated analysis of brain expression profiles reveals <i>YAP1</i> and other prioritized hub genes as important upstream regulators in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2018, 14, 215-229.	0.4	172
7256	PTSD Blood Transcriptome Mega-Analysis: Shared Inflammatory Pathways across Biological Sex and Modes of Trauma. <i>Neuropsychopharmacology</i> , 2018, 43, 469-481.	2.8	92
7257	Correlation analyses revealed global microRNAâ€”mRNA expression associations in human peripheral blood mononuclear cells. <i>Molecular Genetics and Genomics</i> , 2018, 293, 95-105.	1.0	12
7258	Visualizing omics and clinical data: Which challenges for dealing with their variety?. <i>Methods</i> , 2018, 132, 3-18.	1.9	7



#	ARTICLE	IF	CITATIONS
7259	Initial gut microbiota structure affects sensitivity to DSS-induced colitis in a mouse model. <i>Science China Life Sciences</i> , 2018, 61, 762-769.	2.3	70
7260	Opening Pandora's Box: Mechanisms of <i>Mycobacterium tuberculosis</i> Resuscitation. <i>Trends in Microbiology</i> , 2018, 26, 145-157.	3.5	44
7261	Integrating Imaging Genomic Data in the Quest for Biomarkers of Schizophrenia Disease. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1480-1491.	1.9	13
7262	Acetylome Profiling Reveals Extensive Lysine Acetylation of the Fatty Acid Metabolism Pathway in the Diatom <i>Phaeodactylum tricornutum</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 399-412.	2.5	26
7263	The social networks and distinctive experiences of intensively involved online gamers: A novel mixed methods approach. <i>Computers in Human Behavior</i> , 2018, 80, 229-242.	5.1	6
7264	Extended Metabolic Space Modeling. <i>Methods in Molecular Biology</i> , 2018, 1671, 83-96.	0.4	1
7265	An immune-related lncRNA signature for patients with anaplastic gliomas. <i>Journal of Neuro-Oncology</i> , 2018, 136, 263-271.	1.4	129
7266	Alterations in gut microbiota associated with a cafeteria diet and the physiological consequences in the host. <i>International Journal of Obesity</i> , 2018, 42, 746-754.	1.6	31
7267	Annotating gene sets by mining large literature collections with protein networks. , 2018, , .		6
7268	Fluoxetine, not donepezil, reverses anhedonia, cognitive dysfunctions and hippocampal proteome changes during repeated social defeat exposure. <i>European Neuropsychopharmacology</i> , 2018, 28, 195-210.	0.3	13
7269	Proteomic analysis of six- and twelve-month hippocampus and cerebellum in a murine Down syndrome model. <i>Neurobiology of Aging</i> , 2018, 63, 96-109.	1.5	14
7270	Population mitogenomics provides insights into evolutionary history, source of invasions and diversifying selection in the House Crow ( <i>Corvus splendens</i> ). <i>Heredity</i> , 2018, 120, 296-309.	1.2	6
7271	Sex-specific transcript expression in the hepatopancreas of the banana shrimp ( <i>Fenneropenaeus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	1.0	5
7272	The Intestinal Microbiome in Nonalcoholic Fatty Liver Disease. <i>Clinics in Liver Disease</i> , 2018, 22, 121-132.	1.0	25
7273	Systems-level mechanisms of action of <i>Panax ginseng</i> : a network pharmacological approach. <i>Journal of Ginseng Research</i> , 2018, 42, 98-106.	3.0	55
7274	Identification of genes involved in the four stages of colorectal cancer: Gene expression profiling. <i>Molecular and Cellular Probes</i> , 2018, 37, 39-47.	0.9	11
7275	Advances in Text Mining and Visualization for Precision Medicine. , 2018, , .		3
7276	HDAC11 is a regulator of diverse immune functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 54-59.	0.9	70



#	ARTICLE	IF	CITATIONS
7277	The interactome of intact mitochondria by cross-linking mass spectrometry provides evidence for coexisting respiratory supercomplexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 216-232.	2.5	142
7278	Cyclic Concatenated Genetic Encoder: A mathematical proposal for biological inferences. <i>BioSystems</i> , 2018, 163, 47-58.	0.9	5
7279	Biochar application influences microbial assemblage complexity and composition due to soil and bioenergy crop type interactions. <i>Soil Biology and Biochemistry</i> , 2018, 117, 97-107.	4.2	75
7280	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018, 24, 103-112.	15.2	525
7281	The N-Terminal CCHC Zinc Finger Motif Mediates Homodimerization of Transcription Factor BCL11B. <i>Molecular and Cellular Biology</i> , 2018, 38, .	1.1	15
7282	Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. <i>Analytical Chemistry</i> , 2018, 90, 1325-1333.	3.2	27
7283	Race Disparities in the Contribution of miRNA Isoforms and tRNA-Derived Fragments to Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2018, 78, 1140-1154.	0.4	90
7284	Discovery of 2-arylquinazoline derivatives as a new class of ASK1 inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 400-404.	1.0	10
7285	In silico drug design for <i>Staphylococcus aureus</i> and development of host-pathogen interaction network. <i>Informatics in Medicine Unlocked</i> , 2018, 10, 58-70.	1.9	40
7286	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <i>Environmental Microbiology</i> , 2018, 20, 734-754.	1.8	53
7287	Dual Targeting of Oncogenic Activation and Inflammatory Signaling Increases Therapeutic Efficacy in Myeloproliferative Neoplasms. <i>Cancer Cell</i> , 2018, 33, 29-43.e7.	7.7	186
7288	Structure-Based Kinase Profiling To Understand the Polypharmacological Behavior of Therapeutic Molecules. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 68-89.	2.5	5
7289	Proteomic Mapping of Dental Enamel Matrix from Inbred Mouse Strains: Unraveling Potential New Players in Enamel. <i>Caries Research</i> , 2018, 52, 78-87.	0.9	6
7290	Estrogen Receptor $\beta$ Signaling Exacerbates Immune-Mediated Nephropathies through Alteration of Metabolic Activity. <i>Journal of Immunology</i> , 2018, 200, 512-522.	0.4	13
7291	Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. , 2018, , .		5
7292	ZikaBase: An integrated ZIKV- Human Interactome Map database. <i>Virology</i> , 2018, 514, 203-210.	1.1	13
7293	Proteinâ€“protein interaction networks and different clustering analysis in Burkittâ€™s lymphoma. <i>Hematology</i> , 2018, 23, 391-398.	0.7	6
7294	Mechanisms underlying the impact of exercise training in pulmonary arterial hypertension. <i>Respiratory Medicine</i> , 2018, 134, 70-78.	1.3	24

#	ARTICLE	IF	CITATIONS
7295	Multi-omics Approach Reveals Distinct Differences in Left- and Right-Sided Colon Cancer. <i>Molecular Cancer Research</i> , 2018, 16, 476-485.	1.5	47
7296	Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. <i>Journal of Proteome Research</i> , 2018, 17, 568-578.	1.8	40
7297	Sperm RNA elements as markers of health. <i>Systems Biology in Reproductive Medicine</i> , 2018, 64, 25-38.	1.0	32
7298	The impact of artificial surfaces on marine bacterial and eukaryotic biofouling assemblages: A high-throughput sequencing analysis. <i>Marine Environmental Research</i> , 2018, 133, 57-66.	1.1	54
7299	Effects of Alanyl-Glutamine Treatment on the Peritoneal Dialysis Effluent Proteome Reveal Pathomechanism-Associated Molecular Signatures. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 516-532.	2.5	32
7300	Environmental factors shaping the archaeal community structure and ether lipid distribution in a subtropic river and estuary, China. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 461-474.	1.7	7
7301	Multivariate statistical analysis of a large odorants database aimed at revealing similarities and links between odorants and odors. <i>Flavour and Fragrance Journal</i> , 2018, 33, 106-126.	1.2	9
7302	Ecological Patterns Among Bacteria and Microbial Eukaryotes Derived from Network Analyses in a Low-Salinity Lake. <i>Microbial Ecology</i> , 2018, 75, 917-929.	1.4	39
7303	Data-driven Confounder Selection via Markov and Bayesian Networks. <i>Biometrics</i> , 2018, 74, 389-398.	0.8	25
7304	Chloride Intracellular Channel 4 Overexpression in the Proximal Tubules of Kidneys from the Spontaneously Hypertensive Rat: Insight from Proteomic Analysis. <i>Nephron</i> , 2018, 138, 60-70.	0.9	8
7305	Dietary Glycation Products Regulate Immune Homeostasis: Early Glycation Products Promote Prostate Cancer Cell Proliferation through Modulating Macrophages. <i>Molecular Nutrition and Food Research</i> , 2018, 62, 1700641.	1.5	16
7306	Identification of circular RNAs and their targets during tomato fruit ripening. <i>Postharvest Biology and Technology</i> , 2018, 136, 90-98.	2.9	74
7307	A Network-Based Integrative Workflow to Unravel Mechanisms Underlying Disease Progression. <i>Methods in Molecular Biology</i> , 2018, 1702, 247-276.	0.4	6
7308	Physicochemical characteristics of stored cattle manure affect methane emissions by inducing divergence of methanogens that have different interactions with bacteria. <i>Agriculture, Ecosystems and Environment</i> , 2018, 253, 38-47.	2.5	16
7309	Conserving migration in a changing climate, a case study: The Eurasian spoonbill, <i>Platalea leucorodia leucorodia</i> . <i>Biological Conservation</i> , 2018, 217, 222-231.	1.9	8
7310	Deep RNAseq indicates protective mechanisms of cold-tolerant indica rice plants during early vegetative stage. <i>Plant Cell Reports</i> , 2018, 37, 347-375.	2.8	31
7311	Contextual factors and motivations affecting rural community sanitation in low- and middle-income countries: A systematic review. <i>International Journal of Hygiene and Environmental Health</i> , 2018, 221, 121-133.	2.1	44
7312	Allosteric mechanism of quinoline inhibitors for $\text{HIV RT}$ -associated $\text{RNase H}$ with $\text{MD}$ simulation and dynamics fluctuation network. <i>Chemical Biology and Drug Design</i> , 2018, 91, 805-816.	1.5	6

#	ARTICLE	IF	CITATIONS
7313	Cartilage MicroRNA Dysregulation During the Onset and Progression of Mouse Osteoarthritis Is Independent of Aggrecanolytic and Overlaps With Candidates From End-stage Human Disease. <i>Arthritis and Rheumatology</i> , 2018, 70, 383-395.	2.9	21
7314	Transient leaf endophytes are the most active fungi in 1-year-old beech leaf litter. <i>Fungal Diversity</i> , 2018, 89, 237-251.	4.7	62
7315	A methodological evaluation of natural user interfaces for immersive 3D Graph explorations. <i>Journal of Visual Languages and Computing</i> , 2018, 44, 13-27.	1.8	17
7316	Integrative omics data analyses of repeated dose toxicity of valproic acid in vitro reveal new mechanisms of steatosis induction. <i>Toxicology</i> , 2018, 393, 160-170.	2.0	35
7317	Ethylene Receptors Signal via a Noncanonical Pathway to Regulate Abscisic Acid Responses. <i>Plant Physiology</i> , 2018, 176, 910-929.	2.3	45
7318	Azole resistance in a <i>Candida albicans</i> mutant lacking the ABC transporter CDR6/ROA1 depends on TOR signaling. <i>Journal of Biological Chemistry</i> , 2018, 293, 412-432.	1.6	42
7319	Apple fruit superficial scald resistance mediated by ethylene inhibition is associated with diverse metabolic processes. <i>Plant Journal</i> , 2018, 93, 270-285.	2.8	76
7320	Exploring the effect of D61G mutation on SHP2 cause gain of function activity by a molecular dynamics study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 3856-3868.	2.0	18
7321	Golgi stress-induced transcriptional changes mediated by MAPK signaling and three ETS transcription factors regulate MCL1 splicing. <i>Molecular Biology of the Cell</i> , 2018, 29, 42-52.	0.9	31
7322	Oxidative stress-triggered interactions between the succinyl- and acetyl-proteomes of rice leaves. <i>Plant, Cell and Environment</i> , 2018, 41, 1139-1153.	2.8	79
7323	Proteomic analysis of lysine acetylation provides strong evidence for involvement of acetylated proteins in plant meiosis and tapetum function. <i>Plant Journal</i> , 2018, 93, 142-154.	2.8	30
7324	A loss-of-function homozygous mutation in <i>DDX59</i> implicates a conserved DEAD-box RNA helicase in nervous system development and function. <i>Human Mutation</i> , 2018, 39, 187-192.	1.1	44
7325	Effect of abiotic and biotic stress factors analysis using machine learning methods in zebrafish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 62-72.	0.4	1
7326	Identification of key microRNAs associated with diffuse large B-cell lymphoma by analyzing serum microRNA expressions. <i>Gene</i> , 2018, 642, 205-211.	1.0	36
7327	Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. <i>Gene</i> , 2018, 642, 84-94.	1.0	117
7328	Systems genetic analysis of brown adipose tissue function. <i>Physiological Genomics</i> , 2018, 50, 52-66.	1.0	11
7329	Metabolomic and physiological changes of <i>Chlamydomonas reinhardtii</i> (Chlorophyceae, Chlorophyta) during batch culture development. <i>Journal of Applied Phycology</i> , 2018, 30, 803-818.	1.5	22
7330	Quantitative and systems pharmacology 2. In silico polypharmacology of G protein-coupled receptor ligands via network-based approaches. <i>Pharmacological Research</i> , 2018, 129, 400-413.	3.1	28

#	ARTICLE	IF	CITATIONS
7331	Pyk2 and FAK differentially regulate invadopodia formation and function in breast cancer cells. <i>Journal of Cell Biology</i> , 2018, 217, 375-395.	2.3	47
7332	Network of anatomical texts (NAnaTex), an open-source project for visualizing the interaction between anatomical terms. <i>Anatomical Science International</i> , 2018, 93, 149-153.	0.5	5
7333	Identification and functional analysis of a potential key lncRNA involved in fat loss of cancer cachexia. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 1679-1688.	1.2	19
7334	In silico approaches for unveiling novel glycomarkers in cancer. <i>Journal of Proteomics</i> , 2018, 171, 95-106.	1.2	14
7335	Discovering Regulators in Post-Transcriptional Control of the Biological Clock of <i>Neurospora crassa</i> Using Variable Topology Ensemble Methods on GPUs. <i>IEEE Access</i> , 2018, 6, 54582-54594.	2.6	6
7336	Pathway Analysis of Marker Genes for Leukemia Cancer using Enhanced Genetic Algorithm-Neural Network (enGANN)., 2018, , .		0
7337	High-Throughput Architecture for Discovering Combination Cancer Therapeutics. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-12.	1.0	9
7338	An Integrative Framework for the Construction of Big Functional Networks. , 2018, , .		1
7339	Hub Genes of Astrocyte Involved in Glaucoma with Ocular Hypertension by Integrated Bioinformatics Analysis. <i>Digital Chinese Medicine</i> , 2018, 1, 280-288.	0.5	1
7340	Normal pregnancy induced glucose metabolic stress in a longitudinal cohort of healthy women. <i>Medicine (United States)</i> , 2018, 97, e12417.	0.4	25
7341	Screening pathogenic genes in oral squamous cell carcinoma based on the mRNA expression microarray data. <i>International Journal of Molecular Medicine</i> , 2018, 41, 3597-3603.	1.8	9
7342	Bioinformatics analysis of the molecular mechanisms underlying traumatic spinal cord injury. <i>Molecular Medicine Reports</i> , 2018, 17, 8484-8492.	1.1	9
7343	Identification and prediction of novel non-coding and coding RNA-associated competing endogenous RNA networks in colorectal cancer. <i>World Journal of Gastroenterology</i> , 2018, 24, 5259-5270.	1.4	30
7344	Bioinformatics prediction and annotation of cherry ( <i>Prunus avium</i> L.) microRNAs and their targeted proteins. <i>Turkish Journal of Botany</i> , 2018, 42, 382-399.	0.5	4
7345	Dropout-Based Active Learning for Regression. <i>Lecture Notes in Computer Science</i> , 2018, , 247-258.	1.0	21
7346	Towards a Model and Graph Representation for Smart Homes in the IoT. , 2018, , .		10
7347	Genome-wide association study of carcass weight in commercial Hanwoo cattle. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 327-334.	2.4	23
7348	Visualising the global structure of search landscapes: genetic improvement as a case study. <i>Genetic Programming and Evolvable Machines</i> , 2018, 19, 317-349.	1.5	12

#	ARTICLE	IF	CITATIONS
7349	Identification of the key transcription factors in esophageal squamous cell carcinoma. <i>Journal of Thoracic Disease</i> , 2018, 10, 148-161.	0.6	27
7350	Bronchoalveolar lavage fluid microbiota dysbiosis in infants with protracted bacterial bronchitis. <i>Journal of Thoracic Disease</i> , 2018, 10, 168-174.	0.6	15
7351	Five-CpG-based prognostic signature for predicting survival in hepatocellular carcinoma patients. <i>Cancer Biology and Medicine</i> , 2018, 15, 425.	1.4	30
7352	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. <i>BMC Medical Genomics</i> , 2018, 11, 112.	0.7	8
7353	Search of Allosteric Inhibitors and Associated Proteins of an AKT-like Kinase from <i>Trypanosoma cruzi</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3951.	1.8	6
7354	NetDriller Version 2: A Powerful Social Network Analysis Tool. , 2018, , .		2
7355	Comparison of Disease Specific Sub-Network Identification Programs. , 2018, , .		0
7356	CrowdLayout. , 2018, , .		6
7357	Genome-wide identification, molecular evolution, and expression analysis of auxin response factor (ARF) gene family in <i>Brachypodium distachyon</i> L. <i>BMC Plant Biology</i> , 2018, 18, 336.	1.6	31
7358	Effects of Space Flight on Mouse Liver versus Kidney: Gene Pathway Analyses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4106.	1.8	17
7359	A strategy to find novel candidate anti-Alzheimer's disease drugs by constructing interaction networks between drug targets and natural compounds in medical plants. <i>PeerJ</i> , 2018, 6, e4756.	0.9	8
7360	Multivariate Entropy Characterizes the Gene Expression and Protein-Protein Networks in Four Types of Cancer. <i>Entropy</i> , 2018, 20, 154.	1.1	4
7361	Proteome data of <i>Anopheles stephensi</i> salivary glands using high-resolution mass spectrometry analysis. <i>Data in Brief</i> , 2018, 21, 2554-2561.	0.5	0
7362	Assessing the bacterial communities of sponges inhabiting the remote western Indian Ocean island of Mayotte. <i>Marine Ecology</i> , 2018, 39, e12517.	0.4	18
7363	Type 2 Diabetes Gene Identification Using an Integrated Approach from Single-Cell RNA Sequencing Data. , 2018, , .		0
7364	GOnet: a tool for interactive Gene Ontology analysis. <i>BMC Bioinformatics</i> , 2018, 19, 470.	1.2	189
7365	Identification of Potential Prostate Cancer-Related Pseudogenes Based on Competitive Endogenous RNA Network Hypothesis. <i>Medical Science Monitor</i> , 2018, 24, 4213-4239.	0.5	31
7366	Understanding Human Deubiquitinases Target Specificity by Network-based Analysis towards their Development as Therapeutics Target. , 2018, , .		1

#	ARTICLE	IF	CITATIONS
7367	Relrank: An Algorithm for Relevance-Based Ranking of Meta-Paths in a Heterogeneous Information Network. , 2018, , .		0
7368	Host species, pathogens and disease associated with divergent nasal microbial communities in tortoises. Royal Society Open Science, 2018, 5, 181068.	1.1	9
7369	Abnormal DNA Methylation in Thoracic Spinal Cord Tissue Following Transection Injury. Medical Science Monitor, 2018, 24, 8878-8890.	0.5	10
7370	Quantitative Phosphoproteome Analysis of Clostridioides difficile Toxin B Treated Human Epithelial Cells. Frontiers in Microbiology, 2018, 9, 3083.	1.5	5
7371	VIA-QMI: A visualized data analytic tool for Quantitative Multiplex Co-Immunoprecipitation(QMI) Platform. , 2018, , .		0
7372	Robust Computational Method for Identification of miRNA-mRNA Modules in Cervical Cancer. , 2018, , .		0
7373	BEL Commons: an environment for exploration and analysis of networks encoded in Biological Expression Language. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	17
7374	High Throughput Screening Technologies in Biomass Characterization. Frontiers in Energy Research, 2018, 6, .	1.2	28
7375	Intestinal Microbiome and the Liver. , 2018, , 37-65.e6.		0
7376	PanoromiX: a time-course network medicine platform integrating molecular assays and pathophenotypic data. BMC Bioinformatics, 2018, 19, 458.	1.2	0
7377	Large-scale mining disease comorbidity relationships from post-market drug adverse events surveillance data. BMC Bioinformatics, 2018, 19, 500.	1.2	21
7378	Defining a Characteristic Gene Expression Set Responsible for Cancer Stem Cell-Like Features in a Sub-Population of Ewing Sarcoma Cells CADO-ES1. International Journal of Molecular Sciences, 2018, 19, 3908.	1.8	13
7379	Understanding molecular mechanisms of Rhodiola rosea for the treatment of acute mountain sickness through computational approaches (a STROBE-compliant article). Medicine (United States), 2018, 97, e11886.	0.4	6
7380	The Cost of Metabolic Interactions in Symbioses between Insects and Bacteria with Reduced Genomes. MBio, 2018, 9, .	1.8	51
7382	Comprehensive analysis of circRNA expression pattern and circRNA-miRNA-mRNA network in the pathogenesis of atherosclerosis in rabbits. Aging, 2018, 10, 2266-2283.	1.4	135
7383	Multiomics biomarkers for the prediction of nonalcoholic fatty liver disease severity. World Journal of Gastroenterology, 2018, 24, 1601-1615.	1.4	60
7384	Drug&ndash;target&ndash;disease network analysis of gene&ndash;phenotype connectivity for genistein in ovarian cancer. OncoTargets and Therapy, 2018, Volume 11, 8901-8908.	1.0	5
7385	Social Risk Dissociates Social Network Structure across Lateralized Behaviors in Spider Monkeys. Symmetry, 2018, 10, 390.	1.1	3

#	ARTICLE	IF	CITATIONS
7386	A Comparative Analysis of Large-scale Network Visualization Tools. , 2018, , .		7
7387	Aberrantly expressed long noncoding RNAs and genes in Parkinson&#39;s disease. <i>Neuropsychiatric Disease and Treatment</i> , 2018, Volume 14, 3219-3229.	1.0	29
7388	Biochemical Characterization and Phylogenetic Analysis of the Virulence Factor Lysine Decarboxylase From <i>Vibrio vulnificus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3082.	1.5	15
7389	Dynamics of Gut Microbiome in Giant Panda Cubs Reveal Transitional Microbes and Pathways in Early Life. <i>Frontiers in Microbiology</i> , 2018, 9, 3138.	1.5	30
7390	Identification of Significant Protein Diabetes Mellitus Type 2 with Fuzzy C- Means and Topological Analysis. , 2018, , .		2
7391	miRBaseConverter: an R/Bioconductor package for converting and retrieving miRNA name, accession, sequence and family information in different versions of miRBase. <i>BMC Bioinformatics</i> , 2018, 19, 514.	1.2	59
7392	Prediction of biochemical mechanism of anti-inflammation explained from two marine-derived bioactive compounds. <i>Agriculture and Natural Resources</i> , 2018, 52, 588-595.	0.4	3
7393	Discovery of Xuantoujiedu Decoction and its Molecular Mechanisms Using Integrated Network Analysis. , 2018, , .		0
7394	Next-generation sequencing analysis reveals high bacterial diversity in wild venomous and non-venomous snakes from India.. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2018, 24, 41.	0.8	11
7395	Gene Network Dysregulation in the Trigeminal Ganglia and Nucleus Accumbens of a Model of Chronic Migraine-Associated Hyperalgesia. <i>Frontiers in Systems Neuroscience</i> , 2018, 12, 63.	1.2	27
7396	NeVOmics: An Enrichment Tool for Gene Ontology and Functional Network Analysis and Visualization of Data from OMICs Technologies. <i>Genes</i> , 2018, 9, 569.	1.0	16
7397	Integrative analysis of gene expression profiles reveals distinct molecular characteristics in oral tongue squamous cell carcinoma. <i>Oncology Letters</i> , 2018, 17, 2377-2387.	0.8	12
7398	Genome-wide analysis of consistently RNA edited sites in human blood reveals interactions with mRNA processing genes and suggests correlations with cell types and biological variables. <i>BMC Genomics</i> , 2018, 19, 963.	1.2	8
7399	Plant stress RNA-seq Nexus: a stress-specific transcriptome database in plant cells. <i>BMC Genomics</i> , 2018, 19, 966.	1.2	24
7400	Investigation of the clinical significance and molecular mechanism of miRâ€‘21â€‘5p in hepatocellular carcinoma: A systematic review based on 24 studies and bioinformatics investigation. <i>Oncology Letters</i> , 2019, 17, 230-246.	0.8	9
7401	Benefits of procyanidins on gut microbiota in Bama minipigs and implications in replacing antibiotics. <i>Journal of Veterinary Science</i> , 2018, 19, 798.	0.5	4
7402	The bacterial community significantly promotes cast iron corrosion in reclaimed wastewater distribution systems. <i>Microbiome</i> , 2018, 6, 222.	4.9	32
7403	Transcriptome analysis of pancreatic cancer cell response to treatment with grape seed proanthocyanidins. <i>Oncology Letters</i> , 2018, 17, 1741-1749.	0.8	8



#	ARTICLE	IF	CITATIONS
7404	Transcriptomics in pain research: insights from new and old technologies. <i>Molecular Omics</i> , 2018, 14, 389-404.	1.4	22
7405	Transcriptomic and microRNAomic profiling reveals molecular mechanisms to cope with silver nanoparticle exposure in the ciliate <i>Euplotes vannus</i> . <i>Environmental Science: Nano</i> , 2018, 5, 2921-2935.	2.2	27
7406	An In Vitro Versus In Vivo Toxicogenomic Investigation of Prenatal Exposures to Tobacco Smoke. <i>Applied in Vitro Toxicology</i> , 2018, 4, 379-388.	0.6	3
7407	Modelling Implicit Content Networks to Track Information Propagation Across Media Sources to Analyze News Events. , 2018, , .		0
7408	FRET-Based Enzyme Activity Reporter: Practical Hints for Kinases as Indicators of Virulence. , 2018, , .		0
7409	The landscape of miRNA-related ceRNA networks for marking different renal cell carcinoma subtypes. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	5
7410	Uterine Microbiota of Dairy Cows With Clinical and Subclinical Endometritis. <i>Frontiers in Microbiology</i> , 2018, 9, 2691.	1.5	54
7411	Identification of key pathways and genes in endometrial cancer using bioinformatics analyses. <i>Oncology Letters</i> , 2018, 17, 897-906.	0.8	18
7412	Generation of a versatile BiFC ORFeome library for analyzing protein-protein interactions in live <i>Drosophila</i> . <i>ELife</i> , 2018, 7, .	2.8	31
7413	Protein Regulating Networks underlying Multiple Actions against Cancer Delivered by Ginseng. , 2018, , .		1
7414	Bioinformatics analysis and verification of key genes associated with recurrent respiratory tract infections. <i>International Journal of Molecular Medicine</i> , 2018, 42, 514-524.	1.8	2
7415	A panel of 7 prognosis-related long non-coding RNAs to improve platinum-based chemoresistance prediction in ovarian cancer. <i>International Journal of Oncology</i> , 2018, 53, 866-876.	1.4	17
7416	Disease outbreak accompanies the dispersive structure of shrimp gut bacterial community with a simple core microbiota. <i>AMB Express</i> , 2018, 8, 120.	1.4	50
7417	Cantharidin Triggers Apoptosis via ALB and PPP2R4 against Lung Cancer. , 2018, , .		0
7418	Visual Analysis of Vertex-Disjoint Path Connectivity in Networks. , 2018, , .		0
7419	A Graph-Theoretic Approach for Identifying Bacterial Inter-correlations and Functional Pathways in Microbiome Data. , 2018, , .		2
7420	Genome-Wide miRNA Expression Alterations in Nucleus Accumbens Provide Insights into Chronic Stress and Treatment in Depression. , 2018, , .		0
7421	Network-based gene function inference method to predict optimal gene functions associated with fetal growth restriction. <i>Molecular Medicine Reports</i> , 2018, 18, 3003-3010.	1.1	3

#	ARTICLE	IF	CITATIONS
7422	Integrative machine learning analysis of multiple gene expression profiles in cervical cancer. PeerJ, 2018, 6, e5285.	0.9	27
7423	Graph Theoretic Concepts as the Building Blocks for Disease Initiation and Progression at Protein Network Level: Identification and Challenges. , 2018, , .		3
7424	Gene expression profiles for predicting antibody-mediated kidney allograft rejection: Analysis of GEO datasets. International Journal of Molecular Medicine, 2018, 42, 2303-2311.	1.8	5
7425	Analysis of NFkB-mediated regulation of mechanisms underlying the development of Hodgkin's lymphoma. Molecular Medicine Reports, 2018, 17, 8129-8136.	1.1	5
7426	Connectivity analysis of ecological landscape networks by cut node ranking. Applied Network Science, 2018, 3, 22.	0.8	11
7427	REMatch: Research Expert Matching System. , 2018, , .		1
7428	A Gene Family-led Meta-Analysis of Drug-Target Interactions. , 2018, , .		1
7429	Biomarker Identification from RNA-Seq Data using a Robust Statistical Approach. Bioinformatics, 2018, 14, 153-163.	0.2	10
7430	RDF Graph Visualization Tools: a Survey. , 2018, , .		13
7431	A survey of simulation provenance systems: modeling, capturing, querying, visualization, and advanced utilization. Human-centric Computing and Information Sciences, 2018, 8, .	6.1	10
7432	Analyzing students' collaboration patterns in a social learning environment using StudentViz platform. Smart Learning Environments, 2018, 5, .	4.3	9
7433	ClustEx2: Gene Module Identification using Density-Based Network Hierarchical Clustering. , 2018, , .		2
7434	Biological Network Analysis and Subnetwork Extraction Tool. , 2018, , .		0
7435	Protein Regulating Network towards Tonifying Primal Qi Delivered by Ginseng. , 2018, , .		0
7436	Complete Genomes of Two Novel Active Prophages Discovered by Bioinformatics Methods from High-Throughput Sequencing Data. IOP Conference Series: Materials Science and Engineering, 2018, 466, 012032.	0.3	1
7438	Several genes involved in the JAK-STAT pathway may act as prognostic markers in pancreatic cancer identified by microarray data analysis. Medicine (United States), 2018, 97, e13297.	0.4	9
7439	Whole-Genome and Expression Analyses of Bamboo Aquaporin Genes Reveal Their Functions Involved in Maintaining Diurnal Water Balance in Bamboo Shoots. Cells, 2018, 7, 195.	1.8	14
7440	Identification of Arbuscular Mycorrhiza Fungi Responsive microRNAs and Their Regulatory Network in Maize. International Journal of Molecular Sciences, 2018, 19, 3201.	1.8	29

#	ARTICLE	IF	CITATIONS
7441	Global Analysis of WOX Transcription Factor Gene Family in Brassica napus Reveals Their Stress- and Hormone-Responsive Patterns. International Journal of Molecular Sciences, 2018, 19, 3470.	1.8	27
7442	Identification of Six Potentially Long Noncoding RNAs as Biomarkers Involved Competitive Endogenous RNA in Clear Cell Renal Cell Carcinoma. BioMed Research International, 2018, 2018, 1-13.	0.9	28
7443	Systems-Mapping of Herbal Effects on Complex Diseases Using the Network-Perturbation Signatures. Frontiers in Pharmacology, 2018, 9, 1174.	1.6	18
7444	Exploring Seipin: From Biochemistry to Bioinformatics Predictions. International Journal of Cell Biology, 2018, 2018, 1-21.	1.0	18
7445	SyNDI: synchronous network data integration framework. BMC Bioinformatics, 2018, 19, 403.	1.2	1
7446	Integrated whole genome microarray analysis and immunohistochemical assay identifies COL11A1, GJB2 and CTRL as predictive biomarkers for pancreatic cancer. Cancer Cell International, 2018, 18, 174.	1.8	28
7447	Identification of critically carcinogenesis-related genes in basal cell carcinoma. OncoTargets and Therapy, 2018, Volume 11, 6957-6967.	1.0	7
7448	Identifying a Novel Biomarker <i>TOP2A</i> of Clear Cell Renal Cell Carcinoma (ccRCC) Associated with Smoking by Co-Expression Network Analysis. Journal of Cancer, 2018, 9, 3912-3922.	1.2	20
7449	Functional annotation of extensively and divergently expressed miRNAs in suprachiasmatic nucleus of <i>Clock<sup>fl<sup>+</sup>/19</sup></i> mutant mice. Bioscience Reports, 2018, 38, .	1.1	5
7450	Spatial Analysis of Functional Enrichment (SAFE) in Large Biological Networks. Methods in Molecular Biology, 2018, 1819, 249-268.	0.4	18
7451	RIP1 Kinase Drives Macrophage-Mediated Adaptive Immune Tolerance in Pancreatic Cancer. Cancer Cell, 2018, 34, 757-774.e7.	7.7	170
7452	Integrated Bioinformatics Analysis for Identificating the Therapeutic Targets of Aspirin in Small Cell Lung Cancer. Journal of Biomedical Informatics, 2018, 88, 20-28.	2.5	26
7453	Identification of key genes and miRNAs markers of papillary thyroid cancer. Biological Research, 2018, 51, 45.	1.5	39
7454	Single cell transcriptome analysis of human, marmoset and mouse embryos reveals common and divergent features of preimplantation development. Development (Cambridge), 2018, 145, .	1.2	167
7455	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	3.8	18
7456	Identification of chemoresistance-associated miRNAs in breast cancer. Cancer Management and Research, 2018, Volume 10, 4747-4757.	0.9	64
7457	Gene Expression Profiling of Lacrimal Glands Identifies the Ectopic Expression of MHC II on Glandular Cells as a Presymptomatic Feature in a Mouse Model of Primary Sjögren's Syndrome. Frontiers in Immunology, 2018, 9, 2362.	2.2	7
7458	Transcriptome and Resistance-Related Genes Analysis of Botrytis cinerea B05.10 Strain to Different Selective Pressures of Cyprodinil and Fenhexamid. Frontiers in Microbiology, 2018, 9, 2591.	1.5	8

#	ARTICLE	IF	CITATIONS
7459	Determining the Balance Between Drug Efficacy and Safety by the Network and Biological System Profile of Its Therapeutic Target. <i>Frontiers in Pharmacology</i> , 2018, 9, 1245.	1.6	28
7460	Temperature-dependent vitamin D signaling regulates developmental trajectory associated with diapause in an annual killifish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12763-12768.	3.3	40
7461	Identification of Potential Prognostic Genes for Neuroblastoma. <i>Frontiers in Genetics</i> , 2018, 9, 589.	1.1	47
7462	Novel drug candidates for treating esophageal carcinoma: A study on differentially expressed genes, using connectivity mapping and molecular docking. <i>International Journal of Oncology</i> , 2019, 54, 152-166.	1.4	17
7463	Cellular metabolism constrains innate immune responses in early human ontogeny. <i>Nature Communications</i> , 2018, 9, 4822.	5.8	35
7464	In silico identification and characterization of a diverse subset of conserved microRNAs in bioenergy crop <i>Arundo donax</i> L.. <i>Scientific Reports</i> , 2018, 8, 16667.	1.6	9
7465	A 15-lncRNA signature predicts survival and functions as a ceRNA in patients with colorectal cancer. <i>Cancer Management and Research</i> , 2018, Volume 10, 5799-5806.	0.9	56
7466	Transcriptome Analysis of Long Non-Coding RNA in the Bovine Mammary Gland Following Dietary Supplementation with Linseed Oil and Safflower Oil. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3610.	1.8	18
7467	Developing Network Models of Multiscale Host Responses Involved in Infections and Diseases. <i>Methods in Molecular Biology</i> , 2018, 1819, 385-402.	0.4	0
7468	Haploinsufficiency of the intellectual disability gene <i>SETD5</i> disturbs developmental gene expression and cognition. <i>Nature Neuroscience</i> , 2018, 21, 1717-1727.	7.1	65
7469	A Network Pharmacology Analysis to Explore the Effect of <i>Astragali Radix-Radix Angelica Sinensis</i> on Traumatic Brain Injury. <i>BioMed Research International</i> , 2018, 2018, 1-13.	0.9	28
7470	Distinct prognostic value of dynactin subunit 4 (DCTN4) and diagnostic value of DCTN1, DCTN2, and DCTN4 in colon adenocarcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 5807-5824.	0.9	17
7471	Damage-responsive elements in <i>Drosophila</i> regeneration. <i>Genome Research</i> , 2018, 28, 1852-1866.	2.4	52
7472	Comprehensive proteome analyses of lysine acetylation in tea leaves by sensing nitrogen nutrition. <i>BMC Genomics</i> , 2018, 19, 840.	1.2	31
7473	Metabolomic Fingerprinting of <i>Salinispora</i> From Atlantic Oceanic Islands. <i>Frontiers in Microbiology</i> , 2018, 9, 3021.	1.5	17
7474	CCNA2 acts as a novel biomarker in regulating the growth and apoptosis of colorectal cancer. <i>Cancer Management and Research</i> , 2018, Volume 10, 5113-5124.	0.9	83
7475	Cacolides: Sesterterpene Butenolides from a Southern Australian Marine Sponge, <i>Cacospongia</i> sp.. <i>Marine Drugs</i> , 2018, 16, 456.	2.2	13
7476	Investigating the Role of MicroRNA and Transcription Factor Co-regulatory Networks in Multiple Sclerosis Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3652.	1.8	40

#	ARTICLE	IF	CITATIONS
7477	Proteome Investigation of Rat Lungs subjected to Ex Vivo Perfusion (EVLP). <i>Molecules</i> , 2018, 23, 3061.	1.7	20
7478	Weighted Correlation Network Analysis (WGCNA) of Japanese Flounder ( <i>Paralichthys olivaceus</i> ) Embryo Transcriptome Provides Crucial Gene Sets for Understanding Haploid Syndrome and Rescue by Diploidization. <i>Journal of Ocean University of China</i> , 2018, 17, 1441-1450.	0.6	7
7479	Assessing the Pharmacological and Therapeutic Efficacy of Traditional Chinese Medicine Liangxue Tongyu Prescription for Intracerebral Hemorrhagic Stroke in Neurological Disease Models. <i>Frontiers in Pharmacology</i> , 2018, 9, 1169.	1.6	20
7480	Protein Profiling of Arabidopsis Roots Treated With Humic Substances: Insights Into the Metabolic and Interactome Networks. <i>Frontiers in Plant Science</i> , 2018, 9, 1812.	1.7	41
7481	Maize multi-omics reveal roles for autophagic recycling in proteome remodelling and lipid turnover. <i>Nature Plants</i> , 2018, 4, 1056-1070.	4.7	124
7482	miRNA Mediated Noise Making of 3'UTR Mutations in Cancer. <i>Genes</i> , 2018, 9, 545.	1.0	12
7483	Gene's hubs in retinal diseases: A retinal disease network. <i>Heliyon</i> , 2018, 4, e00867.	1.4	7
7484	Comprehensive analysis of aberrantly expressed profiles of lncRNAs, miRNAs and mRNAs with associated ceRNA network in cholangiocarcinoma. <i>Cancer Biomarkers</i> , 2018, 23, 549-559.	0.8	25
7485	Aerobic Anoxygenic Phototrophic Bacteria Promote the Development of Biological Soil Crusts. <i>Frontiers in Microbiology</i> , 2018, 9, 2715.	1.5	17
7486	Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. <i>Cell Systems</i> , 2018, 7, 627-642.e6.	2.9	34
7487	Helios is a key transcriptional regulator of outer hair cell maturation. <i>Nature</i> , 2018, 563, 696-700.	13.7	90
7488	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. <i>Scientific Reports</i> , 2018, 8, 17135.	1.6	42
7489	Human Fetal Astrocytes Infected with Zika Virus Exhibit Delayed Apoptosis and Resistance to Interferon: Implications for Persistence. <i>Viruses</i> , 2018, 10, 646.	1.5	47
7490	Bioinformatics-based study to detect chemical compounds that show potential as treatments for pulmonary thromboembolism. <i>International Journal of Molecular Medicine</i> , 2019, 43, 276-284.	1.8	5
7491	N-Prenylation of Tryptophan by an Aromatic Prenyltransferase from the Cyanobactin Biosynthetic Pathway. <i>Biochemistry</i> , 2018, 57, 6860-6867.	1.2	26
7492	Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. <i>Nature Communications</i> , 2018, 9, 4892.	5.8	51
7493	Proteomic Analysis of Plasma Membrane Proteins of Antler Stem Cells Using Label-Free LC-MS/MS. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3477.	1.8	11
7494	Systems Biology Analysis to Understand Regulatory miRNA Networks in Lung Cancer. <i>Methods in Molecular Biology</i> , 2018, 1819, 235-247.	0.4	5

#	ARTICLE	IF	CITATIONS
7495	Increased virulence of the oral microbiome in oral squamous cell carcinoma revealed by metatranscriptome analyses. <i>International Journal of Oral Science</i> , 2018, 10, 32.	3.6	88
7496	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. <i>Scientific Reports</i> , 2018, 8, 16679.	1.6	29
7497	MicroRNA-200a Affects the Proliferation of Airway Smooth Muscle Cells and Airway Remodeling by Targeting FOXC1 via the PI3K/AKT Signaling Pathway in Ovalbumin-Induced Asthmatic Mice. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 2365-2389.	1.1	34
7498	Effect of IAPP on the proteome of cultured Rin-5F cells. <i>BMC Biochemistry</i> , 2018, 19, 9.	4.4	1
7499	Triptolide as a novel agent in pancreatic cancer: the validation using patient derived pancreatic tumor cell line. <i>BMC Cancer</i> , 2018, 18, 1103.	1.1	25
7500	Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. <i>Cell Stem Cell</i> , 2018, 23, 869-881.e8.	5.2	419
7501	Lactobacillus elicits a 'Marmite effect' on the chicken cecal microbiome. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 27.	2.9	18
7502	Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. <i>Nature Medicine</i> , 2018, 24, 978-985.	15.2	1,044
7503	C/VDdb: A multi-omics expression profiling database for a knowledge-driven approach in cardiovascular disease (CVD). <i>PLoS ONE</i> , 2018, 13, e0207371.	1.1	21
7504	Identification of novel candidate genes involved in the progression of emphysema by bioinformatic methods. <i>International Journal of COPD</i> , 2018, Volume 13, 3733-3747.	0.9	12
7505	Optimized Protein-Protein Interaction Network Usage with Context Filtering. <i>Methods in Molecular Biology</i> , 2018, 1819, 33-50.	0.4	2
7506	Signalink: Multilayered Regulatory Networks. <i>Methods in Molecular Biology</i> , 2018, 1819, 53-73.	0.4	17
7507	Revealing the Critical Regulators of Cell Identity in the Mouse Cell Atlas. <i>Cell Reports</i> , 2018, 25, 1436-1445.e3.	2.9	185
7508	Charting an Unexplored Streptococcal Biosynthetic Landscape Reveals a Unique Peptide Cyclization Motif. <i>Journal of the American Chemical Society</i> , 2018, 140, 17674-17684.	6.6	78
7509	Genome-wide Identification, Classification, and Expression Pattern of Homeobox Gene Family in Brassica rapa under Various Stresses. <i>Scientific Reports</i> , 2018, 8, 16265.	1.6	28
7510	Machine Learning Reveals Protein Signatures in CSF and Plasma Fluids of Clinical Value for ALS. <i>Scientific Reports</i> , 2018, 8, 16334.	1.6	30
7511	A group of long noncoding RNAs identified by data mining can predict the prognosis of lung adenocarcinoma. <i>Cancer Science</i> , 2018, 109, 4033-4044.	1.7	15
7512	Norepinephrine triggers an immediate-early regulatory network response in primary human white adipocytes. <i>BMC Genomics</i> , 2018, 19, 794.	1.2	20

#	ARTICLE	IF	CITATIONS
7513	Solute Carrier Family 27 Member 4 (SLC27A4) Enhances Cell Growth, Migration, and Invasion in Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3434.	1.8	54
7514	A Systems-Level Analysis of Mechanisms of <i>Platycodon grandiflorum</i> Based on A Network Pharmacological Approach. <i>Molecules</i> , 2018, 23, 2841.	1.7	36
7515	Mining the potential therapeutic targets for coronary artery disease by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 5069-5075.	1.1	2
7516	Personalized Proteomics for Precision Health: Identifying Biomarkers of Vitreoretinal Disease. <i>Translational Vision Science and Technology</i> , 2018, 7, 12.	1.1	33
7517	3D Network exploration and visualisation for lifespan data. <i>BMC Bioinformatics</i> , 2018, 19, 390.	1.2	5
7518	Independent yet overlapping pathways ensure the robustness and responsiveness of trans-Golgi network functions in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2018, 145, .	1.2	28
7519	AIF1L regulates actomyosin contractility and filopodial extensions in human podocytes. <i>PLoS ONE</i> , 2018, 13, e0200487.	1.1	15
7520	MYC Protein Interactome Profiling Reveals Functionally Distinct Regions that Cooperate to Drive Tumorigenesis. <i>Molecular Cell</i> , 2018, 72, 836-848.e7.	4.5	121
7521	Metabolomics-Driven Discovery of Meroterpenoids from a Mussel-Derived <i>Penicillium ubiqetum</i> . <i>Journal of Natural Products</i> , 2018, 81, 2501-2511.	1.5	31
7522	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840026.	0.3	10
7523	A Novel Systems Pharmacology Method to Investigate Molecular Mechanisms of <i>Scutellaria barbata</i> D. Don for Non-small Cell Lung Cancer. <i>Frontiers in Pharmacology</i> , 2018, 9, 1473.	1.6	25
7524	Sheep skeletal muscle transcriptome analysis reveals muscle growth regulatory lncRNAs. <i>PeerJ</i> , 2018, 6, e4619.	0.9	6
7525	Network proteomics of human dermal wound healing. <i>Physiological Measurement</i> , 2018, 39, 124002.	1.2	10
7526	Diversification of DNA binding specificities enabled SREBP transcription regulators to expand the repertoire of cellular functions that they govern in fungi. <i>PLoS Genetics</i> , 2018, 14, e1007884.	1.5	14
7527	A miRNA Host Response Signature Accurately Discriminates Acute Respiratory Infection Etiologies. <i>Frontiers in Microbiology</i> , 2018, 9, 2957.	1.5	14
7528	Large scale study of anti-sense regulation by differential network analysis. <i>BMC Systems Biology</i> , 2018, 12, 95.	3.0	1
7529	Comparative De Novo transcriptome analysis of the Australian black-lip and Sydney rock oysters reveals expansion of repetitive elements in <i>Saccostrea</i> genomes. <i>PLoS ONE</i> , 2018, 13, e0206417.	1.1	3
7530	Robust analysis of novel mRNA&ndash;lncRNA cross talk based on ceRNA hypothesis uncovers carcinogenic mechanism and promotes diagnostic accuracy in esophageal cancer. <i>Cancer Management and Research</i> , 2019, Volume 11, 347-358.	0.9	16



#	ARTICLE	IF	CITATIONS
7531	Parameter estimation of qualitative biological regulatory networks on high performance computing hardware. <i>BMC Systems Biology</i> , 2018, 12, 146.	3.0	6
7532	Bacterial diversity and community in Qula from the Qinghaiâ€“Tibetan Plateau in China. <i>PeerJ</i> , 2018, 6, e6044.	0.9	22
7533	Six novel susceptibility loci for coronary artery disease and cerebral infarction identified by longitudinal exomeâ€“wide association studies in a Japanese population. <i>Biomedical Reports</i> , 2018, 9, 123-134.	0.9	8
7534	Expression levels and coâ€“targets of miRNAâ€“126â€“3p and miRNAâ€“126â€“5p in lung adenocarcinoma tissues: An exploration with RTâ€“qPCR, microarray and bioinformatic analyses. <i>Oncology Reports</i> , 2019, 41, 939-953.	1.2	13
7535	Bioinformatic and Metabolomic Analysis Reveal Intervention Effects of Chicory in a Quail Model of Hyperuricemia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-13.	0.5	12
7536	Bioinformatics Analysis of the Molecular Mechanism of Aging on Fracture Healing. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	8
7537	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. <i>Clinical Epigenetics</i> , 2018, 10, 161.	1.8	20
7538	Transcriptome analysis of the typical freshwater rhodophytes <i>Sheathia arcuata</i> grown under different light intensities. <i>PLoS ONE</i> , 2018, 13, e0197729.	1.1	12
7539	In silico repositioning of approved drugs against <i>Schistosoma mansoni</i> energy metabolism targets. <i>PLoS ONE</i> , 2018, 13, e0203340.	1.1	5
7540	Temporal dynamics of liver mitochondrial protein acetylation and succinylation and metabolites due to high fat diet and/or excess glucose or fructose. <i>PLoS ONE</i> , 2018, 13, e0208973.	1.1	38
7541	An Alliance of Gel-Based and Gel-Free Proteomic Techniques Displays Substantial Insight Into the Proteome of a Virulent and an Attenuated <i>Histomonas meleagridis</i> Strain. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 407.	1.8	14
7542	Comparative Metabolomic Sampling of Upper and Lower Airways by Four Different Methods to Identify Biochemicals That May Support Bacterial Growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 432.	1.8	18
7543	Temporal Bacterial Surveillance of Salmon Aquaculture Sites Indicates a Long Lasting Benthic Impact With Minimal Recovery. <i>Frontiers in Microbiology</i> , 2018, 9, 3054.	1.5	36
7544	Disorganized Gut Microbiome Contributed to Liver Cirrhosis Progression: A Meta-Omics-Based Study. <i>Frontiers in Microbiology</i> , 2018, 9, 3166.	1.5	57
7545	Integrating Strategies of Herbal Metabolomics, Network Pharmacology, and Experiment Validation to Investigate Frankincense Processing Effects. <i>Frontiers in Pharmacology</i> , 2018, 9, 1482.	1.6	23
7546	Biological Pathways Leading From ANGPTL8 to Diabetes Mellitusâ€“A Co-expression Network Based Analysis. <i>Frontiers in Physiology</i> , 2018, 9, 1841.	1.3	8
7547	Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant <i>Haberlea rhodopensis</i> . <i>BMC Plant Biology</i> , 2018, 18, 351.	1.6	40
7548	Shotgun proteomics data on the impact of hyperglycaemia on platelet protein acetylation by aspirin. <i>Data in Brief</i> , 2018, 21, 2475-2481.	0.5	2

#	ARTICLE	IF	CITATIONS
7549	Protective Effect of Salidroside Against Diabetic Kidney Disease Through Inhibiting BIM-Mediated Apoptosis of Proximal Renal Tubular Cells in Rats. <i>Frontiers in Pharmacology</i> , 2018, 9, 1433.	1.6	23
7550	Data set of differentially expressed microRNAs in sanguinarine-treated <i>Caenorhabditis elegans</i> and its F3 progeny. <i>Data in Brief</i> , 2018, 21, 899-906.	0.5	0
7551	An electrogenic redox loop in sulfate reduction reveals a likely widespread mechanism of energy conservation. <i>Nature Communications</i> , 2018, 9, 5448.	5.8	27
7552	Role of miRNAs in skeletal muscle aging. <i>Clinical Interventions in Aging</i> , 2018, Volume 13, 2407-2419.	1.3	42
7553	Lysosomal protease deficiency or substrate overload induces an oxidative-stress mediated STAT3-dependent pathway of lysosomal homeostasis. <i>Nature Communications</i> , 2018, 9, 5343.	5.8	52
7554	Exploring the rumen fluid metabolome using liquid chromatography-high-resolution mass spectrometry and Molecular Networking. <i>Scientific Reports</i> , 2018, 8, 17971.	1.6	17
7555	Co-expression of long non-coding RNAs and autism risk genes in the developing human brain. <i>BMC Systems Biology</i> , 2018, 12, 91.	3.0	27
7556	Circular RNA regulatory network reveals cell-cell crosstalk in acute myeloid leukemia extramedullary infiltration. <i>Journal of Translational Medicine</i> , 2018, 16, 361.	1.8	45
7557	Identification of alterations in macrophage activation associated with disease activity in systemic lupus erythematosus. <i>PLoS ONE</i> , 2018, 13, e0208132.	1.1	80
7558	Network analysis of differentially expressed smoking-associated mRNAs, lncRNAs and miRNAs reveals key regulators in smoking-associated lung cancer. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 4991-5002.	0.8	11
7559	Phototransduction and circadian entrainment are the key pathways in the signaling mechanism for the baculovirus induced tree-top disease in the lepidopteran larvae. <i>Scientific Reports</i> , 2018, 8, 17528.	1.6	17
7560	Bioinformatic Analyses of Renal Ischaemia-Reperfusion Injury Models: Identification of Key Genes Involved in the Development of Kidney Disease. <i>Kidney and Blood Pressure Research</i> , 2018, 43, 1898-1907.	0.9	13
7561	Identification of differentially expressed miRNAs in early-stage cervical cancer with lymph node metastasis across The Cancer Genome Atlas datasets. <i>Cancer Management and Research</i> , 2018, Volume 10, 6489-6504.	0.9	19
7562	The Core- and Pan-Genomic Analyses of the Genus <i>Comamonas</i> : From Environmental Adaptation to Potential Virulence. <i>Frontiers in Microbiology</i> , 2018, 9, 3096.	1.5	67
7564	Identification of a multidimensional transcriptome signature for survival prediction of postoperative glioblastoma multiforme patients. <i>Journal of Translational Medicine</i> , 2018, 16, 368.	1.8	54
7565	Metabolomics and 16S rRNA sequencing of human colorectal cancers and adjacent mucosa. <i>PLoS ONE</i> , 2018, 13, e0208584.	1.1	39
7566	DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory sensory epithelium. <i>Scientific Reports</i> , 2018, 8, 17348.	1.6	27
7567	Discrimination of contagious and environmental strains of <i>Streptococcus uberis</i> in dairy herds by means of mass spectrometry and machine-learning. <i>Scientific Reports</i> , 2018, 8, 17517.	1.6	25

#	ARTICLE	IF	CITATIONS
7568	Integrated molecular characterization of adult soft tissue sarcoma for therapeutic targets. <i>BMC Medical Genetics</i> , 2018, 19, 216.	2.1	18
7569	scdNet: a computational tool for single-cell differential network analysis. <i>BMC Systems Biology</i> , 2018, 12, 124.	3.0	13
7570	Integrated analysis of dysregulated long non-coding RNAs/microRNAs/mRNAs in metastasis of lung adenocarcinoma. <i>Journal of Translational Medicine</i> , 2018, 16, 372.	1.8	62
7571	Transcriptome and Small RNA Sequencing Analysis Revealed Roles of PaWB-Related miRNAs and Genes in <i>Paulownia fortunei</i> . <i>Forests</i> , 2018, 9, 397.	0.9	5
7572	Investigation into the underlying molecular mechanisms of white adipose tissue through comparative transcriptome analysis of multiple tissues. <i>Molecular Medicine Reports</i> , 2018, 19, 959-966.	1.1	4
7573	Regulation of mycobacterial infection by macrophage Gch1 and tetrahydrobiopterin. <i>Nature Communications</i> , 2018, 9, 5409.	5.8	24
7575	lncRNA profile study reveals the mRNAs and lncRNAs associated with docetaxel resistance in breast cancer cells. <i>Scientific Reports</i> , 2018, 8, 17970.	1.6	52
7576	Interactive Network Visualization of Gene Expression Time-Series Data. , 2018, , .		2
7577	Hunters or farmers? Microbiome characteristics help elucidate the diet composition in an aquatic carnivorous plant. <i>Microbiome</i> , 2018, 6, 225.	4.9	29
7578	Identification of Candidate Genes and Regulatory Factors Underlying Intramuscular Fat Content Through Longissimus Dorsi Transcriptome Analyses in Heavy Iberian Pigs. <i>Frontiers in Genetics</i> , 2018, 9, 608.	1.1	56
7579	Oncogenic Activation of Nrf2, Though as a Master Antioxidant Transcription Factor, Liberated by Specific Knockout of the Full-Length Nrf1 that Acts as a Dominant Tumor Repressor. <i>Cancers</i> , 2018, 10, 520.	1.7	42
7580	A Metabologenomic Approach Reveals Changes in the Intestinal Environment of Mice Fed on American Diet. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4079.	1.8	41
7581	Identification of 12 novel loci that confer susceptibility to early-onset dyslipidemia. <i>International Journal of Molecular Medicine</i> , 2018, 43, 57-82.	1.8	5
7582	Pan-cancer analysis of transcriptional metabolic dysregulation using The Cancer Genome Atlas. <i>Nature Communications</i> , 2018, 9, 5330.	5.8	174
7583	GraphVR: A Virtual Reality Tool for the Exploration of Graphs with HTC Vive System. , 2018, , .		16
7584	Dysregulated miRNAome and Proteome of PPRV Infected Goat PBMCs Reveal a Coordinated Immune Response. <i>Frontiers in Immunology</i> , 2018, 9, 2631.	2.2	22
7585	The Role of Fur in the Transcriptional and Iron Homeostatic Response of <i>Enterococcus faecalis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1580.	1.5	32
7586	Dopamine perturbation of gene co-expression networks reveals differential response in schizophrenia for translational machinery. <i>Translational Psychiatry</i> , 2018, 8, 278.	2.4	8

#	ARTICLE	IF	CITATIONS
7587	Structure-function analysis of Sedolisins: evolution of tripeptidyl peptidase and endopeptidase subfamilies in fungi. <i>BMC Bioinformatics</i> , 2018, 19, 464.	1.2	2
7588	The construction and analysis of ceRNA networks in invasive breast cancer: a study based on The Cancer Genome Atlas. <i>Cancer Management and Research</i> , 2019, Volume 11, 1-11.	0.9	49
7589	Identification of core genes and prediction of miRNAs associated with osteoporosis using a bioinformatics approach. <i>Oncology Letters</i> , 2018, 17, 468-481.	0.8	5
7590	MicroRNA-31 Reduces the Motility of Proinflammatory T Helper 1 Lymphocytes. <i>Frontiers in Immunology</i> , 2018, 9, 2813.	2.2	13
7591	Prognostic value of sorting nexin 10 weak expression in stomach adenocarcinoma revealed by weighted gene co-expression network analysis. <i>World Journal of Gastroenterology</i> , 2018, 24, 4906-4919.	1.4	17
7592	Bone Marrow-Derived Proangiogenic Cells Mediate Pulmonary Arteriole Stiffening via Serotonin 2B Receptor Dependent Mechanism. <i>Circulation Research</i> , 2018, 123, e51-e64.	2.0	17
7593	Centromere protein F (CENPF), a microtubule binding protein, modulates cancer metabolism by regulating pyruvate kinase M2 phosphorylation signaling. <i>Cell Cycle</i> , 2018, 17, 2802-2818.	1.3	51
7594	The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	81
7595	Chronic lifestyle diseases display seasonal sensitive comorbid trend in human population evidence from Google Trends. <i>PLoS ONE</i> , 2018, 13, e0207359.	1.1	15
7596	Natural and molecular history of prolactinoma: insights from a <i>Prlr</i> mouse model. <i>Oncotarget</i> , 2018, 9, 6144-6155.	0.8	14
7597	Evaluating the profound effect of gut microbiome on host appetite in pigs. <i>BMC Microbiology</i> , 2018, 18, 215.	1.3	50
7598	Potential clinical value and putative biological function of miR-122-5p in hepatocellular carcinoma: A comprehensive study using microarray and RNA sequencing data. <i>Oncology Letters</i> , 2018, 16, 6918-6929.	0.8	12
7599	Identifying the key genes and microRNAs in colorectal cancer liver metastasis by bioinformatics analysis and <i>in vitro</i> experiments. <i>Oncology Reports</i> , 2019, 41, 279-291.	1.2	39
7600	Microbial Communities From the World's Largest Lithium Reserve, Salar de Atacama, Chile: Life at High LiCl Concentrations. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2018, 123, 3668-3681.	1.3	29
7601	Pathway sensor-based functional genomics screening identifies modulators of neuronal activity. <i>Scientific Reports</i> , 2018, 8, 17597.	1.6	7
7602	Analysis of the transcriptome data in <i>Litopenaeus vannamei</i> reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. <i>PLoS ONE</i> , 2018, 13, e0207771.	1.1	20
7603	Gut Microbiota Features in Young Children With Autism Spectrum Disorders. <i>Frontiers in Microbiology</i> , 2018, 9, 3146.	1.5	154
7604	Oxytocin Manipulation Alters Neural Activity in Response to Social Stimuli in Eusocial Naked Mole-Rats. <i>Frontiers in Behavioral Neuroscience</i> , 2018, 12, 272.	1.0	5

#	ARTICLE	IF	CITATIONS
7605	Integrated Analysis of MicroRNA (miRNA) and mRNA Profiles Reveals Reduced Correlation between MicroRNA and Target Gene in Cancer. <i>BioMed Research International</i> , 2018, 2018, 1-15.	0.9	24
7606	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. <i>PLoS ONE</i> , 2018, 13, e0208273.	1.1	41
7607	MicroRNAs as Diagnostic and Prognostic Biomarkers in Ischemic Stroke—A Comprehensive Review and Bioinformatic Analysis. <i>Cells</i> , 2018, 7, 249.	1.8	131
7608	Tissue-Specific Down-Regulation of the Long Non-Coding RNAs PCAT18 and LINC01133 in Gastric Cancer Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3881.	1.8	37
7609	Systematic Investigation of <i>Scutellariae Barbatae</i> Herba for Treating Hepatocellular Carcinoma Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-12.	0.5	18
7610	Interactive Responses of <i>Solanum Dulcamara</i> to Drought and Insect Feeding are Herbivore Species-Specific. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3845.	1.8	17
7611	Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , 2018, 8, 267.	2.4	22
7612	Exploration of deep terrestrial subsurface microbiome in Late Cretaceous Deccan traps and underlying Archean basement, India. <i>Scientific Reports</i> , 2018, 8, 17459.	1.6	44
7613	Integration of high-throughput data of microRNA and mRNA expression profiles reveals novel insights into the mechanism of liver fibrosis. <i>Molecular Medicine Reports</i> , 2018, 19, 115-124.	1.1	7
7614	The chicken gut metagenome and the modulatory effects of plant-derived benzyloquinoline alkaloids. <i>Microbiome</i> , 2018, 6, 211.	4.9	204
7615	Rainbow Trout Erythrocytes ex vivo Transfection With a DNA Vaccine Encoding VHSV Glycoprotein G Induces an Antiviral Immune Response. <i>Frontiers in Immunology</i> , 2018, 9, 2477.	2.2	23
7616	CircRNA-associated ceRNA network reveals ErbB and Hippo signaling pathways in hypopharyngeal cancer. <i>International Journal of Molecular Medicine</i> , 2018, 43, 127-142.	1.8	15
7617	Differential expression profiles of long non-coding RNAs during the mouse pronuclear stage under normal gravity and simulated microgravity. <i>Molecular Medicine Reports</i> , 2018, 19, 155-164.	1.1	4
7618	Selective expansion of myeloid and NK cells in humanized mice yields human-like vaccine responses. <i>Nature Communications</i> , 2018, 9, 5031.	5.8	39
7619	Tumour-vasculature development via endothelial-to-mesenchymal transition after radiotherapy controls CD44v6+ cancer cell and macrophage polarization. <i>Nature Communications</i> , 2018, 9, 5108.	5.8	74
7620	RNA Sequencing for Gene Expression Profiles in a Rat Model of Middle Cerebral Artery Occlusion. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	8
7621	Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations: an example for tomato and grapevine. <i>BMC Bioinformatics</i> , 2018, 19, 435.	1.2	9
7622	Alterations of Gut Microbiota in Cholestatic Infants and Their Correlation With Hepatic Function. <i>Frontiers in Microbiology</i> , 2018, 9, 2682.	1.5	42

#	ARTICLE	IF	CITATIONS
7623	The Microbiome of the Cosmopolitan Diatom <i>Leptocylindrus</i> Reveals Significant Spatial and Temporal Variability. <i>Frontiers in Microbiology</i> , 2018, 9, 2758.	1.5	35
7624	Identification of key candidate genes and miRNA-mRNA target pairs in chronic lymphocytic leukemia by integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 362-374.	1.1	16
7625	Potential four-miRNA signature associated with T <sub>1/2</sub> stage and prognosis of patients with pancreatic ductal adenocarcinoma identified by co-expression analysis. <i>Molecular Medicine Reports</i> , 2018, 19, 441-451.	1.1	3
7626	Comparative Proteomic Analysis. , 2018, , .		2
7627	ARP3 Controls the Podocyte Architecture at the Kidney Filtration Barrier. <i>Developmental Cell</i> , 2018, 47, 741-757.e8.	3.1	33
7628	Genome-wide characterization and phylogenetic analysis of GSK gene family in three species of cotton: evidence for a role of some GSKs in fiber development and responses to stress. <i>BMC Plant Biology</i> , 2018, 18, 330.	1.6	34
7629	BioGraph: a web application and a graph database for querying and analyzing bioinformatics resources. <i>BMC Systems Biology</i> , 2018, 12, 98.	3.0	28
7630	The Impact of Changes in Environmental Conditions on Organic Acid Production by Commercial Wine Yeast Strains. <i>South African Journal of Enology and Viticulture</i> , 2018, 39, .	0.8	3
7631	Transcription Factor Co-expression Networks of Adipose RNA-Seq Data Reveal Regulatory Mechanisms of Obesity. <i>Current Genomics</i> , 2018, 19, 289-299.	0.7	9
7632	Microarray analysis of the molecular mechanisms associated with age and body mass index in human meniscal injury. <i>Molecular Medicine Reports</i> , 2018, 19, 93-102.	1.1	4
7633	The Chinese herbal formula <em>Fuzheng</em> <em>Quxie</em> Decoction attenuates cognitive impairment and protects cerebrovascular function in SAMP8 mice. <i>Neuropsychiatric Disease and Treatment</i> , 2018, Volume 14, 3037-3051.	1.0	8
7634	Elevated FAM3C promotes cell epithelial&ndash;mesenchymal transition and cell migration in gastric cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 8491-8505.	1.0	18
7635	Lipidomic Response to Coffee Consumption. <i>Nutrients</i> , 2018, 10, 1851.	1.7	32
7636	A Combination of Proteomic Approaches Identifies A Panel of Circulating Extracellular Vesicle Proteins Related to the Risk of Suffering Cardiovascular Disease in Obese Patients. <i>Proteomics</i> , 2019, 19, e1800248.	1.3	16
7637	Comparative Transcriptome Profiling of mRNA and lncRNA Related to Tail Adipose Tissues of Sheep. <i>Frontiers in Genetics</i> , 2018, 9, 365.	1.1	43
7638	An Improved Method for Prediction of Cancer Prognosis by Network Learning. <i>Genes</i> , 2018, 9, 478.	1.0	33
7639	Enantioselectivity in degradation and ecological risk of the chiral pesticide ethiprole. <i>Land Degradation and Development</i> , 2018, 29, 4242-4251.	1.8	25
7640	Systems biology primer: the basic methods and approaches. <i>Essays in Biochemistry</i> , 2018, 62, 487-500.	2.1	128



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7641	SetCoLa: High-Level Constraints for Graph Layout. <i>Computer Graphics Forum</i> , 2018, 37, 537-548.	1.8	11
7642	Exploration of the Biosynthetic Potential of the <i>Populus</i> Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	34
7643	The Paralogous Genes PDR18 and SNQ2, Encoding Multidrug Resistance ABC Transporters, Derive From a Recent Duplication Event, PDR18 Being Specific to the <i>Saccharomyces</i> Genus. <i>Frontiers in Genetics</i> , 2018, 9, 476.	1.1	14
7644	Long-Term Biogas Production from Glycolate by Diverse and Highly Dynamic Communities. <i>Microorganisms</i> , 2018, 6, 103.	1.6	12
7645	Early Responses to Severe Drought Stress in the <i>Arabidopsis thaliana</i> Cell Suspension Culture Proteome. <i>Proteomes</i> , 2018, 6, 38.	1.7	24
7646	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. <i>Methods in Microbiology</i> , 2018, , 243-290.	0.4	3
7647	Comparing microbial community compositions of biogas and sewage treatment plants by analyzing 16S rRNA gene data. <i>Data in Brief</i> , 2018, 21, 395-402.	0.5	1
7648	Association between PPP2CA expression and colorectal cancer prognosis tumor marker prognostic study. <i>International Journal of Surgery</i> , 2018, 59, 80-89.	1.1	15
7649	MicroRNA-transcription factor network analysis reveals miRNAs cooperatively suppress RORA in oral squamous cell carcinoma. <i>Oncogenesis</i> , 2018, 7, 79.	2.1	29
7650	Early neurogenomic response associated with variation in guppy female mate preference. <i>Nature Ecology and Evolution</i> , 2018, 2, 1772-1781.	3.4	30
7651	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. <i>Nature Ecology and Evolution</i> , 2018, 2, 1700-1708.	3.4	40
7652	Plant Phenotypic Traits Eventually Shape Its Microbiota: A Common Garden Test. <i>Frontiers in Microbiology</i> , 2018, 9, 2479.	1.5	68
7653	Peroxisome Proliferator Activated Receptor Agonists Modulate Transposable Element Expression in Brain and Liver. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 331.	1.4	8
7654	Chimeric Antigen Receptor-T Cells with 4-1BB Co-Stimulatory Domain Present a Superior Treatment Outcome than Those with CD28 Domain Based on Bioinformatics. <i>Acta Haematologica</i> , 2018, 140, 131-140.	0.7	8
7655	Fangjifuling Ameliorates Lipopolysaccharide-Induced Renal Injury via Inhibition of Inflammatory and Apoptotic Response in Mice. <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 2124-2137.	1.1	20
7656	Microbiome Interaction Networks and Community Structure From Laboratory-Reared and Field-Collected <i>Aedes aegypti</i> , <i>Aedes albopictus</i> , and <i>Culex quinquefasciatus</i> Mosquito Vectors. <i>Frontiers in Microbiology</i> , 2018, 9, 2160.	1.5	119
7657	Inhibitory Effect of Methotrexate on Rheumatoid Arthritis Inflammation and Comprehensive Metabolomics Analysis Using Ultra-Performance Liquid Chromatography-Quadrupole Time of Flight-Mass Spectrometry (UPLC-Q/TOF-MS). <i>International Journal of Molecular Sciences</i> , 2018, 19, 2894.	1.8	33
7658	A prognostic mRNA expression signature of four 16q24.3 genes in radio(chemo)therapy-treated head and neck squamous cell carcinoma (HNSCC). <i>Molecular Oncology</i> , 2018, 12, 2085-2101.	2.1	21



#	ARTICLE	IF	CITATIONS
7659	Regulatory mechanisms of incomplete huntingtin mRNA splicing. <i>Nature Communications</i> , 2018, 9, 3955.	5.8	55
7660	Analysis of NRAS RNA G-quadruplex binding proteins reveals DDX3X as a novel interactor of cellular G-quadruplex containing transcripts. <i>Nucleic Acids Research</i> , 2018, 46, 11592-11604.	6.5	106
7661	Control of seminal fluid protein expression via regulatory hubs in <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181681.	1.2	15
7662	Integrated analysis of long noncoding RNA associated competing endogenous RNA as prognostic biomarkers in clear cell renal carcinoma. <i>Cancer Science</i> , 2018, 109, 3336-3349.	1.7	33
7663	Analysis of <i>Drosophila melanogaster</i> testis transcriptome. <i>BMC Genomics</i> , 2018, 19, 697.	1.2	53
7664	Pathway networks generated from human disease phenome. <i>BMC Medical Genomics</i> , 2018, 11, 75.	0.7	10
7665	Maintaining Genome Integrity during Seed Development in <i>Phaseolus vulgaris</i> L.: Evidence from a Transcriptomic Profiling Study. <i>Genes</i> , 2018, 9, 463.	1.0	16
7666	Single-Run Mass Spectrometry Analysis Provides Deep Insight into <i>E. coli</i> Proteome. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2394-2401.	1.2	3
7667	Distribution of Extracellular Flavins in a Coastal Marine Basin and Their Relationship to Redox Gradients and Microbial Community Members. <i>Environmental Science &amp; Technology</i> , 2018, 52, 12265-12274.	4.6	34
7668	Deubiquitinase Usp12 functions noncatalytically to induce autophagy and confer neuroprotection in models of Huntington's disease. <i>Nature Communications</i> , 2018, 9, 3191.	5.8	47
7669	MicroRNAs and histone deacetylase inhibition-mediated protection against inflammatory $\beta$ 2-cell damage. <i>PLoS ONE</i> , 2018, 13, e0203713.	1.1	17
7670	Metabolite-Centric Reporter Pathway and Tripartite Network Analysis of <i>Arabidopsis</i> Under Cold Stress. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 121.	2.0	15
7671	A Comprehensive In Silico Method to Study the QSTR of the Aconitine Alkaloids for Designing Novel Drugs. <i>Molecules</i> , 2018, 23, 2385.	1.7	14
7672	Genome-wide identification of the interactions between key genes and pathways provide new insights into the toxicity of bisphenol F and S during early development in zebrafish. <i>Chemosphere</i> , 2018, 213, 559-567.	4.2	27
7673	Identification of 26 novel loci that confer susceptibility to early-onset coronary artery disease in a Japanese population. <i>Biomedical Reports</i> , 2018, 9, 383-404.	0.9	17
7674	Identification of key genes and associated pathways in KIT/PDGFR $\alpha$ wild-type gastrointestinal stromal tumors through bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 4499-4515.	1.1	5
7675	When the Tree Let Us See the Forest: Systems Biology and Natural Variation Studies in Forest Species. <i>Progress in Botany Fortschritte Der Botanik</i> , 2018, , 353-375.	0.1	2
7676	Genome-wide association studies for tick resistance in <i>Bos taurus</i> $\times$ <i>Bos indicus</i> crossbred cattle: A deeper look into this intricate mechanism. <i>Journal of Dairy Science</i> , 2018, 101, 11020-11032.	1.4	24

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7677	Multomics Data Integration in Time Series Experiments. <i>Comprehensive Analytical Chemistry</i> , 2018, 82, 505-532.	0.7	19
7678	Changes in salivary analytes in canine parvovirus: A high-resolution quantitative proteomic study. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2018, 60, 1-10.	0.7	18
7679	PTMD: A Database of Human Disease-associated Post-translational Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 244-251.	3.0	129
7680	Immune Cell Gene Signatures for Profiling the Microenvironment of Solid Tumors. <i>Cancer Immunology Research</i> , 2018, 6, 1388-1400.	1.6	169
7681	Phosphoproteomic screening identifies physiological substrates of the <scp>CDKL</scp> 5 kinase. <i>EMBO Journal</i> , 2018, 37, .	3.5	56
7682	Identifying novel candidate biomarkers of RCC based on WGCNA analysis. <i>Personalized Medicine</i> , 2018, 15, 381-394.	0.8	12
7683	Transcriptomics and co-expression networks reveal tissue-specific responses and regulatory hubs under mild and severe drought in papaya ( <i>Carica papaya</i> L.). <i>Scientific Reports</i> , 2018, 8, 14539.	1.6	39
7684	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. <i>Molecular Ecology</i> , 2018, 27, 4744-4757.	2.0	30
7685	Sex Differences in Cancer Driver Genes and Biomarkers. <i>Cancer Research</i> , 2018, 78, 5527-5537.	0.4	108
7686	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. <i>Cancer Research</i> , 2018, 78, 5538-5547.	0.4	81
7687	Alterations in gut bacterial and fungal microbiomes are associated with bacterial Keratitis, an inflammatory disease of the human eye. <i>Journal of Biosciences</i> , 2018, 43, 835-856.	0.5	47
7688	Gene Pathways Analysis of the Effects of Suspension Culture on Primary Human Renal Proximal Tubular Cells. <i>Microgravity Science and Technology</i> , 2018, 30, 951-963.	0.7	3
7689	Longitudinal analysis of biomarker data from a personalized nutrition platform in healthy subjects. <i>Scientific Reports</i> , 2018, 8, 14685.	1.6	18
7690	Identification of genes and signaling pathways associated with arthrogyposis&#x2013;renal dysfunction&#x2013;cholestasis syndrome using weighted correlation network analysis. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2238-2246.	1.8	5
7691	Extracellular Vesicles: Potential Participants in Circadian Rhythm Synchronization. <i>International Journal of Biological Sciences</i> , 2018, 14, 1610-1620.	2.6	32
7692	The effect of Hsa_circ_0001451 in clear cell renal cell carcinoma cells and its relationship with clinicopathological features. <i>Journal of Cancer</i> , 2018, 9, 3269-3277.	1.2	36
7693	Disruption of thrombo-inflammatory response and activation of a distinct cytokine cluster after subarachnoid hemorrhage. <i>Cytokine</i> , 2018, 111, 334-341.	1.4	13
7694	Blue Team Communication and Reporting for Enhancing Situational Awareness from White Team Perspective in Cyber Security Exercises. <i>Lecture Notes in Computer Science</i> , 2018, , 277-288.	1.0	5

#	ARTICLE	IF	CITATIONS
7695	Transcriptomic view of survival during early seedling growth of the extremophyte <i>Haloxylon ammodendron</i> . <i>Plant Physiology and Biochemistry</i> , 2018, 132, 475-489.	2.8	21
7696	Substrate Profile of the Phosphotriesterase Homology Protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 6219-6227.	1.2	5
7697	Transcriptomic response to parasite infection in Nile tilapia ( <i>Oreochromis niloticus</i> ) depends on rearing density. <i>BMC Genomics</i> , 2018, 19, 723.	1.2	44
7698	Cholesterol is Inefficiently Converted to Cholesteryl Esters in the Blood of Cardiovascular Disease Patients. <i>Scientific Reports</i> , 2018, 8, 14764.	1.6	44
7699	Screening and identification of potential novel biomarker for diagnosis of complicated <i>Plasmodium vivax</i> malaria. <i>Journal of Translational Medicine</i> , 2018, 16, 272.	1.8	23
7700	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	9.4	97
7701	Association of Pioglitazone with Increased Risk of Prostate Cancer and Pancreatic Cancer: A Functional Network Study. <i>Diabetes Therapy</i> , 2018, 9, 2229-2243.	1.2	7
7702	TED-Seq Identifies the Dynamics of Poly(A) Length during ER Stress. <i>Cell Reports</i> , 2018, 24, 3630-3641.e7.	2.9	54
7703	Highly cited papers in Microbiology: identification and conceptual analysis. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
7704	Key elements involved in Epstein-Barr virus-associated gastric cancer and their network regulation. <i>Cancer Cell International</i> , 2018, 18, 146.	1.8	30
7705	Plastid genome analysis of three Nemaliophycidae red algal species suggests environmental adaptation for iron limited habitats. <i>PLoS ONE</i> , 2018, 13, e0196995.	1.1	9
7706	Identification of novel drug targets in bovine respiratory disease: an essential step in applying biotechnologic techniques to develop more effective therapeutic treatments. <i>Drug Design, Development and Therapy</i> , 2018, Volume 12, 1135-1146.	2.0	2
7707	Expression Profile of <i>Glossina pallidipes</i> MicroRNAs During Symptomatic and Asymptomatic Infection With <i>Glossina pallidipes</i> Salivary Gland Hypertrophy Virus (Hytrosavirus). <i>Frontiers in Microbiology</i> , 2018, 9, 2037.	1.5	7
7708	Keystone Species in Pregnancy Gingivitis: A Snapshot of Oral Microbiome During Pregnancy and Postpartum Period. <i>Frontiers in Microbiology</i> , 2018, 9, 2360.	1.5	59
7709	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519.	1.5	100
7710	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. <i>Cell Reports</i> , 2018, 24, 3607-3618.	2.9	30
7711	Efficient methods and readily customizable libraries for managing complexity of large networks. <i>PLoS ONE</i> , 2018, 13, e0197238.	1.1	8
7712	Analyzing Metabolic Pathways in Microbiomes. <i>Methods in Molecular Biology</i> , 2018, 1849, 291-307.	0.4	0

#	ARTICLE	IF	CITATIONS
7713	Inhibitory mechanism of 5-bromo-3-indoleacetic acid for non-structural-3 helicase hepatitis C virus with dynamics correlation network analysis. <i>Computational Biology and Chemistry</i> , 2018, 77, 167-177.	1.1	2
7714	A rust fungal effector binds plant DNA and modulates transcription. <i>Scientific Reports</i> , 2018, 8, 14718.	1.6	42
7715	The Duality of the MAPK Signaling Pathway in the Control of Metabolic Processes and Cellulase Production in <i>Trichoderma reesei</i> . <i>Scientific Reports</i> , 2018, 8, 14931.	1.6	31
7716	Tomato Seeds Preferably Transmit Plant Beneficial Endophytes. <i>Phytobiomes Journal</i> , 2018, 2, 183-193.	1.4	124
7717	Discovering Causal Relationships in Grapevine Expression Data to Expand Gene Networks. A Case Study: Four Networks Related to Climate Change. <i>Frontiers in Plant Science</i> , 2018, 9, 1385.	1.7	17
7718	Metabotyping of 30 maize hybrids under early-sowing conditions reveals potential marker-metabolites for breeding. <i>Metabolomics</i> , 2018, 14, 132.	1.4	15
7719	Feedbacks from the metabolic network to the genetic network reveal regulatory modules in <i>E. coli</i> and <i>B. subtilis</i> . <i>PLoS ONE</i> , 2018, 13, e0203311.	1.1	8
7720	Prognostic Implications of Heterogeneity in Intra-tumoral Immune Composition for Recurrence in Early Stage Lung Cancer. <i>Frontiers in Immunology</i> , 2018, 9, 2298.	2.2	38
7721	Gene module analysis of juvenile myelomonocytic leukemia and screening of anticancer drugs. <i>Oncology Reports</i> , 2018, 40, 3155-3170.	1.2	1
7722	Gene expression differences between thyroid carcinoma, thyroid adenoma and normal thyroid tissue. <i>Oncology Reports</i> , 2018, 40, 3359-3369.	1.2	24
7723	miRNA-21 and miRNA-223 expression signature as a predictor for lymph node metastasis, distant metastasis and survival in kidney renal clear cell carcinoma. <i>Journal of Cancer</i> , 2018, 9, 3651-3659.	1.2	45
7724	Genome-wide expression profiling of glioblastoma using a large combined cohort. <i>Scientific Reports</i> , 2018, 8, 15104.	1.6	28
7725	Opportunities in Functional Genomics: A Primer on Lab and Computational Aspects. <i>Journal of Shellfish Research</i> , 2018, 37, 747-754.	0.3	1
7726	Loop Motion in Triosephosphate Isomerase Is Not a Simple Open and Shut Case. <i>Journal of the American Chemical Society</i> , 2018, 140, 15889-15903.	6.6	63
7727	Effects of antibiotic on microflora in ileum and cecum for broilers by 16S rRNA sequence analysis. <i>Animal Science Journal</i> , 2018, 89, 1680-1691.	0.6	16
7728	<scp>FMRP</scp> recruitment of $\beta$ -catenin to the translation pre-initiation complex represses translation. <i>EMBO Reports</i> , 2018, 19, .	2.0	15
7729	Root Microbiota in Primary and Secondary Apical Periodontitis. <i>Frontiers in Microbiology</i> , 2018, 9, 2374.	1.5	79
7730	Transcriptomic and functional network features of lung squamous cell carcinoma through integrative analysis of GEO and TCGA data. <i>Scientific Reports</i> , 2018, 8, 15834.	1.6	91

#	ARTICLE	IF	CITATIONS
7731	Candidate Biomarkers and Molecular Mechanism Investigation for Glioblastoma Multiforme Utilizing WGCNA. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	72
7732	wTO: an R package for computing weighted topological overlap and a consensus network with integrated visualization tool. <i>BMC Bioinformatics</i> , 2018, 19, 392.	1.2	44
7733	Application of Proteomics Technologies in Oil Palm Research. <i>Protein Journal</i> , 2018, 37, 473-499.	0.7	7
7734	Single-Stranded Nucleic Acids Regulate TLR3/4/7 Activation through Interference with Clathrin-Mediated Endocytosis. <i>Scientific Reports</i> , 2018, 8, 15841.	1.6	12
7735	Structural and kinetic characterization of (S)-1-amino-2-propanol kinase from the aminoacetone utilization microcompartment of <i>Mycobacterium smegmatis</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 19909-19918.	1.6	14
7736	Elevated Autoantibodies in Subacute Human Spinal Cord Injury Are Naturally Occurring Antibodies. <i>Frontiers in Immunology</i> , 2018, 9, 2365.	2.2	33
7737	mully: An R Package to Create, Modify and Visualize Multilayered Graphs. <i>Genes</i> , 2018, 9, 519.	1.0	11
7738	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. <i>Genome Medicine</i> , 2018, 10, 78.	3.6	107
7739	Transcriptome Profile Analysis Reveals an Estrogen Induced lncRNA Associated with Lipid Metabolism and Carcass Traits in Chickens ( <i>Gallus Gallus</i> ). <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 1638-1658.	1.1	15
7740	Identification of glioblastoma gene prognosis modules based on weighted gene co-expression network analysis. <i>BMC Medical Genomics</i> , 2018, 11, 96.	0.7	57
7741	Possible Molecular Markers for the Diagnosis of Pancreatic Ductal Adenocarcinoma. <i>Medical Science Monitor</i> , 2018, 24, 2368-2376.	0.5	14
7742	Profiling Cellular Processes in Adipose Tissue during Weight Loss Using Time Series Gene Expression. <i>Genes</i> , 2018, 9, 525.	1.0	4
7743	Disease-relevant transcriptional signatures identified in individual smooth muscle cells from healthy mouse vessels. <i>Nature Communications</i> , 2018, 9, 4567.	5.8	219
7744	<i>Bacillus megaterium</i> adapts to acid stress condition through a network of genes: Insight from a genome-wide transcriptome analysis. <i>Scientific Reports</i> , 2018, 8, 16105.	1.6	30
7745	Murine Oviductosomes (OVS) microRNA profiling during the estrous cycle: Delivery of OVS-borne microRNAs to sperm where miR-34c-5p localizes at the centrosome. <i>Scientific Reports</i> , 2018, 8, 16094.	1.6	35
7746	Exploration of the diagnostic value and molecular mechanism of miR-1 in prostate cancer: A study based on meta-analyses and bioinformatics. <i>Molecular Medicine Reports</i> , 2018, 18, 5630-5646.	1.1	12
7747	De novo transcriptome assembly of the bamboo snout beetle <i>Cyrtotrachelus buqueti</i> reveals ability to degrade lignocellulose of bamboo feedstock. <i>Biotechnology for Biofuels</i> , 2018, 11, 292.	6.2	28
7748	Pathways and Network Based Analysis of Candidate Genes to Reveal Cross-Talk and Specificity in the Sorghum ( <i>Sorghum bicolor</i> (L.) Moench) Responses to Drought and It's Co-occurring Stresses. <i>Frontiers in Genetics</i> , 2018, 9, 557.	1.1	22

#	ARTICLE	IF	CITATIONS
7749	Identification of Five Genes as a Potential Biomarker for Predicting Progress and Prognosis in Adrenocortical Carcinoma. <i>Journal of Cancer</i> , 2018, 9, 4484-4495.	1.2	39
7750	Gene-level associations in suicide attempter families show overrepresentation of synaptic genes and genes differentially expressed in brain development. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 774-784.	1.1	19
7751	Sequencing of <i>Euscaphis konishii</i> Endocarp Transcriptome Points to Molecular Mechanisms of Endocarp Coloration. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3209.	1.8	5
7752	Modular bioinformatics analysis demonstrates that a Toll-like receptor signaling pathway is involved in the regulation of macrophage polarization. <i>Molecular Medicine Reports</i> , 2018, 18, 4313-4320.	1.1	15
7753	Drug Target Prioritization for Alzheimer's Disease Using Protein Interaction Network Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 665-677.	1.0	7
7754	Serum Metabolomics Analysis of Asthma in Different Inflammatory Phenotypes: A Cross-Sectional Study in Northeast China. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	29
7755	Network Analysis of RAD51 Proteins in Metazoa and the Evolutionary Relationships With Their Archaeal Homologs. <i>Frontiers in Genetics</i> , 2018, 9, 383.	1.1	3
7756	Genetic expression profile-based screening of genes and pathways associated with papillary thyroid carcinoma. <i>Oncology Letters</i> , 2018, 16, 5723-5732.	0.8	7
7757	Maternal immune activation alters brain microRNA expression in mouse offspring. <i>Annals of Clinical and Translational Neurology</i> , 2018, 5, 1264-1276.	1.7	14
7758	Transcriptional regulation of nitrogen-associated metabolism and growth. <i>Nature</i> , 2018, 563, 259-264.	13.7	222
7759	CD49b defines functionally mature Treg cells that survey skin and vascular tissues. <i>Journal of Experimental Medicine</i> , 2018, 215, 2796-2814.	4.2	37
7760	Global Transcriptome Analysis During Adipogenic Differentiation and Involvement of Transthyretin Gene in Adipogenesis in Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 463.	1.1	25
7761	Organic Particles: Heterogeneous Hubs for Microbial Interactions in Aquatic Ecosystems. <i>Frontiers in Microbiology</i> , 2018, 9, 2569.	1.5	51
7762	Current Applications of Metabolomics in Cirrhosis. <i>Metabolites</i> , 2018, 8, 67.	1.3	10
7763	Diosgenin protects against alveolar bone loss in ovariectomized rats via regulating long non-coding RNAs. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 3939-3950.	0.8	12
7764	The C-terminal D/E-rich domain of MBD3 is a putative Z-DNA mimic that competes for Z-DNA-binding activity. <i>Nucleic Acids Research</i> , 2018, 46, 11806-11821.	6.5	6
7765	Comparative gene expression profile and DNA methylation status in diabetic patients of Kazak and Han people. <i>Medicine (United States)</i> , 2018, 97, e11982.	0.4	7
7766	Comparative Transcriptomic Analysis of Embryo Implantation in Mice and Rats. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 668-678.	1.1	3



#	ARTICLE	IF	CITATIONS
7767	Global Deletome Profile of <i>Saccharomyces cerevisiae</i> Exposed to the Technology-Critical Element Yttrium. <i>Frontiers in Microbiology</i> , 2018, 9, 2005.	1.5	8
7768	Genome-wide analysis of gene expression after one year of venom immunotherapy. <i>Immunology Letters</i> , 2018, 204, 23-28.	1.1	2
7769	Indoleacetate decarboxylase is a glycy radical enzyme catalysing the formation of malodorous skatole. <i>Nature Communications</i> , 2018, 9, 4224.	5.8	37
7770	Identification of potential prognostic long non-coding RNA signatures based on a competing endogenous RNA network in lung adenocarcinoma. <i>Oncology Reports</i> , 2018, 40, 3199-3212.	1.2	8
7771	Feminist designs: modernist digital humanities & Mina Loy: Navigating the Avant-Garde. <i>Feminist Modernist Studies</i> , 2018, 1, 243-256.	0.1	2
7772	Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2018, 19, 745.	1.2	38
7773	Identification of Candidate Biomarkers Correlated With the Pathogenesis and Prognosis of Non-small Cell Lung Cancer via Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2018, 9, 469.	1.1	99
7774	The Inclusion of Water Molecules in Residue Interaction Networks Identifies Additional Central Residues. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 88.	1.6	9
7775	Candidate genes in gastric cancer identified by constructing a weighted gene co-expression network. <i>PeerJ</i> , 2018, 6, e4692.	0.9	54
7776	Exogenous brassinosteroids altered cell length, gibberellin content, and cellulose deposition in promoting carrot petiole elongation. <i>Plant Science</i> , 2018, 277, 110-120.	1.7	27
7777	Construction of a long non-coding RNA-associated ceRNA network reveals potential prognostic lncRNA biomarkers in hepatocellular carcinoma. <i>Pathology Research and Practice</i> , 2018, 214, 2031-2038.	1.0	21
7778	Fibrin-targeting immunotherapy protects against neuroinflammation and neurodegeneration. <i>Nature Immunology</i> , 2018, 19, 1212-1223.	7.0	149
7779	Bacteriocyte Reprogramming to Cope With Nutritional Stress in a Phloem Sap Feeding Hemipteran, the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1498.	1.3	15
7780	Integrated analysis of long noncoding RNA interactions reveals the potential role in progression of human papillary thyroid cancer. <i>Cancer Medicine</i> , 2018, 7, 5394-5410.	1.3	22
7781	Chemical nature of soil organic carbon under different long-term fertilization regimes is coupled with changes in the bacterial community composition in a Calcaric Fluvisol. <i>Biology and Fertility of Soils</i> , 2018, 54, 999-1012.	2.3	27
7782	Bacterial Carbon Cycling in the River Plume in the Northern South China Sea During Summer. <i>Journal of Geophysical Research: Oceans</i> , 2018, 123, 8106-8121.	1.0	15
7783	Identification of genes and analysis of prognostic values in nonsmoking females with non-small cell lung carcinoma by bioinformatics analyses. <i>Cancer Management and Research</i> , 2018, Volume 10, 4287-4295.	0.9	20
7784	Transcriptome and Proteome of Fish-Pathogenic <i>Streptococcus agalactiae</i> Are Modulated by Temperature. <i>Frontiers in Microbiology</i> , 2018, 9, 2639.	1.5	21



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7785	Sterol uptake and sterol biosynthesis act coordinately to mediate antifungal resistance in <i>Candida glabrata</i> under azole and hypoxic stress. <i>Molecular Medicine Reports</i> , 2018, 17, 6585-6597.	1.1	25
7786	RBM17 Interacts with U2SURP and CHERP to Regulate Expression and Splicing of RNA-Processing Proteins. <i>Cell Reports</i> , 2018, 25, 726-736.e7.	2.9	57
7787	Transcriptomic basis for reinforcement of elm antiherbivore defence mediated by insect egg deposition. <i>Molecular Ecology</i> , 2018, 27, 4901-4915.	2.0	18
7788	Proteomic and metabolomic analysis of the cellular biomarkers related to inhibitors tolerance in <i>Zymomonas mobilis</i> ZM4. <i>Biotechnology for Biofuels</i> , 2018, 11, 283.	6.2	14
7789	Cdh1 and Pik3ca Mutations Cooperate to Induce Immune-Related Invasive Lobular Carcinoma of the Breast. <i>Cell Reports</i> , 2018, 25, 702-714.e6.	2.9	47
7790	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 4276.	5.8	46
7791	Evaluation of Serum Apolipoprotein E as a Potential Biomarker for Pharmacological Therapeutic Efficacy Monitoring in Dopamine Dictated Disease Spectrum of Schizophrenia and Parkinson's disease: A Preliminary Study. <i>Journal of Central Nervous System Disease</i> , 2018, 10, 117957351880358.	0.7	6
7792	Leaves of Indoor Ornamentals Are Biodiversity and Functional Hotspots for Fungi. <i>Frontiers in Microbiology</i> , 2018, 9, 2343.	1.5	9
7793	Circular RNA expression profile of spleen in a <i>Clostridium perfringens</i> type C-induced piglet model of necrotizing enteritis. <i>FEBS Open Bio</i> , 2018, 8, 1722-1732.	1.0	26
7794	Transcriptome-wide association study identifies multiple genes and pathways associated with pancreatic cancer. <i>Cancer Medicine</i> , 2018, 7, 5727-5732.	1.3	26
7795	Glutathione Transferases. , 2018, , 326-362.		2
7796	Bacterial community structure in the Bohai Strait provides insights into organic matter niche partitioning. <i>Continental Shelf Research</i> , 2018, 169, 46-54.	0.9	13
7797	Comparative transcriptome analyses of the third and fourth stage larvae of <i>Anisakis simplex</i> (Nematoda: Anisakidae). <i>Molecular and Biochemical Parasitology</i> , 2018, 226, 24-33.	0.5	15
7798	Exploring Pharmacological Mechanisms of Xuefu Zhuyu Decoction in the Treatment of Traumatic Brain Injury via a Network Pharmacology Approach. Evidence-based Complementary and Alternative Medicine, 2018, 2018, 1-20.	0.5	24
7799	Cardiomyocyte gene programs encoding morphological and functional signatures in cardiac hypertrophy and failure. <i>Nature Communications</i> , 2018, 9, 4435.	5.8	201
7800	Computational discovery of dynamic cell line specific Boolean networks from multiplex time-course data. <i>PLoS Computational Biology</i> , 2018, 14, e1006538.	1.5	25
7801	Soil Bacteria Isolated From Tunisian Arid Areas Show Promising Antimicrobial Activities Against Gram-Negatives. <i>Frontiers in Microbiology</i> , 2018, 9, 2742.	1.5	12
7802	Network pharmacology-based strategy to investigate pharmacological mechanisms of Zuojinwan for treatment of gastritis. <i>BMC Complementary and Alternative Medicine</i> , 2018, 18, 292.	3.7	101

#	ARTICLE	IF	CITATIONS
7803	The SRC-family tyrosine kinase HCK shapes the landscape of SKAP2 interactome. <i>Oncotarget</i> , 2018, 9, 13102-13115.	0.8	11
7804	The 7q11.23 Protein DNAJC30 Interacts with ATP Synthase and Links Mitochondria to Brain Development. <i>Cell</i> , 2018, 175, 1088-1104.e23.	13.5	46
7805	N-methyladenine DNA Modification in Glioblastoma. <i>Cell</i> , 2018, 175, 1228-1243.e20.	13.5	236
7806	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. <i>Cell</i> , 2018, 175, 973-983.e14.	13.5	707
7807	US Immigration Westernizes the Human Gut Microbiome. <i>Cell</i> , 2018, 175, 962-972.e10.	13.5	511
7808	Evidence of polygenic adaptation to high altitude from Tibetan and Sherpa genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 2919-2930.	1.1	39
7809	Integrative analysis of gut microbiota composition, host colonic gene expression and intraluminal metabolites in aging C57BL/6J mice. <i>Aging</i> , 2018, 10, 930-950.	1.4	46
7810	An impaired hepatic clock system effects lipid metabolism in rats with nephropathy. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2720-2736.	1.8	6
7811	Identification of COL1A1 as an invasion-related gene in malignant astrocytoma. <i>International Journal of Oncology</i> , 2018, 53, 2542-2554.	1.4	31
7812	Identification of Kinases and Interactors of p53 Using Kinase-Catalyzed Cross-Linking and Immunoprecipitation. <i>Journal of the American Chemical Society</i> , 2018, 140, 16299-16310.	6.6	12
7813	HSP90-incorporating chaperome networks as biosensor for disease-related pathways in patient-specific midbrain dopamine neurons. <i>Nature Communications</i> , 2018, 9, 4345.	5.8	40
7814	Bioinformatics identification of crucial genes and pathways associated with hepatocellular carcinoma. <i>Bioscience Reports</i> , 2018, 38, .	1.1	43
7815	Untargeted lipidomic features associated with colorectal cancer in a prospective cohort. <i>BMC Cancer</i> , 2018, 18, 996.	1.1	21
7816	Spatial Variability and Co-acclimation of Phytoplankton and Bacterioplankton Communities in the Pearl River Estuary, China. <i>Frontiers in Microbiology</i> , 2018, 9, 2503.	1.5	28
7817	Peanut Stunt Virus and Its Satellite RNA Trigger Changes in Phosphorylation in <i>N. benthamiana</i> Infected Plants at the Early Stage of the Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3223.	1.8	7
7818	Genome-Wide Investigation of Genes Regulated by ER $\alpha$ in Breast Cancer Cells. <i>Molecules</i> , 2018, 23, 2543.	1.7	10
7819	A Central Edge Selection Based Overlapping Community Detection Algorithm for the Detection of Overlapping Structures in Protein-Protein Interaction Networks. <i>Molecules</i> , 2018, 23, 2633.	1.7	13
7820	Large De Novo Microdeletion in Epilepsy with Intellectual and Developmental Disabilities, with a Systems Biology Analysis. <i>Advances in Neurobiology</i> , 2018, 21, 247-266.	1.3	13

#	ARTICLE	IF	CITATIONS
7821	Integrated dataset on acute phase protein response in chicken challenged with Escherichia coli lipopolysaccharide endotoxin. Data in Brief, 2018, 21, 684-699.	0.5	11
7822	Revealing the cellular degradome by mass spectrometry analysis of proteasome-cleaved peptides. Nature Biotechnology, 2018, 36, 1110-1116.	9.4	33
7823	Increased transferrin saturation is associated with subgingival microbiota dysbiosis and severe periodontitis in genetic haemochromatosis. Scientific Reports, 2018, 8, 15532.	1.6	19
7824	Module-detection approaches for the integration of multilevel omics data highlight the comprehensive response of Aspergillus fumigatus to caspofungin. BMC Systems Biology, 2018, 12, 88.	3.0	11
7825	Comparative analysis of circular RNAs between soybean cytoplasmic male-sterile line NJCMS1A and its maintainer NJCMS1B by high-throughput sequencing. BMC Genomics, 2018, 19, 663.	1.2	35
7826	DermaGene and VitmiRS: a comprehensive systems analysis of genetic dermatological disorders. Biomedical Dermatology, 2018, 2, .	7.6	1
7827	Defining the genetic components of callus formation: A GWAS approach. PLoS ONE, 2018, 13, e0202519.	1.1	27
7828	Phosphorus and Nitrogen Drive the Seasonal Dynamics of Bacterial Communities in Pinus Forest Rhizospheric Soil of the Qinling Mountains. Frontiers in Microbiology, 2018, 9, 1930.	1.5	25
7829	Integration of miRNA and mRNA Co-Expression Reveals Potential Regulatory Roles of miRNAs in Developmental and Immunological Processes in Calf Ileum during Early Growth. Cells, 2018, 7, 134.	1.8	7
7830	Comparative Transcriptomics Identifies Novel Genes and Pathways Involved in Post-Traumatic Osteoarthritis Development and Progression. International Journal of Molecular Sciences, 2018, 19, 2657.	1.8	27
7831	Identification of Genes and Pathways Involved in Ovarian Epithelial Cancer by Bioinformatics Analysis. Journal of Cancer, 2018, 9, 3016-3022.	1.2	13
7832	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. PLoS ONE, 2018, 13, e0199649.	1.1	13
7833	Structure and Reaction Mechanism of the LigI Hydratase: An Enzyme Critical for the Bacterial Degradation of Lignin in the Protocatechuate 4,5-Cleavage Pathway. Biochemistry, 2018, 57, 5841-5850.	1.2	11
7834	High-Reynolds Microfluidic Sorting of Large Yeast Populations. Scientific Reports, 2018, 8, 13739.	1.6	8
7835	DiNAR: revealing hidden patterns of plant signalling dynamics using Differential Network Analysis in R. Plant Methods, 2018, 14, 78.	1.9	5
7836	Identification of key candidate genes and small molecule drugs in cervical cancer by bioinformatics strategy. Cancer Management and Research, 2018, Volume 10, 3533-3549.	0.9	18
7837	Genome-Wide Identification and Characterization of Aquaporins and Their Role in the Flower Opening Processes in Carnation (Dianthus caryophyllus). Molecules, 2018, 23, 1895.	1.7	42
7838	Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. Theranostics, 2018, 8, 4520-4534.	4.6	40

#	ARTICLE	IF	CITATIONS
7840	Young age at diagnosis is associated with worse prognosis in the Luminal A breast cancer subtype: a retrospective institutional cohort study. <i>Breast Cancer Research and Treatment</i> , 2018, 172, 689-702.	1.1	32
7841	rec-YnH enables simultaneous many-by-many detection of direct protein-protein and protein-RNA interactions. <i>Nature Communications</i> , 2018, 9, 3747.	5.8	26
7842	The genome of <i>Naegleria lovaniensis</i> , the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba <i>N. fowleri</i> . <i>BMC Genomics</i> , 2018, 19, 654.	1.2	23
7843	Regional Differences and Similarities in the Brain Transcriptome for Mice Selected for Ethanol Preference From HS-CC Founders. <i>Frontiers in Genetics</i> , 2018, 9, 300.	1.1	16
7844	Dme-Hsa Disease Database (DHDD): Conserved Human Disease-Related miRNA and Their Targeting Genes in <i>Drosophila melanogaster</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2642.	1.8	6
7845	Analyzing the disease module associated with osteosarcoma via a network and pathway-based approach. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 2584-2592.	0.8	7
7846	Molecular mechanism of activated T cells in breast cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 5015-5024.	1.0	11
7847	EBV Associated Breast Cancer Whole Methylome Analysis Reveals Viral and Developmental Enriched Pathways. <i>Frontiers in Oncology</i> , 2018, 8, 316.	1.3	12
7848	Novel prognostic biomarkers of gastric cancer based on gene expression microarray: COL12A1, GSTA3, FGA and FGG. <i>Molecular Medicine Reports</i> , 2018, 18, 3727-3736.	1.1	48
7849	Identification of novel genes involved in gingival epithelial cells responding to <i>Aggregatibacter actinomycetemcomitans</i> and <i>Porphyromonas gingivalis</i> infections. <i>Archives of Oral Biology</i> , 2018, 96, 113-121.	0.8	4
7850	Identification and Quantification of Murine Mitochondrial Proteoforms Using an Integrated Top-Down and Intact-Mass Strategy. <i>Journal of Proteome Research</i> , 2018, 17, 3526-3536.	1.8	23
7851	Minipuberty and Sexual Dimorphism in the Infant Human Thymus. <i>Scientific Reports</i> , 2018, 8, 13169.	1.6	17
7852	Discovering lncRNA mediated sponge interactions in breast cancer molecular subtypes. <i>BMC Genomics</i> , 2018, 19, 650.	1.2	41
7853	Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs. <i>Cell</i> , 2018, 175, 239-253.e17.	13.5	97
7854	Structure and Dynamics of tRNA <sup>Met</sup> Containing Core Substitutions. <i>ACS Omega</i> , 2018, 3, 10668-10678.	1.6	6
7855	Seasonal succession of small planktonic eukaryotes inhabiting surface waters of a coastal upwelling system. <i>Environmental Microbiology</i> , 2018, 20, 2955-2973.	1.8	44
7856	Proteomic Analysis Reveals That an Extract of the Plant <i>Lippia organoides</i> Suppresses Mitochondrial Metabolism in Triple-Negative Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2018, 17, 3370-3383.	1.8	20
7857	PCYCARD Gene Plays a Key Role in Rapidly Progressive Glomerulonephritis: Results of a Weighted Gene Co-Expression Network Analysis. <i>American Journal of Nephrology</i> , 2018, 48, 193-204.	1.4	6

#	ARTICLE	IF	CITATIONS
7858	In silico Study of Iron, Zinc and Copper Binding Proteins of <i>Pseudomonas syringae</i> pv. <i>lapsa</i> : Emphasis on Secreted Metalloproteins. <i>Frontiers in Microbiology</i> , 2018, 9, 1838.	1.5	28
7859	In silico Prioritization of Transporter-Drug Relationships From Drug Sensitivity Screens. <i>Frontiers in Pharmacology</i> , 2018, 9, 1011.	1.6	23
7860	Omega-3 PUFA attenuate mice myocardial infarction injury by emerging a protective eicosanoid pattern. <i>Prostaglandins and Other Lipid Mediators</i> , 2018, 139, 1-9.	1.0	7
7861	Diversity of Active Viral Infections within the Sphagnum Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	27
7862	Stable Histone Methylation Changes at Proteoglycan Network Genes Following Ethanol Exposure. <i>Frontiers in Genetics</i> , 2018, 9, 346.	1.1	14
7863	Dietary Bile Salt Types Influence the Composition of Biliary Bile Acids and Gut Microbiota in Grass Carp. <i>Frontiers in Microbiology</i> , 2018, 9, 2209.	1.5	31
7864	The clinical importance of a cytokine network in the acute phase of sepsis. <i>Scientific Reports</i> , 2018, 8, 13995.	1.6	114
7865	A Quantitative Chemical Proteomic Strategy for Profiling Phosphoprotein Phosphatases from Yeast to Humans. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2448-2461.	2.5	29
7866	Prioritized High-Confidence Risk Genes for Intellectual Disability Reveal Molecular Convergence During Brain Development. <i>Frontiers in Genetics</i> , 2018, 9, 349.	1.1	12
7867	Aquatic Bacterial Communities Associated With Land Use and Environmental Factors in Agricultural Landscapes Using a Metabarcoding Approach. <i>Frontiers in Microbiology</i> , 2018, 9, 2301.	1.5	44
7868	The PIN-FORMED Auxin Efflux Carriers in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2759.	1.8	113
7869	Identification of 13 novel susceptibility loci for early-onset myocardial infarction, hypertension, or chronic kidney disease. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2415-2436.	1.8	33
7870	Update of the Functional Mitochondrial Human Proteome Network. <i>Journal of Proteome Research</i> , 2018, 17, 4297-4306.	1.8	13
7871	Knock-down of AHCY and depletion of adenosine induces DNA damage and cell cycle arrest. <i>Scientific Reports</i> , 2018, 8, 14012.	1.6	36
7872	Information Feedback in Temporal Networks as a Predictor of Market Crashes. <i>Complexity</i> , 2018, 2018, 1-13.	0.9	18
7873	Transcriptome evolution from breast epithelial cells to basal-like tumors. <i>Oncotarget</i> , 2018, 9, 453-463.	0.8	11
7874	Proteoglycan Chemical Diversity Drives Multifunctional Cell Regulation and Therapeutics. <i>Chemical Reviews</i> , 2018, 118, 9152-9232.	23.0	253
7875	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018, 8, 13314.	1.6	54

#	ARTICLE	IF	CITATIONS
7876	DNA damage-induced dynamic changes in abundance and cytosol-nuclear translocation of proteins involved in translational processes, metabolism, and autophagy. <i>Cell Cycle</i> , 2018, 17, 2146-2163.	1.3	9
7877	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: Boiga). <i>Journal of Molecular Evolution</i> , 2018, 86, 531-545.	0.8	14
7878	Neuronal heterogeneity and stereotyped connectivity in the auditory afferent system. <i>Nature Communications</i> , 2018, 9, 3691.	5.8	195
7879	Effects of exogenous microbial inoculum on the structure and dynamics of bacterial communities in swine carcass composting. <i>Canadian Journal of Microbiology</i> , 2018, 64, 1042-1053.	0.8	9
7880	A Time-Series Analysis of Severe Burned Injury of Skin Gene Expression Profiles. <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 1492-1498.	1.1	6
7881	COL1A1: A potential therapeutic target for colorectal cancer expressing wild-type or mutant KRAS. <i>International Journal of Oncology</i> , 2018, 53, 1869-1880.	1.4	24
7882	Knowledge networks for innovation in the forestry sector: Multinational companies in Uruguay. <i>Forest Policy and Economics</i> , 2018, 97, 9-20.	1.5	8
7883	Application of Environmental DNA Metabarcoding for Predicting Anthropogenic Pollution in Rivers. <i>Environmental Science &amp; Technology</i> , 2018, 52, 11708-11719.	4.6	44
7884	Identification of differentially methylated region (DMR) networks associated with progression of nonalcoholic fatty liver disease. <i>Scientific Reports</i> , 2018, 8, 13567.	1.6	33
7885	Doxorubicin induces an extensive transcriptional and metabolic rewiring in yeast cells. <i>Scientific Reports</i> , 2018, 8, 13672.	1.6	104
7886	Transcriptomic analyses of cacao cell suspensions in light and dark provide target genes for controlled flavonoid production. <i>Scientific Reports</i> , 2018, 8, 13575.	1.6	14
7887	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus Host Protein Network. <i>Cancer Discovery</i> , 2018, 8, 1474-1489.	7.7	67
7888	Biclustering of transcriptome sequencing data reveals human tissue-specific circular RNAs. <i>BMC Genomics</i> , 2018, 19, 958.	1.2	9
7889	In ovo exposure to triclosan alters the hepatic proteome in chicken embryos. <i>Ecotoxicology and Environmental Safety</i> , 2018, 165, 495-504.	2.9	14
7890	Identification and differential expression of microRNAs in the testis of chicken with high and low sperm motility. <i>Theriogenology</i> , 2018, 122, 94-101.	0.9	21
7891	The collaborative effect of scientific meetings: A study of the International Milk Genomics Consortium. <i>PLoS ONE</i> , 2018, 13, e0201637.	1.1	7
7892	T cell microvilli constitute immunological synaptosomes that carry messages to antigen-presenting cells. <i>Nature Communications</i> , 2018, 9, 3630.	5.8	81
7893	Comparative transcriptome analysis to identify putative genes involved in thymol biosynthesis pathway in medicinal plant <i>Trachyspermum ammi</i> L.. <i>Scientific Reports</i> , 2018, 8, 13405.	1.6	24



#	ARTICLE	IF	CITATIONS
7894	Long-chain acyl-CoA synthetase 1 interacts with key proteins that activate and direct fatty acids into niche hepatic pathways. <i>Journal of Biological Chemistry</i> , 2018, 293, 16724-16740.	1.6	67
7895	Adaptive Steered Molecular Dynamics Combined With Protein Structure Networks Revealing the Mechanism of Y68I/G109P Mutations That Enhance the Catalytic Activity of D-psicose 3-Epimerase From <i>Clostridium Bolteae</i> . <i>Frontiers in Chemistry</i> , 2018, 6, 437.	1.8	18
7896	Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling. <i>Cancer Cell</i> , 2018, 34, 379-395.e7.	7.7	104
7897	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018, 34, 396-410.e8.	7.7	146
7898	Distinct gene signatures predict insulin resistance in young mice with high fat diet-induced obesity. <i>Physiological Genomics</i> , 2018, 50, 144-157.	1.0	7
7899	Small RNAs from cereal powdery mildew pathogens may target host plant genes. <i>Fungal Biology</i> , 2018, 122, 1050-1063.	1.1	41
7900	Quantitative RNA-seq Analysis Unveils Osmotic and Thermal Adaptation Mechanisms Relevant for Ectoine Production in <i>Chromohalobacter salexigens</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1845.	1.5	21
7901	Exploring the Mechanism of Flavonoids Through Systematic Bioinformatics Analysis. <i>Frontiers in Pharmacology</i> , 2018, 9, 918.	1.6	36
7902	FDHE-IW: A Fast Approach for Detecting High-Order Epistasis in Genome-Wide Case-Control Studies. <i>Genes</i> , 2018, 9, 435.	1.0	26
7903	All-Round Manipulation of the Actin Cytoskeleton by HIV. <i>Viruses</i> , 2018, 10, 63.	1.5	46
7904	Deciphering the Human Virome with Single-Virus Genomics and Metagenomics. <i>Viruses</i> , 2018, 10, 113.	1.5	31
7905	Transcriptome sequencing identifies key pathways and genes involved in gastric adenocarcinoma. <i>Molecular Medicine Reports</i> , 2018, 18, 3673-3682.	1.1	13
7906	Developing DNA methylation-based prognostic biomarkers of acute myeloid leukemia. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 10041-10050.	1.2	4
7907	Identification of hub genes and analysis of prognostic values in pancreatic ductal adenocarcinoma by integrated bioinformatics methods. <i>Molecular Biology Reports</i> , 2018, 45, 1799-1807.	1.0	22
7908	Identification of novel variants associated with osteoporosis, type 2 diabetes and potentially pleiotropic loci using pleiotropic cFDR method. <i>Bone</i> , 2018, 117, 6-14.	1.4	19
7909	Label-free quantitative proteome data associated with MSP1 and flg22 induced signaling in rice leaves. <i>Data in Brief</i> , 2018, 20, 204-209.	0.5	10
7910	Protective effects of 2,3,5,4-tetrahydroxystilbene-2-O- $\beta$ -D-glucoside against osteoporosis: Current knowledge and proposed mechanisms. <i>International Journal of Rheumatic Diseases</i> , 2018, 21, 1504-1513.	0.9	4
7911	Insights into archaeal chaperone machinery: a network-based approach. <i>Cell Stress and Chaperones</i> , 2018, 23, 1257-1274.	1.2	1



#	ARTICLE	IF	CITATIONS
7912	The <i>Xenopus</i> animal cap transcriptome: building a mucociliary epithelium. <i>Nucleic Acids Research</i> , 2018, 46, 8772-8787.	6.5	14
7913	RepTB: a gene ontology based drug repurposing approach for tuberculosis. <i>Journal of Cheminformatics</i> , 2018, 10, 24.	2.8	27
7914	Proteome-wide analysis of phospho-regulated <scp>PDZ</scp> domain interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8129.	3.2	48
7915	Upregulated <em>VEGFA</em> and <em>DLL4</em> act as potential prognostic genes for clear cell renal cell carcinoma. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 1697-1706.	1.0	16
7916	Integrated profiling of long non-coding RNAs and mRNAs identifies novel regulators associated with liver fibrosis. <i>Pathology Research and Practice</i> , 2018, 214, 1794-1803.	1.0	7
7917	Modulation of the transcriptomic profile of the R2C tumor Leydig cell line by the adipose tissue derived hormone leptin. <i>Reproductive Biology</i> , 2018, 18, 440-449.	0.9	2
7918	Antibiotic resistance genes and associated bacterial communities in agricultural soils amended with different sources of animal manures. <i>Soil Biology and Biochemistry</i> , 2018, 126, 91-102.	4.2	170
7919	Integrated analysis of a competing endogenous RNA network reveals key lncRNAs as potential prognostic biomarkers for human bladder cancer. <i>Medicine (United States)</i> , 2018, 97, e11887.	0.4	39
7920	Impact of non-LTR retrotransposons in the differentiation and evolution of anatomically modern humans. <i>Mobile DNA</i> , 2018, 9, 28.	1.3	18
7921	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. <i>PLoS Computational Biology</i> , 2018, 14, e1006372.	1.5	8
7922	A network-based signature to predict the survival of non-smoking lung adenocarcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 2683-2693.	0.9	9
7923	Potential role of LINC00996 in colorectal cancer: a study based on data mining and bioinformatics. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 4845-4855.	1.0	37
7924	Microarray data analysis to identify differentially expressed genes and biological pathways associated with asthma. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1613-1620.	0.8	2
7925	Establishment of a SVM classifier to predict recurrence of ovarian cancer. <i>Molecular Medicine Reports</i> , 2018, 18, 3589-3598.	1.1	17
7926	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. <i>Cell Reports</i> , 2018, 24, 2493-2505.e4.	2.9	123
7927	High-resolution repertoire analysis reveals a major bystander activation of Tfh and Tfr cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9604-9609.	3.3	62
7928	Comparative transcriptome of neurons after oxygen-glucose deprivation: Potential differences in neuroprotection versus reperfusion. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2018, 38, 2236-2250.	2.4	13
7929	Understanding the World Economy in Terms of Networks: A Survey of Data-Based Network Science Approaches on Economic Networks. <i>Frontiers in Applied Mathematics and Statistics</i> , 2018, 4, .	0.7	7

#	ARTICLE	IF	CITATIONS
7930	Oral Microbiome Shifts From Caries-Free to Caries-Affected Status in 3-Year-Old Chinese Children: A Longitudinal Study. <i>Frontiers in Microbiology</i> , 2018, 9, 2009.	1.5	42
7931	Co-Expression Network Analysis Identifies miRNA-mRNA Networks Potentially Regulating Milk Traits and Blood Metabolites. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2500.	1.8	14
7932	Analysis and Visualization of Dynamic Networks Using the DyNet App for Cytoscape. <i>Current Protocols in Bioinformatics</i> , 2018, 63, e55.	25.8	5
7933	miR-124-3p is a chronic regulator of gene expression after brain injury. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 4557-4581.	2.4	40
7934	Epigenetic and Transcriptomic Profiling of Mammary Gland Development and Tumor Models Disclose Regulators of Cell State Plasticity. <i>Cancer Cell</i> , 2018, 34, 466-482.e6.	7.7	111
7935	iTRAQ-based secretome reveals that SiO <sub>2</sub> induces the polarization of RAW264.7 macrophages by activation of the NOD-RIP2-NF- $\kappa$ B signaling pathway. <i>Environmental Toxicology and Pharmacology</i> , 2018, 63, 92-102.	2.0	14
7936	The NF- $\kappa$ B subunit RELA is a master transcriptional regulator of the committed epithelial-mesenchymal transition in airway epithelial cells. <i>Journal of Biological Chemistry</i> , 2018, 293, 16528-16545.	1.6	44
7937	Transcriptional survey of alveolar macrophages in a murine model of chronic granulomatous inflammation reveals common themes with human sarcoidosis. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 314, L617-L625.	1.3	14
7938	Integrating MicroRNA Expression Profiling Studies to Systematically Evaluate the Diagnostic Value of MicroRNAs in Pancreatic Cancer and Validate Their Prognostic Significance with the Cancer Genome Atlas Data. <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 678-695.	1.1	28
7939	Stratification of candidate genes for Parkinson's disease using weighted protein-protein interaction network analysis. <i>BMC Genomics</i> , 2018, 19, 452.	1.2	35
7940	A network pharmacology approach to explore the mechanisms of Erxian decoction in polycystic ovary syndrome. <i>Chinese Medicine</i> , 2018, 13, 46.	1.6	25
7941	Bio-production of gaseous alkenes: ethylene, isoprene, isobutene. <i>Biotechnology for Biofuels</i> , 2018, 11, 234.	6.2	14
7942	CRL4 <sup>AMBRA1</sup> targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. <i>EMBO Journal</i> , 2018, 37, .	3.5	13
7943	GWAS with Heterogeneous Data: Estimating the Fraction of Phenotypic Variation Mediated by Gene Expression Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3059-3068.	0.8	28
7944	Supervised Machine Learning with Protein Structural and Network Topological Features Predicts Physical Interactors of the Human Huntingtons Disease Protein. , 2018, , .		1
7945	An Evaluation of the Information Technology of Gene Expression Profiles Processing Stability for Different Levels of Noise Components. <i>Data</i> , 2018, 3, 48.	1.2	19
7946	Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. <i>Computers in Biology and Medicine</i> , 2018, 99, 76-84.	3.9	8
7947	Comparative Transcriptome Profiling Analysis of Red- and White-Fleshed Strawberry ( <i>Fragaria ananassa</i> ) Provides New Insight into the Regulation of the Anthocyanin Pathway. <i>Plant and Cell Physiology</i> , 2018, 59, 1844-1859.	1.5	48

#	ARTICLE	IF	CITATIONS
7948	Quantitative Proteomics Study Reveals Changes in the Molecular Landscape of Human Embryonic Stem Cells with Impaired Stem Cell Differentiation upon Exposure to Titanium Dioxide Nanoparticles. <i>Small</i> , 2018, 14, e1800190.	5.2	20
7949	Starvation stress affects the interplay among shrimp gut microbiota, digestion and immune activities. <i>Fish and Shellfish Immunology</i> , 2018, 80, 191-199.	1.6	61
7950	High-serum MMP-8 levels are associated with decreased survival and systemic inflammation in colorectal cancer. <i>British Journal of Cancer</i> , 2018, 119, 213-219.	2.9	45
7951	Mapping <sc>DNA</sc> damage-dependent genetic interactions in yeast via party mating and barcode fusion genetics. <i>Molecular Systems Biology</i> , 2018, 14, e7985.	3.2	25
7952	Integrated bioinformatics analysis reveals that the expression of cathepsin B is associated with lymph node metastasis and poor prognosis in papillary thyroid cancer. <i>Oncology Reports</i> , 2018, 40, 111-122.	1.2	29
7953	A combined tissue-engineered/ in silico signature tool patient stratification in lung cancer. <i>Molecular Oncology</i> , 2018, 12, 1264-1285.	2.1	8
7954	Comparative analysis of long non-coding RNAs in Atlantic and Coho salmon reveals divergent transcriptome responses associated with immunity and tissue repair during sea lice infestation. <i>Developmental and Comparative Immunology</i> , 2018, 87, 36-50.	1.0	40
7955	The basic principles of topology-dynamics relations in networks: An empirical approach. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 508, 584-594.	1.2	7
7956	TISSUES 2.0: an integrative web resource on mammalian tissue expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	137
7957	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	3.5	122
7958	eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. <i>Nucleic Acids Research</i> , 2018, 46, W171-W179.	6.5	127
7959	PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data. <i>Nucleic Acids Research</i> , 2018, 46, W503-W509.	6.5	143
7960	Analysis of gene expression profiles of multiple skin diseases identifies a conserved signature of disrupted homeostasis. <i>Experimental Dermatology</i> , 2018, 27, 1000-1008.	1.4	12
7961	Identification and ultra-high-performance liquid chromatography coupled with high-resolution mass spectrometry characterization of biosurfactants, including a new surfactin, isolated from oil-contaminated environments. <i>Microbial Biotechnology</i> , 2018, 11, 759-769.	2.0	36
7962	Global assessment of its network dynamics reveals that the kinase Plk1 inhibits the phosphatase PP6 to promote Aurora A activity. <i>Science Signaling</i> , 2018, 11, .	1.6	25
7963	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
7964	Visualization of Biomedical Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 275-304.	2.8	63
7965	Integrating multi-source information on a single network to detect disease-related clusters of molecular mechanisms. <i>Journal of Proteomics</i> , 2018, 188, 15-29.	1.2	37

#	ARTICLE	IF	CITATIONS
7966	Active and total microbial community dynamics and the role of functional genes bamA and mcrA during anaerobic digestion of phenol and p-cresol. <i>Bioresource Technology</i> , 2018, 264, 290-297.	4.8	31
7967	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> , 2018, 173, 1796-1809.e17.	13.5	165
7968	p300-Mediated Lysine 2-Hydroxyisobutyrylation Regulates Glycolysis. <i>Molecular Cell</i> , 2018, 70, 663-678.e6.	4.5	126
7969	SNAP23-Kif5 complex controls mGlu1 receptor trafficking. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 423-436.	1.5	20
7970	Distinct epigenetic landscapes underlie the pathobiology of pancreatic cancer subtypes. <i>Nature Communications</i> , 2018, 9, 1978.	5.8	177
7971	A Five-microRNA Signature for Survival Prognosis in Pancreatic Adenocarcinoma based on TCGA Data. <i>Scientific Reports</i> , 2018, 8, 7638.	1.6	51
7972	The Ancient Phosphatidylinositol 3-Kinase Signaling System Is a Master Regulator of Energy and Carbon Metabolism in Algae. <i>Plant Physiology</i> , 2018, 177, 1050-1065.	2.3	16
7973	Anti-tumor efficacy of a novel CLK inhibitor via targeting RNA splicing and MYC-dependent vulnerability. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	65
7974	BioModelKit: Spatial Modelling of Complex Multiscale Molecular Biosystems Based on Modular Models. <i>Fundamenta Informaticae</i> , 2018, 160, 221-254.	0.3	1
7975	Leveraging Experimental Details for an Improved Understanding of Host-Pathogen Interactome. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.26.1-8.26.12.	25.8	2
7976	EuPathDB: The Eukaryotic Pathogen Genomics Database Resource. <i>Methods in Molecular Biology</i> , 2018, 1757, 69-113.	0.4	80
7977	Long-term application of lime or pig manure rather than plant residues suppressed diazotroph abundance and diversity and altered community structure in an acidic Ultisol. <i>Soil Biology and Biochemistry</i> , 2018, 123, 218-228.	4.2	107
7978	miCLIP-MaPseq, a Substrate Identification Approach for Radical SAM RNA Methylating Enzymes. <i>Journal of the American Chemical Society</i> , 2018, 140, 7135-7143.	6.6	11
7979	Gene expression microarray analysis reveals prognostic markers of survival in high grade astrocytomas. <i>Neurological Research</i> , 2018, 40, 744-751.	0.6	1
7980	Pigmentation Is Associated with Stemness Hierarchy of Progenitor Cells Within Cultured Limbal Epithelial Cells. <i>Stem Cells</i> , 2018, 36, 1411-1420.	1.4	17
7981	Bromate and Nitrate Bioreduction Coupled with Poly- $\beta$ -hydroxybutyrate Production in a Methane-Based Membrane Biofilm Reactor. <i>Environmental Science &amp; Technology</i> , 2018, 52, 7024-7031.	4.6	54
7982	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W537-W544.	6.5	3,003
7983	Soy protein isolate feeding does not result in reproductive toxicity in the pre-pubertal rat testis. <i>Experimental Biology and Medicine</i> , 2018, 243, 695-707.	1.1	4

#	ARTICLE	IF	CITATIONS
7984	LRRK2 is a negative regulator of <i>Mycobacterium tuberculosis</i> phagosome maturation in macrophages. <i>EMBO Journal</i> , 2018, 37, .	3.5	140
7985	Integrated analysis of the gene expression profile and DNA methylation profile of obese patients with type 2 diabetes. <i>Molecular Medicine Reports</i> , 2018, 17, 7636-7644.	1.1	17
7986	Prioritization of reproductive toxicants in unconventional oil and gas operations using a multi-country regulatory data-driven hazard assessment. <i>Environment International</i> , 2018, 117, 348-358.	4.8	9
7987	Systems-level analysis of risk genes reveals the modular nature of schizophrenia. <i>Schizophrenia Research</i> , 2018, 201, 261-269.	1.1	20
7988	iPTMnet: an integrated resource for protein post-translational modification network discovery. <i>Nucleic Acids Research</i> , 2018, 46, D542-D550.	6.5	120
7989	The Defense Phytohormone Signaling Network Enables Rapid, High-Amplitude Transcriptional Reprogramming during Effector-Triggered Immunity. <i>Plant Cell</i> , 2018, 30, 1199-1219.	3.1	169
7990	Provenance Analytics for Workflow-Based Computational Experiments. <i>ACM Computing Surveys</i> , 2019, 51, 1-25.	16.1	18
7991	Tau Mutations Serve as a Novel Risk Factor for Cancer. <i>Cancer Research</i> , 2018, 78, 3731-3739.	0.4	30
7992	A Primer for the Rat Genome Database (RGD). <i>Methods in Molecular Biology</i> , 2018, 1757, 163-209.	0.4	11
7993	Aerobic Glycolysis Controls Myeloid-Derived Suppressor Cells and Tumor Immunity via a Specific CEBPB Isoform in Triple-Negative Breast Cancer. <i>Cell Metabolism</i> , 2018, 28, 87-103.e6.	7.2	263
7994	Molecular characterization of physis tissue by RNA sequencing. <i>Gene</i> , 2018, 668, 87-96.	1.0	18
7995	Network-Based Disease Module Discovery by a Novel Seed Connector Algorithm with Pathobiological Implications. <i>Journal of Molecular Biology</i> , 2018, 430, 2939-2950.	2.0	41
7996	Guiding biomedical clustering with ClustEval. <i>Nature Protocols</i> , 2018, 13, 1429-1444.	5.5	3
7997	Species-specific transcriptomic network inference of interspecies interactions. <i>ISME Journal</i> , 2018, 12, 2011-2023.	4.4	22
7998	Intron retention and nuclear loss of SFPQ are molecular hallmarks of ALS. <i>Nature Communications</i> , 2018, 9, 2010.	5.8	116
7999	Screening of prognostic risk microRNAs for acute myeloid leukemia. <i>Hematology</i> , 2018, 23, 747-755.	0.7	8
8000	Activation of the Arterial Program Drives Development of Definitive Hemogenic Endothelium with Lymphoid Potential. <i>Cell Reports</i> , 2018, 23, 2467-2481.	2.9	51
8001	Effects on the hepatic transcriptome of chicken embryos in ovo exposed to phenobarbital. <i>Ecotoxicology and Environmental Safety</i> , 2018, 160, 94-103.	2.9	6

#	ARTICLE	IF	CITATIONS
8002	A functional glycoproteomics approach identifies CD13 as a novel E-selectin ligand in breast cancer. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2069-2080.	1.1	23
8003	Quantitative SUMO proteomics reveals the modulation of several PML nuclear body associated proteins and an anti-senescence function of UBC9. <i>Scientific Reports</i> , 2018, 8, 7754.	1.6	26
8004	Integrated proteomics, genomics, metabolomics approaches reveal oxalic acid as pathogenicity factor in <i>Tilletia indica</i> inciting Karnal bunt disease of wheat. <i>Scientific Reports</i> , 2018, 8, 7826.	1.6	21
8005	Adipose tissue proteomic analyses to study puberty in Brahman heifers. <i>Journal of Animal Science</i> , 2018, 96, 2392-2398.	0.2	21
8006	Network Visualization and Analysis of Spatially Aware Gene Expression Data with InsituNet. <i>Cell Systems</i> , 2018, 6, 626-630.e3.	2.9	13
8007	Factor XIIIa-expressing inflammatory monocytes promote lung squamous cancer through fibrin cross-linking. <i>Nature Communications</i> , 2018, 9, 1988.	5.8	69
8008	Pluripotent stem cells: induction and self-renewal. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170213.	1.8	28
8009	An Open-Source Desktop Application for Generating Arc-Routing Benchmark Instances. <i>INFORMS Journal on Computing</i> , 2018, 30, 361-370.	1.0	7
8010	Network analysis of a proposed exit pathway for protons to the P-side of cytochrome c oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 997-1005.	0.5	35
8011	Functional role of a long non-coding RNA LIFR-AS1/miR-29a/TNFAIP3 axis in colorectal cancer resistance to photodynamic therapy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2871-2880.	1.8	56
8012	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. <i>Cell Reports</i> , 2018, 23, 2819-2831.e5.	2.9	36
8013	Anaerobic production of medium-chain fatty alcohols via a $\hat{1}^2$ -reduction pathway. <i>Metabolic Engineering</i> , 2018, 48, 63-71.	3.6	53
8014	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	1.6	11
8015	Gene-gene interaction network analysis of hepatocellular carcinoma using bioinformatic software. <i>Oncology Letters</i> , 2018, 15, 8371-8377.	0.8	5
8016	Bioinformatics and functional analyses of key genes and pathways in human clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2018, 15, 9133-9141.	0.8	11
8017	Redefining the Protein Kinase Conformational Space with Machine Learning. <i>Cell Chemical Biology</i> , 2018, 25, 916-924.e2.	2.5	65
8018	Convergent Pathways in Idiopathic Autism Revealed by Time Course Transcriptomic Analysis of Patient-Derived Neurons. <i>Scientific Reports</i> , 2018, 8, 8423.	1.6	67
8019	BRCA1 Mutation Status and Follicular Fluid Exposure Alters NF $\kappa$ B Signaling and ISGylation in Human Fallopian Tube Epithelial Cells. <i>Neoplasia</i> , 2018, 20, 697-709.	2.3	8



#	ARTICLE	IF	CITATIONS
8020	Tomato proteomics: Tomato as a model for crop proteomics. <i>Scientia Horticulturae</i> , 2018, 239, 224-233.	1.7	25
8021	In silico experiment system for testing hypothesis on gene functions using three condition specific biological networks. <i>Methods</i> , 2018, 145, 10-15.	1.9	1
8022	Identification of key genes in rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Medicine (United States)</i> , 2018, 97, e10997.	0.4	27
8023	Bmp2 and Notch cooperate to pattern the embryonic endocardium. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	30
8024	Genetic dissection of the signaling pathway required for the cell wall integrity checkpoint. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	6
8025	Potential mechanism and drug candidates for sepsis-induced acute lung injury. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4689-4696.	0.8	6
8026	Identification of key candidate genes and pathways in hepatocellular carcinoma by integrated bioinformatical analysis. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4932-4942.	0.8	15
8027	Microarray analysis for the identification of specific proteins and functional modules involved in the process of hepatocellular carcinoma originating from cirrhotic liver. <i>Molecular Medicine Reports</i> , 2018, 17, 5619-5626.	1.1	8
8028	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , 2018, 1794, 97-117.	0.4	6
8029	GRAM. , 2018, , .		6
8030	Quantitative proteomics and biochemical analyses reveal the role of endoplasmic reticulum in the regulation of the expression and secretion of A Disintegrin And Metalloproteinase 12. <i>Journal of Proteomics</i> , 2018, 182, 34-44.	1.2	4
8031	An intersection network based on combining SNP coassociation and RNA coexpression networks for feed utilization traits in Japanese Black cattle. <i>Journal of Animal Science</i> , 2018, 96, 2553-2566.	0.2	11
8032	Structure and Kinetics of the S-(+)-1-Amino-2-propanol Dehydrogenase from the RMM Microcompartment of <i>Mycobacterium smegmatis</i> . <i>Biochemistry</i> , 2018, 57, 3780-3789.	1.2	16
8033	The novel 19q13 KRAB zinc-finger tumour suppressor ZNF382 is frequently methylated in oesophageal squamous cell carcinoma and antagonises Wnt/ $\beta$ -catenin signalling. <i>Cell Death and Disease</i> , 2018, 9, 573.	2.7	26
8034	FACS-Seq analysis of Pax3-derived cells identifies non-myogenic lineages in the embryonic forelimb. <i>Scientific Reports</i> , 2018, 8, 7670.	1.6	10
8035	A study of transcriptome in leaf rust infected bread wheat involving seedling resistance gene Lr28. <i>Functional Plant Biology</i> , 2018, 45, 1046.	1.1	25
8036	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. <i>Bioinformatics</i> , 2018, 34, 3764-3765.	1.8	0
8037	The Extra-Pathway Interactome of the TCA Cycle: Expected and Unexpected Metabolic Interactions. <i>Plant Physiology</i> , 2018, 177, 966-979.	2.3	81



#	ARTICLE	IF	CITATIONS
8038	Identification of key pathways and genes in the progression of cervical cancer using bioinformatics analysis. <i>Oncology Letters</i> , 2018, 16, 1003-1009.	0.8	20
8039	Proteome response of dental pulp cells to exogenous FGF8. <i>Journal of Proteomics</i> , 2018, 183, 14-24.	1.2	11
8040	The role of p38 MAPK pathway in p53 compromised state and telomere mediated DNA damage response. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2018, 836, 89-97.	0.9	28
8041	Systems Pharmacology-Based Approach of Connecting Disease Genes in Genome-Wide Association Studies with Traditional Chinese Medicine. <i>International Journal of Genomics</i> , 2018, 2018, 1-11.	0.8	7
8042	Deep RNA Sequencing Reveals a Repertoire of Human Fibroblast Circular RNAs Associated with Cellular Responses to Herpes Simplex Virus 1 Infection. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 2031-2045.	1.1	44
8043	miR-876-3p regulates glucose homeostasis and insulin sensitivity by targeting adiponectin. <i>Journal of Endocrinology</i> , 2018, 239, 1-17.	1.2	15
8044	Poly(ADP-ribosyl)ation associated changes in CTCF-chromatin binding and gene expression in breast cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 718-730.	0.9	17
8045	Gold-containing compound BDG-I inhibits the growth of A549 lung cancer cells through the deregulation of miRNA expression. <i>Saudi Pharmaceutical Journal</i> , 2018, 26, 1035-1043.	1.2	6
8046	Consequences of blunting the mevalonate pathway in cancer identified by a pluri-omics approach. <i>Cell Death and Disease</i> , 2018, 9, 745.	2.7	12
8047	Assessment of the key regulatory genes and their Interologs for Turner Syndrome employing network approach. <i>Scientific Reports</i> , 2018, 8, 10091.	1.6	26
8048	Identification of a noncoding RNA-mediated gene pair-based regulatory module in Alzheimer's disease. <i>Molecular Medicine Reports</i> , 2018, 18, 2164-2170.	1.1	1
8049	Formal Modeling of the Key Determinants of Hepatitis C Virus (HCV) Induced Adaptive Immune Response Network: An Integrative Approach to Map the Cellular and Cytokine-Mediated Host Immune Regulations. <i>Lecture Notes in Computer Science</i> , 2018, , 635-649.	1.0	1
8050	Identification of Hub Genes and Key Pathways Associated with Two Subtypes of Diffuse Large B-Cell Lymphoma Based on Gene Expression Profiling via Integrated Bioinformatics. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	31
8051	Weighted gene co-expression network analysis in identification of key genes and networks for ischemic reperfusion remodeling myocardium. <i>Molecular Medicine Reports</i> , 2018, 18, 1955-1962.	1.1	9
8052	Transcriptome profiling analysis reveals biomarkers in colon cancer samples of various differentiation. <i>Oncology Letters</i> , 2018, 16, 48-54.	0.8	7
8053	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018, 7, .	2.8	30
8054	Targeting miRNA for Therapeutics Using a Micronome Based Method for Identification of miRNA-mRNA Pairs and Validation of Key Regulator miRNA. <i>Methods in Molecular Biology</i> , 2018, 1823, 185-195.	0.4	3
8055	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 631-640.	3.6	341

#	ARTICLE	IF	CITATIONS
8056	Microarray Analysis of the Molecular Mechanism Involved in Parkinson's Disease. <i>Parkinson's Disease</i> , 2018, 2018, 1-12.	0.6	22
8057	Systems Pharmacology Dissection of Traditional Chinese Medicine Wen-Dan Decoction for Treatment of Cardiovascular Diseases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-14.	0.5	9
8058	Cytogenomic Integrative Network Analysis of the Critical Region Associated with Wolf-Hirschhorn Syndrome. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	6
8059	A Network Pharmacology Approach to Uncover the Multiple Mechanisms of <i>Hedyotis diffusa</i> Willd. on Colorectal Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-12.	0.5	38
8060	Effect of Freeze-Thaw on a Midtemperate Soil Bacterial Community and the Correlation Network of Its Members. <i>BioMed Research International</i> , 2018, 2018, 1-13.	0.9	12
8061	Meta-Analysis of miRNAs and Their Involvement as Biomarkers in Oral Cancers. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	13
8062	Profiling and Bioinformatic Analyses Indicate Differential circRNA and miRNA/isomiR Expression and Interactions. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	7
8063	Identification of genes and signaling pathways associated with the pathogenesis of juvenile spondyloarthritis. <i>Molecular Medicine Reports</i> , 2018, 18, 1263-1270.	1.1	8
8064	Identification of Key Genes and miRNAs in Osteosarcoma Patients with Chemoresistance by Bioinformatics Analysis. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	24
8065	Identification of key genes in cleft lip with or without cleft palate regulated by miR-199a-5p. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2018, 111, 128-137.	0.4	14
8066	Expression network of transcription factors in resistant and susceptible tung trees responding to Fusarium wilt disease. <i>Industrial Crops and Products</i> , 2018, 122, 716-725.	2.5	8
8067	Distinct biogeographic patterns of rhizobia and non-rhizobial endophytes associated with soybean nodules across China. <i>Science of the Total Environment</i> , 2018, 643, 569-578.	3.9	39
8068	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6526-E6535.	3.3	115
8069	Graph Summarization Methods and Applications. <i>ACM Computing Surveys</i> , 2019, 51, 1-34.	16.1	172
8070	Hsa_circ_0001859 Regulates ATF2 Expression by Functioning as an MiR-204/211 Sponge in Human Rheumatoid Arthritis. <i>Journal of Immunology Research</i> , 2018, 2018, 1-8.	0.9	43
8071	Genomewide phenotypic analysis of growth, cell morphogenesis, and cell cycle events in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2018, 14, e7573.	3.2	69
8072	Bio-modeling Using Petri Nets: A Computational Approach. <i>Computational Biology</i> , 2018, , 3-26.	0.1	4
8073	Analytic Methods in Microbiome Studies. , 2018, , 29-42.		0

#	ARTICLE	IF	CITATIONS
8074	Integrated transcriptomics and metabolomics reveal signatures of lipid metabolism dysregulation in HepaRG liver cells exposed to PCB 126. <i>Archives of Toxicology</i> , 2018, 92, 2533-2547.	1.9	48
8075	Proteomic study of endothelial dysfunction induced by AGEs and its possible role in diabetic cardiovascular complications. <i>Journal of Proteomics</i> , 2018, 187, 69-79.	1.2	37
8076	Toward an Intensive Longitudinal Understanding of Activated Sludge Bacterial Assembly and Dynamics. <i>Environmental Science &amp; Technology</i> , 2018, 52, 8224-8232.	4.6	32
8077	Probing the Protein-Protein Interaction Network of Proteins Causing Maturity Onset Diabetes of the Young. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 110, 167-202.	1.0	15
8078	The Stringent Response Determines the Ability of a Commensal Bacterium to Survive Starvation and to Persist in the Gut. <i>Cell Host and Microbe</i> , 2018, 24, 120-132.e6.	5.1	50
8079	Identification of the extracellular matrix protein Fibulin-2 as a regulator of spinal nerve organization. <i>Developmental Biology</i> , 2018, 442, 101-114.	0.9	21
8080	Transcriptomic and Network Analyses Reveal Mechanistic-Based Biomarkers of Endocrine Disruption in the Marine Mussel, <i>Mytilus edulis</i> . <i>Environmental Science &amp; Technology</i> , 2018, 52, 9419-9430.	4.6	42
8081	Sea cucumber genome provides insights into saponin biosynthesis and aestivation regulation. <i>Cell Discovery</i> , 2018, 4, 29.	3.1	71
8082	Time-resolved transcriptomics in neural stem cells identifies a v-ATPase/Notch regulatory loop. <i>Journal of Cell Biology</i> , 2018, 217, 3285-3300.	2.3	26
8083	Idiopathic Scoliosis Families Highlight Actin-Based and Microtubule-Based Cellular Projections and Extracellular Matrix in Disease Etiology. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2663-2672.	0.8	19
8084	SMILE: a novel procedure for subcellular module identification with localisation expansion. <i>IET Systems Biology</i> , 2018, 12, 55-61.	0.8	21
8085	Network Modeling Unravels Mechanisms of Crosstalk between Ethylene and Salicylate Signaling in Potato. <i>Plant Physiology</i> , 2018, 178, 488-499.	2.3	28
8086	A bi-stable feedback loop between GDNF, EGR1, and ER $\alpha$ contribute to endocrine resistant breast cancer. <i>PLoS ONE</i> , 2018, 13, e0194522.	1.1	5
8087	Systemic bioinformatics analysis of skeletal muscle gene expression profiles of sepsis. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4637-4642.	0.8	1
8088	Novel insights into biomarkers associated with renal cell carcinoma. <i>Oncology Letters</i> , 2018, 16, 83-90.	0.8	16
8089	Computational Modeling of Multidrug-Resistant Bacteria. <i>Computational Biology</i> , 2018, , 195-220.	0.1	4
8090	Progression Rate Associated Peripheral Blood Biomarkers of Parkinson's Disease. <i>Journal of Molecular Neuroscience</i> , 2018, 65, 312-318.	1.1	12
8091	Crystal structure of the flavin reductase of <i>Acinetobacter baumannii</i> p-hydroxyphenylacetate 3-hydroxylase (HPAH) and identification of amino acid residues underlying its regulation by aromatic ligands. <i>Archives of Biochemistry and Biophysics</i> , 2018, 653, 24-38.	1.4	6

#	ARTICLE	IF	CITATIONS
8092	A novel integrated action crossing method for drug-drug interaction prediction in non-communicable diseases. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 163, 183-193.	2.6	11
8093	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. <i>Data in Brief</i> , 2018, 19, 1314-1317.	0.5	6
8094	Gravitational waves and the long relativity revolution. <i>Nature Astronomy</i> , 2018, 2, 534-543.	4.2	15
8095	Hierarchical core decomposition of RING structure as a method to capture novel functional residues within RING-type E3 ligases: a structural systems biology approach. <i>Computers in Biology and Medicine</i> , 2018, 100, 86-91.	3.9	9
8096	Odor mitigation and bacterial community dynamics in on-site biocovers at a sanitary landfill in South Korea. <i>Environmental Research</i> , 2018, 166, 516-528.	3.7	21
8097	Screenplay of flax phloem fiber behavior during gravitropic reaction. <i>Plant Signaling and Behavior</i> , 2018, 13, e1486144.	1.2	2
8098	A network-based zoning for parallel whole-cell simulation. <i>Bioinformatics</i> , 2019, 35, 88-94.	1.8	7
8099	Identification of Key Candidate Proteins and Pathways Associated with Temozolomide Resistance in Glioblastoma Based on Subcellular Proteomics and Bioinformatical Analysis. <i>BioMed Research International</i> , 2018, 2018, 1-12.	0.9	33
8100	Forniceal deep brain stimulation induces gene expression and splicing changes that promote neurogenesis and plasticity. <i>ELife</i> , 2018, 7, .	2.8	39
8101	KCNJ11 gene expression is associated to feed consumption and growth traits in Nelore beef cattle. <i>Agri Gene</i> , 2018, 9, 1-4.	1.9	1
8102	Enhancer-driven transcriptional regulation is a potential key determinant for human visceral and subcutaneous adipocytes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 826-840.	0.9	1
8103	Species-specific activity of antibacterial drug combinations. <i>Nature</i> , 2018, 559, 259-263.	13.7	276
8104	Temporal transcriptomic analysis of metabolic genes in maternal organs and placenta during murine pregnancy. <i>Biology of Reproduction</i> , 2018, 99, 1255-1265.	1.2	9
8105	<i>HEAT INDUCIBLE LIPASE1</i> Remodels Chloroplastic Monogalactosyldiacylglycerol by Liberating $\pm$ -Linolenic Acid in Arabidopsis Leaves under Heat Stress. <i>Plant Cell</i> , 2018, 30, 1887-1905.	3.1	71
8106	Molecular insights into paediatric breast fibroepithelial tumours. <i>Histopathology</i> , 2018, 73, 809-818.	1.6	11
8107	Protein Domain Level Cancer Drug Targets in the Network of MAPK pathways. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 16, 1-1.	1.9	0
8108	Data Mining Mycobacterium tuberculosis Pathogenic Gene Transcription Factors and Their Regulatory Network Nodes. <i>International Journal of Genomics</i> , 2018, 2018, 1-9.	0.8	6
8109	ex-FTCD: A novel mapreduce model for distributed multi source shortest path problem. <i>Journal of Intelligent and Fuzzy Systems</i> , 2018, 34, 1643-1652.	0.8	5

#	ARTICLE	IF	CITATIONS
8110	Association between pathologic factors and ERG expression in prostate cancer: finding pivotal networking. <i>Journal of Cancer Research and Clinical Oncology</i> , 2018, 144, 1665-1683.	1.2	8
8111	Differences in microbial key players in anaerobic degradation between biogas and sewage treatment plants. <i>International Biodeterioration and Biodegradation</i> , 2018, 133, 124-132.	1.9	33
8112	High-throughput analysis of the RNA-induced silencing complex in myotonic dystrophy type 1 patients identifies the dysregulation of miR-29c and its target ASB2. <i>Cell Death and Disease</i> , 2018, 9, 729.	2.7	17
8113	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. <i>Nature Communications</i> , 2018, 9, 2526.	5.8	48
8114	Untargeted metabolic profiling reveals geography as the strongest predictor of metabolic phenotypes of a cosmopolitan weed. <i>Ecology and Evolution</i> , 2018, 8, 6812-6826.	0.8	22
8115	Impaired Angiogenic Supportive Capacity and Altered Gene Expression Profile of Resident CD146+ Mesenchymal Stromal Cells Isolated from Hyperoxia-Injured Neonatal Rat Lungs. <i>Stem Cells and Development</i> , 2018, 27, 1109-1124.	1.1	25
8116	Identification of a novel tRNA wobble uridine modifying activity in the biosynthesis of 5-methoxyuridine. <i>Nucleic Acids Research</i> , 2018, 46, 9160-9169.	6.5	13
8117	Novel 1q22-q23.1 duplication in a patient with lambdoid and metopic craniosynostosis, muscular hypotonia, and psychomotor retardation. <i>Journal of Applied Genetics</i> , 2018, 59, 281-289.	1.0	9
8118	Arabidopsis response to the spider mite <i>Tetranychus urticae</i> depends on the regulation of reactive oxygen species homeostasis. <i>Scientific Reports</i> , 2018, 8, 9432.	1.6	33
8119	Alterations in the gut bacterial microbiome in fungal Keratitis patients. <i>PLoS ONE</i> , 2018, 13, e0199640.	1.1	65
8120	Aberrantly expressed genes and miRNAs in human hypopharyngeal squamous cell carcinoma based on RNA-seq analysis. <i>Oncology Reports</i> , 2018, 40, 647-658.	1.2	5
8121	Network Pharmacology-Based Approach to Investigate the Mechanisms of <i>Hedyotis diffusa</i> Willd. in the Treatment of Gastric Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-17.	0.5	39
8122	Disruption of the Protein Complexes from Weighted Complex Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	2
8123	A Component Formula of Chinese Medicine for Hypercholesterolemia Based on Virtual Screening and Biology Network. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-11.	0.5	8
8124	Metagenomic Analysis of Bacteria, Fungi, Bacteriophages, and Helminths in the Gut of Giant Pandas. <i>Frontiers in Microbiology</i> , 2018, 9, 1717.	1.5	55
8125	2D-DIGE comparative proteomic analysis of developing wheat grains under high-nitrogen fertilization revealed key differentially accumulated proteins that promote storage protein and starch biosyntheses. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 6219-6235.	1.9	12
8126	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. <i>Cell Reports</i> , 2018, 24, 1190-1202.e5.	2.9	56
8127	Species-Specific Changes in a Primate Transcription Factor Network Provide Insights into the Molecular Evolution of the Primate Prefrontal Cortex. <i>Genome Biology and Evolution</i> , 2018, 10, 2023-2036.	1.1	19

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8128	Genome-wide identification and characterization of InDels and SNPs in Glycine max and Glycine soja for contrasting seed permeability traits. <i>BMC Plant Biology</i> , 2018, 18, 141.	1.6	25
8129	Comparative iTRAQ proteomics revealed proteins associated with horn development in yak. <i>Proteome Science</i> , 2018, 16, 14.	0.7	11
8130	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> ANGUSTIFOLIA Protein. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2631-2641.	0.8	9
8131	<i>Herbaspirillum seropedicae</i> Differentially Expressed Genes in Response to Iron Availability. <i>Frontiers in Microbiology</i> , 2018, 9, 1430.	1.5	10
8132	Computational Approaches in Reproductomics. , 2018, , 347-383.		0
8133	Combined Enrichment/Enzymatic Approach To Study Tightly Clustered Multisite Phosphorylation on Ser-Rich Domains. <i>Journal of Proteome Research</i> , 2018, 17, 3050-3060.	1.8	3
8134	Abnormal Small Intestinal Epithelial Microvilli in Patients With Crohn's Disease. <i>Gastroenterology</i> , 2018, 155, 815-828.	0.6	75
8135	Identifying Differentially Expressed MicroRNAs Between Cirrhotic and Non-Cirrhotic Hepatocellular Carcinoma and Exploring Their Functions Using Bioinformatic Analysis. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1443-1456.	1.1	16
8136	Proteome-wide analysis of human motif-domain interactions mapped on influenza A virus. <i>BMC Bioinformatics</i> , 2018, 19, 238.	1.2	8
8137	Functional annotation of hypothetical proteins from the <i>Exiguobacterium antarcticum</i> strain B7 reveals proteins involved in adaptation to extreme environments, including high arsenic resistance. <i>PLoS ONE</i> , 2018, 13, e0198965.	1.1	52
8138	Bioinformatics-based identification of potential microRNA biomarkers in frequent and non-frequent exacerbators of COPD. <i>International Journal of COPD</i> , 2018, Volume 13, 1217-1228.	0.9	24
8139	Manzamine A Exerts Anticancer Activity against Human Colorectal Cancer Cells. <i>Marine Drugs</i> , 2018, 16, 252.	2.2	39
8140	Expression and network analysis of YBX1 interactors for identification of new drug targets in lung adenocarcinoma. <i>Journal of Genomics</i> , 2018, 6, 103-112.	0.6	10
8141	Proteomic interaction profiling reveals KIFC1 as a factor involved in early targeting of F508del-CFTR to degradation. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 4495-4509.	2.4	22
8142	Molecular mechanisms of autophagic memory in pathogenic T cells in human arthritis. <i>Journal of Autoimmunity</i> , 2018, 94, 90-98.	3.0	11
8143	Overexpression of the MADS-box gene K-domain increases the yield potential of blueberry. <i>Plant Science</i> , 2018, 276, 22-31.	1.7	24
8144	From hairballs to hypotheses—biological insights from microbial networks. <i>FEMS Microbiology Reviews</i> , 2018, 42, 761-780.	3.9	374
8145	Heterosis-related genes under different planting densities in maize. <i>Journal of Experimental Botany</i> , 2018, 69, 5077-5087.	2.4	25



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8146	Integrated ovarian mRNA and miRNA transcriptome profiling characterizes the genetic basis of prolificacy traits in sheep ( <i>Ovis aries</i> ). <i>BMC Genomics</i> , 2018, 19, 104.	1.2	38
8147	Novel proteome and acetylome of <i>Bemisia tabaci</i> Q in response to <i>Cardinium</i> infection. <i>BMC Genomics</i> , 2018, 19, 523.	1.2	16
8148	Structure and dynamics of a human myelin protein P2 portal region mutant indicate opening of the $\hat{I}^2$ barrel in fatty acid binding proteins. <i>BMC Structural Biology</i> , 2018, 18, 8.	2.3	19
8149	Differentially expressed genes related to major depressive disorder and antidepressant response: genome-wide gene expression analysis. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-11.	3.2	33
8150	Omics and bioinformatics applied to vaccine development against <i>Borrelia</i> . <i>Molecular Omics</i> , 2018, 14, 330-340.	1.4	11
8151	Candidate genes and microRNAs for glioma pathogenesis and prognosis based on gene expression profiles. <i>Molecular Medicine Reports</i> , 2018, 18, 2715-2723.	1.1	5
8152	Bioinformatics-based interaction analysis of miR-92a-3p and key genes in tamoxifen-resistant breast cancer cells. <i>Biomedicine and Pharmacotherapy</i> , 2018, 107, 117-128.	2.5	33
8153	Transcriptomic sequencing reveals diverse adaptive gene expression responses of human vascular smooth muscle cells to nitro-conjugated linoleic acid. <i>Physiological Genomics</i> , 2018, 50, 287-295.	1.0	8
8154	Molecular Network-Based Identification of Competing Endogenous RNAs in Thyroid Carcinoma. <i>Genes</i> , 2018, 9, 44.	1.0	23
8155	Targeted Isolation of Tsitsikammamines from the Antarctic Deep-Sea Sponge <i>Latrunculia biformis</i> by Molecular Networking and Anticancer Activity. <i>Marine Drugs</i> , 2018, 16, 268.	2.2	42
8156	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	0.4	99
8157	Single-Cell Transcriptomes Distinguish Stem Cell State Changes and Lineage Specification Programs in Early Mammary Gland Development. <i>Cell Reports</i> , 2018, 24, 1653-1666.e7.	2.9	125
8158	MicroRNA signatures in cardiac biopsies and detection of allograft rejection. <i>Journal of Heart and Lung Transplantation</i> , 2018, 37, 1329-1340.	0.3	34
8159	The reciprocal interplay between TNF $\alpha$ and the circadian clock impacts on cell proliferation and migration in Hodgkin lymphoma cells. <i>Scientific Reports</i> , 2018, 8, 11474.	1.6	26
8160	Gene expression analysis indicates reduced memory and cognitive functions in the hippocampus and increase in synaptic reorganization in the frontal cortex 3 weeks after MDMA administration in Dark Agouti rats. <i>BMC Genomics</i> , 2018, 19, 580.	1.2	12
8161	Family specific genetic predisposition to breast cancer: results from Tunisian whole exome sequenced breast cancer cases. <i>Journal of Translational Medicine</i> , 2018, 16, 158.	1.8	32
8162	A new dynamic correlation algorithm reveals novel functional aspects in single cell and bulk RNA-seq data. <i>PLoS Computational Biology</i> , 2018, 14, e1006391.	1.5	29
8163	Circular RNA Signature Predicts Gemcitabine Resistance of Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2018, 9, 584.	1.6	77



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8164	Characterizing the Key Metabolic Pathways of the Neonatal Mouse Heart Using a Quantitative Combinatorial Omics Approach. <i>Frontiers in Physiology</i> , 2018, 9, 365.	1.3	34
8165	Circulating miRNAs as Putative Biomarkers of Exercise Adaptation in Endurance Horses. <i>Frontiers in Physiology</i> , 2018, 9, 429.	1.3	10
8166	Transcriptome Reveals Long Non-coding RNAs and mRNAs Involved in Primary Wool Follicle Induction in Carpet Sheep Fetal Skin. <i>Frontiers in Physiology</i> , 2018, 9, 446.	1.3	72
8167	Interactive Effects of CO <sub>2</sub> Concentration and Water Regime on Stable Isotope Signatures, Nitrogen Assimilation and Growth in Sweet Pepper. <i>Frontiers in Plant Science</i> , 2017, 8, 2180.	1.7	33
8168	Transcriptomic Analysis Reveal the Molecular Mechanisms of Wheat Higher-Temperature Seedling-Plant Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 240.	1.7	18
8169	Integrative Transcriptomic Analysis Uncovers Novel Gene Modules That Underlie the Sulfate Response in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 470.	1.7	44
8170	Gene Discovery of Characteristic Metabolic Pathways in the Tea Plant ( <i>Camellia sinensis</i> ) Using <sup>13</sup> C-Omics-Based Network Approaches: A Future Perspective. <i>Frontiers in Plant Science</i> , 2018, 9, 480.	1.7	33
8171	Integration of the Pokeweed miRNA and mRNA Transcriptomes Reveals Targeting of Jasmonic Acid-Responsive Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 589.	1.7	10
8172	Metabolic Responses to Low Temperature of Three Peach Fruit Cultivars Differently Sensitive to Cold Storage. <i>Frontiers in Plant Science</i> , 2018, 9, 706.	1.7	63
8173	An Integration of Genome-Wide Association Study and Gene Co-expression Network Analysis Identifies Candidate Genes of Stem Lodging-Related Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 796.	1.7	36
8174	Inventory of ABC proteins and their putative role in salt and drug tolerance in <i>Debaryomyces hansenii</i> . <i>Gene</i> , 2018, 676, 227-242.	1.0	7
8175	Global Involvement of Lysine Cronylation in Protein Modification and Transcription Regulation in Rice. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1922-1936.	2.5	62
8176	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. <i>Microbiome</i> , 2018, 6, 130.	4.9	83
8177	Independent effects of dietary fat and sucrose content on chondrocyte metabolism and osteoarthritis pathology in mice. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	20
8178	A Network Approach to Understanding Patterns of Coflowering in Diverse Communities. <i>International Journal of Plant Sciences</i> , 2018, 179, 569-582.	0.6	21
8179	Characterization of long non-coding RNA and messenger RNA profiles in follicular fluid from mature and immature ovarian follicles of healthy women and women with polycystic ovary syndrome. <i>Human Reproduction</i> , 2018, 33, 1735-1748.	0.4	65
8180	GeneXX: an online tool for the exploration of transcript changes in skeletal muscle associated with exercise. <i>Physiological Genomics</i> , 2018, 50, 376-384.	1.0	10
8181	SWATH-MS based quantitative proteomics analysis reveals that curcumin alters the metabolic enzyme profile of CML cells by affecting the activity of miR-22/IPO7/HIF-1 $\alpha$ axis. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 170.	3.5	30

#	ARTICLE	IF	CITATIONS
8182	Diarrhea-Associated Intestinal Microbiota in Captive Sichuan Golden Snub-Nosed Monkeys (&lt;i>Rhinopithecus roxellana&lt;/i>). <i>Microbes and Environments</i> , 2018, 33, 249-256.	0.7	14
8183	Traceability, reproducibility and wiki-exploration for "à-la-carte" reconstructions of genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2018, 14, e1006146.	1.5	89
8184	Identifying miRNA and gene modules of colon cancer associated with pathological stage by weighted gene co-expression network analysis. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 2815-2830.	1.0	120
8185	Identification of Potential Key Genes Associated With the Pathogenesis and Prognosis of Gastric Cancer Based on Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2018, 9, 265.	1.1	154
8186	Splenectomy Leads to Amelioration of Altered Gut Microbiota and Metabolome in Liver Cirrhosis Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 963.	1.5	38
8187	Single Cell Analysis Identifies the miRNA Expression Profile of a Subpopulation of Muscle Precursor Cells Unique to Humans With Type 2 Diabetes. <i>Frontiers in Physiology</i> , 2018, 9, 883.	1.3	5
8188	Comparative analysis of human and mouse transcriptional cofactors (TcoFs) with special emphasis on intrinsically disordered regions and their associated regulating post-translational modifications. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 8531-8546.	1.2	1
8189	Acute changes in DNA methylation in relation to 24-h personal air pollution exposure measurements: A panel study in four European countries. <i>Environment International</i> , 2018, 120, 11-21.	4.8	48
8190	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. <i>Biochemistry</i> , 2018, 57, 4651-4662.	1.2	58
8191	Determination of system level alterations in host transcriptome due to Zika virus (ZIKV) Infection in retinal pigment epithelium. <i>Scientific Reports</i> , 2018, 8, 11209.	1.6	37
8192	Proteomics reveals Rictor as a noncanonical TGF- $\beta^2$ signaling target during aneurysm progression in Marfan mice. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 315, H1112-H1126.	1.5	20
8193	Transcriptome response of human skeletal muscle to divergent exercise stimuli. <i>Journal of Applied Physiology</i> , 2018, 124, 1529-1540.	1.2	61
8194	<i>Zuo Gui Wan</i> Alters Expression of Energy Metabolism Genes and Prevents Cell Death in High-Glucose Loaded Mouse Embryos. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 1-11.	0.5	2
8195	Systems Pharmacological Approach to Investigate the Mechanism of <i>Acori Tatarinowii Rhizoma</i> for Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-20.	0.5	20
8196	In Silico Investigation of the Pharmacological Mechanisms of Beneficial Effects of Ginkgo biloba L. on Alzheimer's Disease. <i>Nutrients</i> , 2018, 10, 589.	1.7	24
8197	Burkitt lymphoma-associated network construction and important network motif analysis. <i>Oncology Letters</i> , 2018, 16, 3054-3062.	0.8	1
8198	In silico prediction of novel residues involved in amyloid primary nucleation of human I56T and D67H lysozyme. <i>BMC Structural Biology</i> , 2018, 18, 9.	2.3	6
8199	QTL Alignment for Seed Yield and Yield Related Traits in Brassica napus. <i>Frontiers in Plant Science</i> , 2018, 9, 1127.	1.7	43

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8201	Molecular characterization of Brassica napus stress related transcription factors, BnMYB44 and BnVIP1, selected based on comparative analysis of Arabidopsis thaliana and Eutrema salsugineum transcriptomes. <i>Molecular Biology Reports</i> , 2018, 45, 1111-1124.	1.0	21
8202	Insights into the Temporal Gene Expression Pattern in <i>Lymantria dispar</i> Larvae During the Baculovirus Induced Hyperactive Stage. <i>Virologica Sinica</i> , 2018, 33, 345-358.	1.2	8
8203	Activation of membrane-bound and soluble Toll-like Receptors 5 in <i>Salmo salar</i> depends on the MyD88 signalling pathway. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2215-2225.	1.1	10
8204	Microbial uniqueness of architecture modified loofah sponge as biological filler for efficient nitrogen removal. <i>Bioresource Technology Reports</i> , 2018, 3, 95-101.	1.5	17
8205	Long-term organic fertilization increased antibiotic resistome in phyllosphere of maize. <i>Science of the Total Environment</i> , 2018, 645, 1230-1237.	3.9	97
8206	Bone marrow characterization in COPD: a multi-level network analysis. <i>Respiratory Research</i> , 2018, 19, 118.	1.4	8
8207	Construction and analysis of a ceRNA-ceRNA network reveals two potential prognostic modules regulated by hsa-miR-335-5p in osteosarcoma. <i>International Journal of Molecular Medicine</i> , 2018, 42, 1237-1246.	1.8	6
8208	Biological networks integration based on dense module identification for gene prioritization from microarray data. <i>Gene Reports</i> , 2018, 12, 276-288.	0.4	14
8209	NRG1 signalling regulates the establishment of Sertoli cell stock in the mouse testis. <i>Molecular and Cellular Endocrinology</i> , 2018, 478, 17-31.	1.6	4
8210	Network-based genetic investigation of virulence-associated phenotypes in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2018, 8, 10796.	1.6	5
8211	Analysis of the Cancer Genome Atlas Data Reveals Novel Putative ncRNAs Targets in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	16
8212	Weighted Gene Co-Expression Network Analysis Identifies Specific Modules and Hub Genes Related to Hyperlipidemia. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1151-1163.	1.1	40
8213	Distinct tissue-specific transcriptional regulation revealed by gene regulatory networks in maize. <i>BMC Plant Biology</i> , 2018, 18, 111.	1.6	41
8214	Comprehensive analysis of a long noncoding RNA-associated competing endogenous RNA network in colorectal cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 2453-2466.	1.0	27
8215	Identification of genomic expression differences between right-sided and left-sided colon cancer based on bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 609-618.	1.0	14
8216	The R2R3MYB Gene Family in <i>Phyllostachys edulis</i> : Genome-Wide Analysis and Identification of Stress or Development-Related R2R3MYBs. <i>Frontiers in Plant Science</i> , 2018, 9, 738.	1.7	45
8217	Characterizing functional consequences of DNA copy number alterations in breast and ovarian tumors by spaceMap. <i>Journal of Genetics and Genomics</i> , 2018, 45, 361-371.	1.7	1
8218	Bioinformatics analysis of gene expression profiles to diagnose crucial and novel genes in glioblastoma multiform. <i>Pathology Research and Practice</i> , 2018, 214, 1395-1461.	1.0	7

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8219	Structural development and assembly patterns of the root-associated microbiomes during phytoremediation. <i>Science of the Total Environment</i> , 2018, 644, 1591-1601.	3.9	60
8220	Transcriptome and metabolome analysis reveal candidate genes and biochemicals involved in tea geometrid defense in <i>Camellia sinensis</i> . <i>PLoS ONE</i> , 2018, 13, e0201670.	1.1	38
8221	The <sc>ATP</sc>ase <sc>VCP</sc>/p97 functions as a disaggregase against toxic Huntingtinâ€œexon1 aggregates. <i>FEBS Letters</i> , 2018, 592, 2680-2692.	1.3	28
8222	Network Pharmacology in the Study of TCM Formulae. , 2018, , 69-95.		1
8223	Succession of bacterioplankton community in intensive shrimp ( <i>Litopenaeus vannamei</i> ) aquaculture systems. <i>Aquaculture</i> , 2018, 497, 200-213.	1.7	35
8224	OCT4 directly regulates stemness and extracellular matrix-related genes in human germ cell tumours. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 1980-1986.	1.0	17
8225	Analysis of diet-induced differential methylation, expression, and interactions of lncRNA and protein-coding genes in mouse liver. <i>Scientific Reports</i> , 2018, 8, 11537.	1.6	10
8226	Advances in computational modeling approaches of pituitary gonadotropin signaling. <i>Expert Opinion on Drug Discovery</i> , 2018, 13, 799-813.	2.5	4
8227	Response of hostâ€œbacterial colonization in shrimp to developmental stage, environment and disease. <i>Molecular Ecology</i> , 2018, 27, 3686-3699.	2.0	82
8228	Stable, Environmental Specific and Novel QTL Identification as Well as Genetic Dissection of Fatty Acid Metabolism in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1018.	1.7	35
8229	Identification of transcription factors responsible for dysregulated networks in human osteoarthritis cartilage by global gene expression analysis. <i>Osteoarthritis and Cartilage</i> , 2018, 26, 1531-1538.	0.6	143
8230	First comprehensive analysis of lysine acetylation in <i>Alvinocaris longirostris</i> from the deep-sea hydrothermal vents. <i>BMC Genomics</i> , 2018, 19, 352.	1.2	14
8231	Bioinformatics Analysis Identifies p53 as a Candidate Prognostic Biomarker for Neuropathic Pain. <i>Frontiers in Genetics</i> , 2018, 9, 320.	1.1	40
8232	The Binding Mechanism Between Inositol Phosphate (InsP) and the Jasmonate Receptor Complex: A Computational Study. <i>Frontiers in Plant Science</i> , 2018, 9, 963.	1.7	9
8233	Chronic Rhinosinusitis: Potential Role of Microbial Dysbiosis and Recommendations for Sampling Sites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 57.	1.8	75
8234	Use of Haploid Model of <i>Candida albicans</i> to Uncover Mechanism of Action of a Novel Antifungal Agent. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 164.	1.8	15
8235	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	32
8236	Identification of Shared Molecular Signatures Indicate the Susceptibility of Endometriosis to Multiple Sclerosis. <i>Frontiers in Genetics</i> , 2018, 9, 42.	1.1	16

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8237	STAT6, PBX2, and PBRM1 Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018, 9, 87.	1.1	34
8238	Identification and Functional Analysis of Long Intergenic Non-coding RNAs Underlying Intramuscular Fat Content in Pigs. <i>Frontiers in Genetics</i> , 2018, 9, 102.	1.1	39
8239	The Interactomic Analysis Reveals Pathogenic Protein Networks in <i>Phomopsis longicolla</i> Underlying Seed Decay of Soybean. <i>Frontiers in Genetics</i> , 2018, 9, 104.	1.1	37
8240	Identification of Central Regulators of Calcium Signaling and ECM Receptor Interaction Genetically Associated With the Progression and Recurrence of Atrial Fibrillation. <i>Frontiers in Genetics</i> , 2018, 9, 162.	1.1	18
8241	Id Proteins Suppress E2A-Driven Invariant Natural Killer T Cell Development prior to TCR Selection. <i>Frontiers in Immunology</i> , 2018, 9, 42.	2.2	13
8242	Genome-Wide Bimolecular Fluorescence Complementation-Based Proteomic Analysis of <i>Toxoplasma gondii</i> ROP18's Human Interactome Shows Its Key Role in Regulation of Cell Immunity and Apoptosis. <i>Frontiers in Immunology</i> , 2018, 9, 61.	2.2	25
8243	Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 224.	2.2	164
8244	Immunotopographical Differences of Human Skin. <i>Frontiers in Immunology</i> , 2018, 9, 424.	2.2	32
8245	RNAi-Based Identification of Gene-Specific Nuclear Cofactor Networks Regulating Interleukin-1 Target Genes. <i>Frontiers in Immunology</i> , 2018, 9, 775.	2.2	7
8246	Molecular and Cellular Dynamics in the Skin, the Lymph Nodes, and the Blood of the Immune Response to Intradermal Injection of Modified Vaccinia Ankara Vaccine. <i>Frontiers in Immunology</i> , 2018, 9, 870.	2.2	7
8247	Gingival Periodontal Disease (PD) Level-Butyric Acid Affects the Systemic Blood and Brain Organ: Insights Into the Systemic Inflammation of Periodontal Disease. <i>Frontiers in Immunology</i> , 2018, 9, 1158.	2.2	27
8248	Tomato Apical Leaf Curl Virus: A Novel, Monopartite Geminivirus Detected in Tomatoes in Argentina. <i>Frontiers in Microbiology</i> , 2017, 8, 2665.	1.5	43
8249	Collection and Curation of Transcriptional Regulatory Interactions in <i>Aspergillus nidulans</i> and <i>Neurospora crassa</i> Reveal Structural and Evolutionary Features of the Regulatory Networks. <i>Frontiers in Microbiology</i> , 2018, 9, 27.	1.5	10
8250	Alanine Enhances Aminoglycosides-Induced ROS Production as Revealed by Proteomic Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 29.	1.5	77
8251	1-((2,4-Dichlorophenethyl)Amino)-3-Phenoxypropan-2-ol Kills <i>Pseudomonas aeruginosa</i> through Extensive Membrane Damage. <i>Frontiers in Microbiology</i> , 2018, 9, 129.	1.5	9
8252	Rapid Formation of Microbe-Oil Aggregates and Changes in Community Composition in Coastal Surface Water Following Exposure to Oil and the Dispersant Corexit. <i>Frontiers in Microbiology</i> , 2018, 9, 689.	1.5	72
8253	Cyanobacterial Community Composition and Bacteria-Bacteria Interactions Promote the Stable Occurrence of Particle-Associated Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 777.	1.5	40
8254	Water Masses and Depth Structure Prokaryotic and T4-Like Viral Communities Around Hydrothermal Systems of the Nordic Seas. <i>Frontiers in Microbiology</i> , 2018, 9, 1002.	1.5	6

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8255	An Engineered Distant Homolog of <i>Pseudomonas syringae</i> TTSS Effector From <i>Physcomitrella patens</i> Can Act as a Bacterial Virulence Factor. <i>Frontiers in Microbiology</i> , 2018, 9, 1060.	1.5	4
8256	Differentially Expressed Genes in Osteomyelitis Induced by <i>Staphylococcus aureus</i> Infection. <i>Frontiers in Microbiology</i> , 2018, 9, 1093.	1.5	10
8257	Evolution and Diversity of Biosynthetic Gene Clusters in <i>Fusarium</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1158.	1.5	41
8258	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1187.	1.5	56
8259	Persistence of Cellulolytic Bacteria <i>Fibrobacter</i> and <i>Treponema</i> After Short-Term Corn Stover-Based Dietary Intervention Reveals the Potential to Improve Rumen Fibrolytic Function. <i>Frontiers in Microbiology</i> , 2018, 9, 1363.	1.5	92
8260	Integrated Analysis and Identification of Novel Biomarkers in Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 178.	1.7	39
8261	Systematic Analysis of mRNA and miRNA Expression of 3D-Cultured Neural Stem Cells (NSCs) in Spaceflight. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 434.	1.8	10
8262	The Pathoconnectivity Profile of Alzheimer's Disease: A Morphometric Coalteration Network Analysis. <i>Frontiers in Neurology</i> , 2018, 8, 739.	1.1	25
8263	Identification of the CFTR c.1666A>G Mutation in Hereditary Inclusion Body Myopathy Using Next-Generation Sequencing Analysis. <i>Frontiers in Neuroscience</i> , 2018, 12, 329.	1.4	2
8264	Regulation of Adult CNS Axonal Regeneration by the Post-transcriptional Regulator <i>Cpeb1</i> . <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 445.	1.4	7
8265	Nonredundant, Highly Connected MicroRNAs Control Functionality in Breast Cancer Networks. <i>International Journal of Genomics</i> , 2018, 2018, 1-10.	0.8	22
8266	Dynamic transcriptome profiling towards understanding the morphogenesis and development of diverse feather in domestic duck. <i>BMC Genomics</i> , 2018, 19, 391.	1.2	10
8267	Aspirin is Involved in the Cell Cycle Arrest, Apoptosis, Cell Migration, and Invasion of Oral Squamous Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2029.	1.8	28
8268	Identification and Characterization of Malate Dehydrogenases and the Lactate-Biosynthetic Pathway in <i>Leuconostoc mesenteroides</i> ATCC 8293. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 8086-8093.	2.4	12
8269	Time-lapse imaging of molecular evolution by high-throughput sequencing. <i>Nucleic Acids Research</i> , 2018, 46, 7480-7494.	6.5	11
8270	Harnessing single-cell genomics to improve the physiological fidelity of organoid-derived cell types. <i>BMC Biology</i> , 2018, 16, 62.	1.7	35
8271	In silico approach in reveal traditional medicine plants pharmacological material basis. <i>Chinese Medicine</i> , 2018, 13, 33.	1.6	75
8272	Diversification of Secondary Metabolite Biosynthetic Gene Clusters Coincides with Lineage Divergence in <i>Streptomyces</i> . <i>Antibiotics</i> , 2018, 7, 12.	1.5	46



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8273	Construction and Analysis of Gene Co-Expression Networks in Escherichia coli. <i>Cells</i> , 2018, 7, 19.	1.8	39
8274	Shape-Shifted Red Blood Cells: A Novel Red Blood Cell Stage?. <i>Cells</i> , 2018, 7, 31.	1.8	37
8275	Tamarix microRNA Profiling Reveals New Insight into Salt Tolerance. <i>Forests</i> , 2018, 9, 180.	0.9	11
8276	Transcription Factor and lncRNA Regulatory Networks Identify Key Elements in Lung Adenocarcinoma. <i>Genes</i> , 2018, 9, 12.	1.0	15
8277	Integration of lncRNA and mRNA Transcriptome Analyses Reveals Genes and Pathways Potentially Involved in Calf Intestinal Growth and Development during the Early Weeks of Life. <i>Genes</i> , 2018, 9, 142.	1.0	20
8278	Genome-Wide Analysis of the PYL Gene Family and Identification of PYL Genes That Respond to Abiotic Stress in <i>Brassica napus</i> . <i>Genes</i> , 2018, 9, 156.	1.0	55
8279	In Silico Functional Networks Identified in Fish Nucleated Red Blood Cells by Means of Transcriptomic and Proteomic Profiling. <i>Genes</i> , 2018, 9, 202.	1.0	55
8280	Integrative Analysis of Dysregulated lncRNA-Associated ceRNA Network Reveals Functional lncRNAs in Gastric Cancer. <i>Genes</i> , 2018, 9, 303.	1.0	60
8281	Transcriptional responses of soybean roots to colonization with the root endophytic fungus <i>Piriformospora indica</i> reveals altered phenylpropanoid and secondary metabolism. <i>Scientific Reports</i> , 2018, 8, 10227.	1.6	64
8282	A system-based analysis of the genetic determinism of udder conformation and health phenotypes across three French dairy cattle breeds. <i>PLoS ONE</i> , 2018, 13, e0199931.	1.1	25
8283	Thermal proteome profiling in bacteria: probing protein state <i>in vivo</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8242.	3.2	130
8284	Responses of fungal bacterial community and network to organic inputs vary among different spatial habitats in soil. <i>Soil Biology and Biochemistry</i> , 2018, 125, 54-63.	4.2	142
8285	Strand-Specific Dual RNA Sequencing of Bronchial Epithelial Cells Infected with Influenza A/H3N2 Viruses Reveals Splicing of Gene Segment 6 and Novel Host-Virus Interactions. <i>Journal of Virology</i> , 2018, 92, .	1.5	51
8286	A common molecular signature of patients with sickle cell disease revealed by microarray meta-analysis and a genome-wide association study. <i>PLoS ONE</i> , 2018, 13, e0199461.	1.1	12
8287	Classification of Single Particles from Human Cell Extract Reveals Distinct Structures. <i>Cell Reports</i> , 2018, 24, 259-268.e3.	2.9	32
8288	Influenza A Virus Induces Autophagosomal Targeting of Ribosomal Proteins. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1909-1921.	2.5	22
8289	Metabolic phenotype of skeletal muscle in early critical illness. <i>Thorax</i> , 2018, 73, 926-935.	2.7	135
8290	Effects of cover crop in an apple orchard on microbial community composition, networks, and potential genes involved with degradation of crop residues in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 743-759.	2.3	85



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8291	Bioturbation by the razor clam ( <i>Sinonovacula constricta</i> ) on the microbial community and enzymatic activities in the sediment of an ecological aquaculture wastewater treatment system. <i>Science of the Total Environment</i> , 2018, 643, 1098-1107.	3.9	57
8292	Comprehensive analysis of the clinical significance and prospective molecular mechanisms of differentially expressed autophagy-related genes in thyroid cancer. <i>International Journal of Oncology</i> , 2018, 53, 603-619.	1.4	14
8293	Transcriptome-Wide Identification and Characterization of Potato Circular RNAs in Response to <i>Pectobacterium carotovorum</i> Subspecies <i>brasiliense</i> Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 71.	1.8	47
8294	Transcriptomics Evidence for Common Pathways in Human Major Depressive Disorder and Glioblastoma. <i>International Journal of Molecular Sciences</i> , 2018, 19, 234.	1.8	12
8295	Study of Imidazolium Salt Derivatives as PIK3CA Inhibitors Using a Comprehensive in Silico Method. <i>International Journal of Molecular Sciences</i> , 2018, 19, 896.	1.8	1
8296	Calcium-Dependent Protein Kinase Family Genes Involved in Ethylene-Induced Natural Rubber Production in Different <i>Hevea brasiliensis</i> Cultivars. <i>International Journal of Molecular Sciences</i> , 2018, 19, 947.	1.8	11
8297	Identification of Blueberry miRNAs and Their Targets Based on High-Throughput Sequencing and Degradome Analyses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 983.	1.8	9
8298	Radiation-Induced Gene Expression Changes in High and Low Grade Breast Cancer Cell Types. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1084.	1.8	28
8299	Comparative microRNA-seq Analysis Depicts Candidate miRNAs Involved in Skin Color Differentiation in Red Tilapia. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1209.	1.8	38
8300	The Cold-Regulated Genes of Blueberry and Their Response to Overexpression of VcDDF1 in Several Tissues. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1553.	1.8	11
8301	Candidate Genes for Yellow Leaf Color in Common Wheat ( <i>Triticum aestivum</i> L.) and Major Related Metabolic Pathways according to Transcriptome Profiling. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1594.	1.8	66
8302	Transcriptome Analysis Provides Insight into the Molecular Mechanisms Underlying gametophyte factor 2-Mediated Cross-Incompatibility in Maize. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1757.	1.8	9
8303	The Diverging Routes of BORIS and CTCF: An Interactomic and Phylogenomic Analysis. <i>Life</i> , 2018, 8, 4.	1.1	9
8304	Testing the Domino Theory of Gene Loss in <i>Buchnera aphidicola</i> : The Relevance of Epistatic Interactions. <i>Life</i> , 2018, 8, 17.	1.1	2
8305	Machine Learning Methods for Analysis of Metabolic Data and Metabolic Pathway Modeling. <i>Metabolites</i> , 2018, 8, 4.	1.3	115
8306	Core Sulphate-Reducing Microorganisms in Metal-Removing Semi-Passive Biochemical Reactors and the Co-Occurrence of Methanogens. <i>Microorganisms</i> , 2018, 6, 16.	1.6	31
8307	MicroRNA and Transcriptomic Profiling Showed miRNA-Dependent Impairment of Systemic Regulation and Synthesis of Biomolecules in Rag2 KO Mice. <i>Molecules</i> , 2018, 23, 527.	1.7	2
8308	Knowledge-Based Neuroendocrine Immunomodulation (NIM) Molecular Network Construction and Its Application. <i>Molecules</i> , 2018, 23, 1312.	1.7	7

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8309	Sponge Long Non-Coding RNAs Are Expressed in Specific Cell Types and Conserved Networks. <i>Non-coding RNA</i> , 2018, 4, 6.	1.3	8
8310	Changing Trends in Computational Drug Repositioning. <i>Pharmaceuticals</i> , 2018, 11, 57.	1.7	127
8311	Seed Dormancy Involves a Transcriptional Program That Supports Early Plastid Functionality during Imbibition. <i>Plants</i> , 2018, 7, 35.	1.6	16
8312	Carbon Dioxide Mediates the Response to Temperature and Water Activity Levels in <i>Aspergillus flavus</i> during Infection of Maize Kernels. <i>Toxins</i> , 2018, 10, 5.	1.5	31
8313	Involvement of Pro-Inflammatory Macrophages in Liver Pathology of Pirital Virus-Infected Syrian Hamsters. <i>Viruses</i> , 2018, 10, 232.	1.5	4
8314	Gene Expression Profiling and Assessment of Vitamin D and Serotonin Pathway Variations in Patients With Irritable Bowel Syndrome. <i>Journal of Neurogastroenterology and Motility</i> , 2018, 24, 96-106.	0.8	20
8315	Genome-Wide Regulatory Network Mapping of miRNA and Transcription Factors in Banana Roots. <i>Tropical Plant Biology</i> , 2018, 11, 141-153.	1.0	5
8316	Comparison of metabolite networks from four German population-based studies. <i>International Journal of Epidemiology</i> , 2018, 47, 2070-2081.	0.9	9
8317	Comprehensive and integrative analysis identifies microRNA-106 as a novel non-invasive biomarker for detection of gastric cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 127.	1.8	23
8318	Radio-sensitizing effects of VE-821 and beyond: Distinct phosphoproteomic and metabolomic changes after ATR inhibition in irradiated MOLT-4 cells. <i>PLoS ONE</i> , 2018, 13, e0199349.	1.1	8
8319	Coral Bacterial-Core Abundance and Network Complexity as Proxies for Anthropogenic Pollution. <i>Frontiers in Microbiology</i> , 2018, 9, 833.	1.5	70
8320	Differential lncRNA expression profiles reveal the potential roles of lncRNAs in antiviral immune response of <i>Crassostrea gigas</i> . <i>Fish and Shellfish Immunology</i> , 2018, 81, 233-241.	1.6	47
8321	Catalytic, Computational, and Evolutionary Analysis of the <scpd</scpd>-Lactate Dehydrogenases Responsible for <scpd</scpd>-Lactic Acid Production in Lactic Acid Bacteria. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 8371-8381.	2.4	22
8322	Transcriptome Analysis of Adipose Tissue Indicates That the cAMP Signaling Pathway Affects the Feed Efficiency of Pigs. <i>Genes</i> , 2018, 9, 336.	1.0	26
8323	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. <i>Pharmaceuticals</i> , 2018, 11, 61.	1.7	32
8324	Assembling the jigsaw puzzle: <scpd</scpd>CBX</scpd>2 isoform 2 and its targets in disorders/differences of sex development. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2018, 6, 785-795.	0.6	16
8325	An integrative, multi-omics approach towards the prioritization of <i>Klebsiella pneumoniae</i> drug targets. <i>Scientific Reports</i> , 2018, 8, 10755.	1.6	50
8326	Integrating Rio1 activities discloses its nutrient-activated network in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2018, 46, 7586-7611.	6.5	19

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8327	Metabolomics Based Profiling of Dexamethasone Side Effects in Rats. <i>Frontiers in Pharmacology</i> , 2018, 9, 46.	1.6	75
8328	A hnRNP K $\alpha$ -AR-Related Signature Reflects Progression toward Castration-Resistant Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1920.	1.8	19
8329	Identifying autophagy gene-associated module biomarkers through construction and analysis of an autophagy-mediated ceRNA $\leftrightarrow$ ceRNA interaction network in colorectal cancer. <i>International Journal of Oncology</i> , 2018, 53, 1083-1093.	1.4	6
8330	Hub genes and key pathways of non-small lung cancer identified using bioinformatics. <i>Oncology Letters</i> , 2018, 16, 2344-2354.	0.8	22
8331	Identification of potential target genes in pancreatic ductal adenocarcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2018, 16, 2453-2461.	0.8	26
8332	Computational Analysis of RNA-Seq Data from Airway Epithelial Cells for Studying Lung Disease. <i>Methods in Molecular Biology</i> , 2018, 1809, 203-235.	0.4	0
8333	Identification of lung cancer specific differentially methylated regions using genome-wide DNA methylation study. <i>Molecular and Cellular Toxicology</i> , 2018, 14, 315-322.	0.8	11
8334	Distinctions and associations between the microbiota of saliva and supragingival plaque of permanent and deciduous teeth. <i>PLoS ONE</i> , 2018, 13, e0200337.	1.1	43
8335	Dissecting Multi-protein Signaling Complexes by Bimolecular Complementation Affinity Purification (BiCAP). <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	3
8336	Three-Dimensional Cell Culture Conditions Affect the Proteome of Cancer-Associated Fibroblasts. <i>Journal of Proteome Research</i> , 2018, 17, 2780-2789.	1.8	19
8337	Genome instability is a consequence of transcription deficiency in patients with bone marrow failure harboring biallelic <i>ERCC6L2</i> variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7777-7782.	3.3	37
8338	Tools, Databases, and Applications of Immunoinformatics. , 2018, , 159-174.		0
8339	Expression patterns and genetic variation of the ovine skeletal muscle transcriptome of sheep from five Spanish meat breeds. <i>Scientific Reports</i> , 2018, 8, 10486.	1.6	8
8340	Atlas of <i>Schistosoma mansoni</i> long non-coding RNAs and their expression correlation to protein-coding genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	9
8341	Discovery and characterization of a prevalent human gut bacterial enzyme sufficient for the inactivation of a family of plant toxins. <i>ELife</i> , 2018, 7, .	2.8	93
8342	Co-expression network of transcription factors reveal ethylene-responsive element-binding factor as key regulator of wood phenotype in <i>Eucalyptus tereticornis</i> . <i>3 Biotech</i> , 2018, 8, 315.	1.1	5
8343	Multilayer View of Pathogenic SNVs in Human Interactome through In Silico Edgetic Profiling. <i>Journal of Molecular Biology</i> , 2018, 430, 2974-2992.	2.0	10
8344	Proteomic Analysis of NCK1/2 Adaptors Uncovers Paralog-specific Interactions That Reveal a New Role for NCK2 in Cell Abscission During Cytokinesis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1979-1990.	2.5	21

#	ARTICLE	IF	CITATIONS
8345	Histone Interaction Landscapes Visualized by Crosslinking Mass Spectrometry in Intact Cell Nuclei. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2018-2033.	2.5	103
8346	Identification of Methylated Gene Markers in Childhood Atopic Asthma by Integrating Gene Expression and Methylation Profiles Based on Bioinformatic Analysis. <i>Pediatric, Allergy, Immunology, and Pulmonology</i> , 2018, 31, 97-106.	0.3	1
8347	Comparative transcriptome analysis of nonchilled, chilled, and late-pink bud reveals flowering pathway genes involved in chilling-mediated flowering in blueberry. <i>BMC Plant Biology</i> , 2018, 18, 98.	1.6	31
8348	Potential biomarkers and therapeutic targets in cervical cancer: Insights from the meta-analysis of transcriptomics data within network biomedicine perspective. <i>PLoS ONE</i> , 2018, 13, e0200717.	1.1	89
8349	Hepatitis C virus enters liver cells using the CD81 receptor complex proteins calpain-5 and CBLB. <i>PLoS Pathogens</i> , 2018, 14, e1007111.	2.1	46
8350	Aux/IAA Gene Family in Plants: Molecular Structure, Regulation, and Function. <i>International Journal of Molecular Sciences</i> , 2018, 19, 259.	1.8	277
8351	A complex of C9ORF72 and p62 uses arginine methylation to eliminate stress granules by autophagy. <i>Nature Communications</i> , 2018, 9, 2794.	5.8	126
8352	Homeologous-specific expression divergence in the recently formed tetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>New Phytologist</i> , 2018, 220, 624-635.	3.5	10
8353	Computational characterization of the binding mode between oncoprotein Ets1 and DNA repair enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1055-1063.	1.5	4
8354	Metagenomic Functional Potential Predicts Degradation Rates of a Model Organophosphorus Xenobiotic in Pesticide Contaminated Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 147.	1.5	67
8355	Preservation Method and Phosphate Buffered Saline Washing Affect the Acute Myeloid Leukemia Proteome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 296.	1.8	3
8356	Identification of a 5' lncRNA signature-based risk scoring system for survival prediction in colorectal cancer. <i>Molecular Medicine Reports</i> , 2018, 18, 279-291.	1.1	7
8357	Identification of key genes and pathways in human clear cell renal cell carcinoma (ccRCC) by co-expression analysis. <i>International Journal of Biological Sciences</i> , 2018, 14, 266-279.	2.6	60
8358	HIRA directly targets the enhancers of selected cardiac transcription factors during in vitro differentiation of mouse embryonic stem cells. <i>Molecular Biology Reports</i> , 2018, 45, 1001-1011.	1.0	5
8359	FPR1 gene silencing suppresses cardiomyocyte apoptosis and ventricular remodeling in rats with ischemia/reperfusion injury through the inhibition of MAPK signaling pathway. <i>Experimental Cell Research</i> , 2018, 370, 506-518.	1.2	35
8360	Genetic variation in transcription factors and photosynthesis light-reaction genes regulates photosynthetic traits. <i>Tree Physiology</i> , 2018, 38, 1871-1885.	1.4	6
8361	Identification of the Key MicroRNAs and the miRNA-mRNA Regulatory Pathways in Prostate Cancer by Bioinformatics Methods. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	29
8362	Molecular mechanism of estrogen-mediated neuroprotection in the relief of brain ischemic injury. <i>BMC Genetics</i> , 2018, 19, 46.	2.7	8

#	ARTICLE	IF	CITATIONS
8363	Structure and transcriptional regulation of the major intrinsic protein gene family in grapevine. <i>BMC Genomics</i> , 2018, 19, 248.	1.2	43
8364	Identification of H <sub>2</sub> O <sub>2</sub> induced oxidative stress associated microRNAs in HLE-B3 cells and their clinical relevance to the progression of age-related nuclear cataract. <i>BMC Ophthalmology</i> , 2018, 18, 93.	0.6	28
8365	Identification of four differentially methylated genes as prognostic signatures for stage I lung adenocarcinoma. <i>Cancer Cell International</i> , 2018, 18, 60.	1.8	15
8366	The phospholipase DDHD1 as a new target in colorectal cancer therapy. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 82.	3.5	8
8367	QAPA: a new method for the systematic analysis of alternative polyadenylation from RNA-seq data. <i>Genome Biology</i> , 2018, 19, 45.	3.8	176
8368	Holobionts and ecological speciation: the intestinal microbiota of lake whitefish species pairs. <i>Microbiome</i> , 2018, 6, 47.	4.9	67
8369	Network analysis of microRNAs, transcription factors, and target genes involved in axon regeneration. <i>Journal of Zhejiang University: Science B</i> , 2018, 19, 293-304.	1.3	25
8370	Comparative Transcriptomic Response of Primary and Immortalized Macrophages to Murine Norovirus Infection. <i>Journal of Immunology</i> , 2018, 200, 4157-4169.	0.4	16
8371	Computational Resources for Predicting Protein-Protein Interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 110, 251-275.	1.0	11
8372	The Spring of Systems Biology-Driven Breeding. <i>Trends in Plant Science</i> , 2018, 23, 706-720.	4.3	37
8373	New imine-reducing enzymes from <i>l</i> -hydroxyacid dehydrogenases by single amino acid substitutions. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 109-120.	1.0	33
8374	Global analysis of prokaryotic tRNA-derived cyclodipeptide biosynthesis. <i>BMC Genomics</i> , 2018, 19, 45.	1.2	35
8375	Ouroboros resembling competitive endogenous loop (ORCEL) in circular RNAs revealed through transcriptome sequencing dataset analysis. <i>BMC Genomics</i> , 2018, 19, 171.	1.2	6
8376	Circular RNA expression and regulatory network prediction in posterior cingulate astrocytes in elderly subjects. <i>BMC Genomics</i> , 2018, 19, 340.	1.2	38
8377	Human angiogenin is a potent cytotoxin in the absence of ribonuclease inhibitor. <i>Rna</i> , 2018, 24, 1018-1027.	1.6	39
8378	Infant Viral Respiratory Infection Nasal Immune-Response Patterns and Their Association with Subsequent Childhood Recurrent Wheeze. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1064-1073.	2.5	56
8379	Identification and functional analysis of a core gene module associated with hepatitis C virus-induced human hepatocellular carcinoma progression. <i>Oncology Letters</i> , 2018, 15, 6815-6824.	0.8	6
8380	Reconstruction and analysis of the aberrant lncRNA-miRNA-mRNA network based on competitive endogenous RNA in CESC. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 6665-6673.	1.2	82

#	ARTICLE	IF	CITATIONS
8381	MIKCC-type MADS-box genes in <i>Rosa chinensis</i> : the remarkable expansion of ABCDE model genes and their roles in floral organogenesis. <i>Horticulture Research</i> , 2018, 5, 25.	2.9	41
8382	Cattle infection response network and its functional modules. <i>BMC Immunology</i> , 2018, 19, 2.	0.9	7
8383	Identification of AUXIN RESPONSE FACTOR gene family from <i>Prunus sibirica</i> and its expression analysis during mesocarp and kernel development. <i>BMC Plant Biology</i> , 2018, 18, 21.	1.6	16
8384	A three-lncRNA signature predicts overall survival and disease-free survival in patients with esophageal squamous cell carcinoma. <i>BMC Cancer</i> , 2018, 18, 147.	1.1	57
8385	Integration analysis of microRNA and mRNA paired expression profiling identifies deregulated microRNA-transcription factor-gene regulatory networks in ovarian endometriosis. <i>Reproductive Biology and Endocrinology</i> , 2018, 16, 4.	1.4	59
8386	Molecular and functional signatures in a novel Alzheimer's disease mouse model assessed by quantitative proteomics. <i>Molecular Neurodegeneration</i> , 2018, 13, 2.	4.4	62
8387	Analysis of microRNA profile of <i>Anopheles sinensis</i> by deep sequencing and bioinformatic approaches. <i>Parasites and Vectors</i> , 2018, 11, 172.	1.0	7
8388	An integrative functional genomics framework for effective identification of novel regulatory variants in genome-phenome studies. <i>Genome Medicine</i> , 2018, 10, 7.	3.6	29
8389	The dynamic intein landscape of eukaryotes. <i>Mobile DNA</i> , 2018, 9, 4.	1.3	18
8390	Binding and entry of peste des petits ruminants virus into caprine endometrial epithelial cells profoundly affect early cellular gene expression. <i>Veterinary Research</i> , 2018, 49, 8.	1.1	10
8391	Characterization and selective incorporation of small non-coding RNAs in non-small cell lung cancer extracellular vesicles. <i>Cell and Bioscience</i> , 2018, 8, 2.	2.1	58
8392	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	4.9	208
8393	<i>Haemophilus</i> is overrepresented in the nasopharynx of infants hospitalized with RSV infection and associated with increased viral load and enhanced mucosal CXCL8 responses. <i>Microbiome</i> , 2018, 6, 10.	4.9	49
8394	A human gut phage catalog correlates the gut phageome with type 2 diabetes. <i>Microbiome</i> , 2018, 6, 24.	4.9	146
8395	Individual and household attributes influence the dynamics of the personal skin microbiota and its association network. <i>Microbiome</i> , 2018, 6, 26.	4.9	48
8396	Identify Down syndrome transcriptome associations using integrative analysis of microarray database and correlation-interaction network. <i>Human Genomics</i> , 2018, 12, 2.	1.4	14
8397	A reservoir of "historical" antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	4.9	244
8398	Analysis of metastasis associated signal regulatory network in colorectal cancer. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 113-118.	1.0	14



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8399	The antibiotic resistome of free-living and particle-attached bacteria under a reservoir cyanobacterial bloom. <i>Environment International</i> , 2018, 117, 107-115.	4.8	95
8400	Characterization of odor emissions and microbial community structure during degradation of pig carcasses using the soil burial-composting method. <i>Waste Management</i> , 2018, 77, 30-42.	3.7	14
8401	Similar bowtie structures and distinct largest strong components are identified in the transcriptional regulatory networks of <i>Arabidopsis thaliana</i> during photomorphogenesis and heat shock. <i>BioSystems</i> , 2018, 168, 1-7.	0.9	2
8402	Personalization of prostate cancer therapy through phosphoproteomics. <i>Nature Reviews Urology</i> , 2018, 15, 483-497.	1.9	25
8403	Dramatic dysbalancing of the Wnt pathway in breast cancers. <i>Scientific Reports</i> , 2018, 8, 7329.	1.6	60
8404	An Integrated Study on the Antitumor Effect and Mechanism of Triphala Against Gynecological Cancers Based on Network Pharmacological Prediction and In Vitro Experimental Validation. <i>Integrative Cancer Therapies</i> , 2018, 17, 894-901.	0.8	18
8405	Key signaling pathways, genes and transcription factors associated with hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2018, 17, 8153-8160.	1.1	21
8406	Organic carbon source and salinity shape sediment bacterial composition in two China marginal seas and their major tributaries. <i>Science of the Total Environment</i> , 2018, 633, 1510-1517.	3.9	15
8407	Proteomic Analysis and NIR-II Imaging of MCM2 Protein in Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2018, 17, 2428-2439.	1.8	51
8408	BMTK: a toolkit for determining modules in biological bipartite networks. <i>Quantitative Biology</i> , 2018, 6, 186-192.	0.3	0
8409	Leukaemic alterations of IKZF1 prime stemness and malignancy programs in human lymphocytes. <i>Cell Death and Disease</i> , 2018, 9, 526.	2.7	6
8410	Potential molecular mechanisms of overgrazing-induced dwarfism in sheepgrass ( <i>Leymus chinensis</i> ) analyzed using proteomic data. <i>BMC Plant Biology</i> , 2018, 18, 81.	1.6	6
8411	Prokaryotic community successions and interactions in marine biofilms: the key role of Flavobacteriia. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	51
8412	Unsupervised, Statistically Based Systems Biology Approach for Unraveling the Genetics of Complex Traits: A Demonstration with Ethanol Metabolism. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 1177-1191.	1.4	7
8413	Contrasting prevalence of selection and drift in the community structuring of bacteria and microbial eukaryotes. <i>Environmental Microbiology</i> , 2018, 20, 2231-2240.	1.8	153
8414	Detection of major loci associated with the variation of 18 important agronomic traits between <i>Solanum pimpinellifolium</i> and cultivated tomatoes. <i>Plant Journal</i> , 2018, 95, 312-323.	2.8	26
8415	Differential expression networks and inheritance patterns of long non-coding RNAs in castor bean seeds. <i>Plant Journal</i> , 2018, 95, 324-340.	2.8	43
8416	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 207-234.	2.8	108



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8417	PPI network analyses of human WD40 protein family systematically reveal their tendency to assemble complexes and facilitate the complex predictions. <i>BMC Systems Biology</i> , 2018, 12, 41.	3.0	9
8418	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2205-2214.	0.8	22
8419	MicroRNA expression in cervical cancer: Novel diagnostic and prognostic biomarkers. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 7080-7090.	1.2	82
8420	Evaluating the microbial ecology and metabolite profile in Kazak artisanal cheeses from Xinjiang, China. <i>Food Research International</i> , 2018, 111, 130-136.	2.9	38
8421	NOTCH signaling specifies arterial-type definitive hemogenic endothelium from human pluripotent stem cells. <i>Nature Communications</i> , 2018, 9, 1828.	5.8	97
8422	Identification and characterization of the BRI2 interactome in the brain. <i>Scientific Reports</i> , 2018, 8, 3548.	1.6	12
8423	An Integrated, High-Throughput Strategy for Multiomic Systems Level Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 3396-3408.	1.8	32
8424	Actinobacteria associated with Chinaberry tree are diverse and show antimicrobial activity. <i>Scientific Reports</i> , 2018, 8, 11103.	1.6	12
8425	Gene co-expression network analysis reveals coordinated regulation of three characteristic secondary biosynthetic pathways in tea plant ( <i>Camellia sinensis</i> ). <i>BMC Genomics</i> , 2018, 19, 616.	1.2	71
8426	Identification of target genes in cardiomyopathy with fibrosis and cardiac remodeling. <i>Journal of Biomedical Science</i> , 2018, 25, 63.	2.6	54
8427	Prediction of novel pluripotent proteins involved in reprogramming of male Germline stem cells (GSCs) into multipotent adult Germline stem cells (maGSCs) by network analysis. <i>Computational Biology and Chemistry</i> , 2018, 76, 302-309.	1.1	7
8428	A New Strategy to Uncover the Anticancer Mechanism of Chinese Compound Formula by Integrating Systems Pharmacology and Bioinformatics. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-19.	0.5	8
8429	Biomarker panels for characterizing microbial community biofilm formation as composite molecular process. <i>PLoS ONE</i> , 2018, 13, e0202032.	1.1	4
8430	Bacterial Biomarkers of Marcellus Shale Activity in Pennsylvania. <i>Frontiers in Microbiology</i> , 2018, 9, 1697.	1.5	11
8431	Computational analysis of micro RNAs compatibility in pharmacogenomic based regulatory networks of psoriatic arthritis: An initiation towards identifying a potential miRNA to treat psoriatic arthritis. <i>Biocatalysis and Agricultural Biotechnology</i> , 2018, 16, 545-547.	1.5	2
8432	<i>Klebsiella oxytoca</i> expands in cancer cachexia and acts as a gut pathobiont contributing to intestinal dysfunction. <i>Scientific Reports</i> , 2018, 8, 12321.	1.6	71
8433	Characterization of protistan plankton diversity in ancient salt evaporation ponds located in a volcanic crater on the island Sal, Cape Verde. <i>Extremophiles</i> , 2018, 22, 943-954.	0.9	3
8434	Proteomics: Clinical and research applications in respiratory diseases. <i>Respirology</i> , 2018, 23, 993-1003.	1.3	15

#	ARTICLE	IF	CITATIONS
8435	Umbilical cord blood metabolomics reveal distinct signatures of dyslipidemia prior to bronchopulmonary dysplasia and pulmonary hypertension. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L870-L881.	1.3	34
8436	A Minimal lncRNA-mRNA Signature Predicts Sensitivity to Neoadjuvant Chemotherapy in Triple-Negative Breast Cancer. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 2539-2548.	1.1	15
8437	Identification and Validation of Two Novel Prognostic lncRNAs in Kidney Renal Clear Cell Carcinoma. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 2549-2562.	1.1	24
8438	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. <i>PLoS ONE</i> , 2018, 13, e0193515.	1.1	34
8439	Shedding Light on Chemically Mediated Tri-Trophic Interactions: A 1H-NMR Network Approach to Identify Compound Structural Features and Associated Biological Activity. <i>Frontiers in Plant Science</i> , 2018, 9, 1155.	1.7	12
8440	A Novel Iron Transporter SPD_1590 in <i>Streptococcus pneumoniae</i> Contributing to Bacterial Virulence Properties. <i>Frontiers in Microbiology</i> , 2018, 9, 1624.	1.5	15
8441	A Quantitative Proteomics View on the Function of Qfhb1, a Major QTL for Fusarium Head Blight Resistance in Wheat. <i>Pathogens</i> , 2018, 7, 58.	1.2	19
8442	An integrated deep sequencing analysis of microRNAs in transplanted corneas. <i>Molecular Immunology</i> , 2018, 101, 429-439.	1.0	6
8443	Analysis of differentially expressed genes among human hair follicle-derived iPSCs, induced hepatocyte-like cells, and primary hepatocytes. <i>Stem Cell Research and Therapy</i> , 2018, 9, 211.	2.4	10
8444	Identification of potential prognostic microRNA biomarkers for predicting survival in patients with hepatocellular carcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 787-803.	0.9	48
8445	An integrated analysis of key microRNAs, regulatory pathways and clinical relevance in bladder cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 3075-3085.	1.0	7
8446	Bioinformatic analysis of microRNA expression in Huntington's disease. <i>Molecular Medicine Reports</i> , 2018, 18, 2857-2865.	1.1	9
8447	Candidate gene and mechanism investigations in congenital obstructive nephropathy based on bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 2651-2660.	1.1	1
8448	MetaboCraft: building a Minecraft plugin for metabolomics. <i>Bioinformatics</i> , 2018, 34, 2693-2694.	1.8	3
8449	Evaluation of the airway microbiome in nontuberculous mycobacteria disease. <i>European Respiratory Journal</i> , 2018, 52, 1800810.	3.1	69
8450	Metabotypes Related to Meat and Vegetable Intake Reflect Microbial, Lipid and Amino Acid Metabolism in Healthy People. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1800583.	1.5	17
8451	Celiac disease biomarkers identified by transcriptome analysis of small intestinal biopsies. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 4385-4401.	2.4	41
8452	Genome-wide haplotype association study identifies risk genes for non-small cell lung cancer. <i>Journal of Theoretical Biology</i> , 2018, 456, 84-90.	0.8	10

#	ARTICLE	IF	CITATIONS
8453	Sexually dimorphic behavior, neuronal activity, and gene expression in Chd8-mutant mice. <i>Nature Neuroscience</i> , 2018, 21, 1218-1228.	7.1	128
8454	The role of triiodothyronine hormone and mechanically-stressed endothelial cell paracrine signalling synergism in gene reprogramming during hBMSC-stimulated osteogenic phenotype in vitro. <i>Molecular and Cellular Endocrinology</i> , 2018, 478, 151-167.	1.6	16
8455	Asthma MicroRNA Regulome Development Using Validated miRNA-Target Interaction Visualization. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 607-615.	1.0	9
8456	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. <i>Environmental Microbiology Reports</i> , 2018, 10, 673-685.	1.0	22
8457	Identification of a co-target for enhancing efficacy of sorafenib in HCC through a quantitative modeling approach. <i>FEBS Journal</i> , 2018, 285, 3977-3992.	2.2	8
8458	Is the Nutritional Value of Fish Fillet Related to Fish Maturation or Fish Age? Integrated Analysis of Transcriptomics and Metabolomics in Blunt Snout Bream ( <i>Megalobrama amblycephala</i> ). <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 17-39.	1.1	7
8459	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. <i>Frontiers in Genetics</i> , 2018, 9, 281.	1.1	30
8460	Interleukin 33 regulates gene expression in intestinal epithelial cells independently of its nuclear localization. <i>Cytokine</i> , 2018, 111, 146-153.	1.4	18
8461	Network pharmacology study reveals energy metabolism and apoptosis pathways-mediated cardioprotective effects of Shenqi Fuzheng. <i>Journal of Ethnopharmacology</i> , 2018, 227, 155-165.	2.0	28
8462	Zearalenone exposure elevated the expression of tumorigenesis genes in mouse ovarian granulosa cells. <i>Toxicology and Applied Pharmacology</i> , 2018, 356, 191-203.	1.3	29
8463	<i>In Vitro</i> Reconstitution of the Remaining Steps in Ovosulfonolipin A Biosynthesis: C-S Lyase and Methyltransferase Reactions. <i>Organic Letters</i> , 2018, 20, 5427-5430.	2.4	26
8464	An analysis of aging-related genes derived from the Genotype-Tissue Expression project (GTEx). <i>Cell Death Discovery</i> , 2018, 4, 26.	2.0	30
8465	Microbial Community Composition Reveals Spatial Variation and Distinctive Core Microbiome of the Weaver Ant <i>Oecophylla smaragdina</i> in Malaysia. <i>Scientific Reports</i> , 2018, 8, 10777.	1.6	22
8466	CBP and P300 regulate distinct gene networks required for human primary myoblast differentiation and muscle integrity. <i>Scientific Reports</i> , 2018, 8, 12629.	1.6	39
8467	Incorporating molecular-based functional and co-occurrence network properties into benthic marine impact assessments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	22
8468	Prediction of key genes and pathways involved in trastuzumab-resistant gastric cancer. <i>World Journal of Surgical Oncology</i> , 2018, 16, 174.	0.8	20
8469	Before platelets: the production of platelet-activating factor during growth and stress in a basal marine organism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181307.	1.2	20
8470	NF- $\kappa$ B inhibition rescues cardiac function by remodeling calcium genes in a Duchenne muscular dystrophy model. <i>Nature Communications</i> , 2018, 9, 3431.	5.8	35

#	ARTICLE	IF	CITATIONS
8471	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. <i>Scientific Reports</i> , 2018, 8, 12727.	1.6	141
8472	Host-parasite interaction: changes in human placental gene expression induced by <i>Trypanosoma cruzi</i> . <i>Parasites and Vectors</i> , 2018, 11, 479.	1.0	32
8473	Analysis of the miRNA and mRNA involved in osteogenesis of adipose-derived mesenchymal stem cells. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1111-1120.	0.8	22
8474	RNA sequencing and bioinformatics analysis of the long noncoding RNA-mRNA network in colorectal cancer. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9957-9966.	1.2	16
8475	<i>In silico</i> identification and characterization of sensory motifs in the transcriptional regulators of the ArsR-SmtB family. <i>Metallomics</i> , 2018, 10, 1476-1500.	1.0	14
8476	Disease gene identification by walking on multilayer heterogeneous networks. , 2018, , .		0
8477	Three-lncRNA signature is a potential prognostic biomarker for pancreatic adenocarcinoma. <i>Oncotarget</i> , 2018, 9, 24248-24259.	0.8	30
8478	Across-Experiment Transcriptomics of Sheep Rumen Identifies Expression of Lipid/Oxo-Acid Metabolism and Muscle Cell Junction Genes Associated With Variation in Methane-Related Phenotypes. <i>Frontiers in Genetics</i> , 2018, 9, 330.	1.1	13
8479	Integrated proteomic and phosphoproteomic analyses of cisplatin-sensitive and resistant bladder cancer cells reveal CDK2 network as a key therapeutic target. <i>Cancer Letters</i> , 2018, 437, 1-12.	3.2	21
8480	Systematic Identification and Analysis of Lysine Succinylation in Strawberry Stigmata. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 13310-13320.	2.4	14
8481	Evolutionary, structural and expression analysis of core genes involved in starch synthesis. <i>Scientific Reports</i> , 2018, 8, 12736.	1.6	70
8482	TGF- $\beta$ -mediated enhancement of T <sub>H</sub> 17 cell generation is inhibited by bone morphogenetic protein receptor 1 signaling. <i>Science Signaling</i> , 2018, 11, .	1.6	15
8483	Creation of Individual Scientific Concept-Centered Semantic Maps Based on Automated Text-Mining Analysis of PubMed. <i>Advances in Bioinformatics</i> , 2018, 2018, 1-10.	5.7	12
8484	Landscape of transcription and long non-coding RNAs reveals new insights into the inflammatory and fibrotic response following ventilator-induced lung injury. <i>Respiratory Research</i> , 2018, 19, 122.	1.4	14
8485	Decoding methylation patterns in ovarian cancer using publicly available Next-Gen sequencing data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2018, 7, 1.	1.2	5
8486	Identification of Skt11-regulated genes in chondrocytes by integrated bioinformatics analysis. <i>Gene</i> , 2018, 677, 340-348.	1.0	9
8487	Comprehensive and in-depth analysis of microRNA and mRNA expression profile in salivary adenoid cystic carcinoma. <i>Gene</i> , 2018, 678, 349-360.	1.0	12
8488	Circular RNA alterations in the <i>Bombyx mori</i> midgut following <i>B. mori</i> nucleopolyhedrovirus infection. <i>Molecular Immunology</i> , 2018, 101, 461-470.	1.0	26

#	ARTICLE	IF	CITATIONS
8489	Targeted Isolation of Neuroprotective Dicoumaroyl Neolignans and Lignans from <i>Sageretia theezans</i> Using <i>in Silico</i> Molecular Network Annotation Propagation-Based Dereplication. <i>Journal of Natural Products</i> , 2018, 81, 1819-1828.	1.5	44
8490	Pathogenic genes related to the progression of actinic keratoses to cutaneous squamous cell carcinoma. <i>International Journal of Dermatology</i> , 2018, 57, 1208-1217.	0.5	16
8491	Integration of Gene Expression Profile Data to Screen and Verify Hub Genes Involved in Osteoarthritis. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	22
8492	SILGGM: An extensive R package for efficient statistical inference in large-scale gene networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006369.	1.5	33
8493	Identification of prognostic risk factors for esophageal adenocarcinoma using bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 4327-4337.	1.0	17
8494	Rhamnelloides A and B, 7-Phenylpentaene Fatty Acid Amide Diglycosides from the Fruits of <i>Rhamnella franguloides</i> . <i>Molecules</i> , 2018, 23, 752.	1.7	3
8495	A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project. <i>Journal of Proteome Research</i> , 2018, 17, 4345-4357.	1.8	7
8496	Influence of Temperature on the Bacterial Community in Substrate and Extracellular Enzyme Activity of <i>Auricularia cornea</i> . <i>Mycobiology</i> , 2018, 46, 224-235.	0.6	7
8497	Comprehensive evaluation of coding region point mutations in microsatellite-unstable colorectal cancer. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	10
8498	The transcription and expression profile of p53 N236S mutant reveals new aspects of gain of function for mutant p53. <i>FEBS Letters</i> , 2018, 592, 3183-3197.	1.3	5
8499	Cranberry-derived proanthocyanidins induce a differential transcriptomic response within <i>Candida albicans</i> urinary biofilms. <i>PLoS ONE</i> , 2018, 13, e0201969.	1.1	3
8500	Zearalenone Exposure Enhanced the Expression of Tumorigenesis Genes in Donkey Granulosa Cells via the PTEN/PI3K/AKT Signaling Pathway. <i>Frontiers in Genetics</i> , 2018, 9, 293.	1.1	16
8501	Molecular profiles of tumor contrast enhancement: A radiogenomic analysis in anaplastic gliomas. <i>Cancer Medicine</i> , 2018, 7, 4273-4283.	1.3	9
8502	System Pharmacology-Based Strategy to Decode the Synergistic Mechanism of Zhi-zhu Wan for Functional Dyspepsia. <i>Frontiers in Pharmacology</i> , 2018, 9, 841.	1.6	49
8503	Identification of Antifungal Targets Based on Computer Modeling. <i>Journal of Fungi (Basel)</i> , 2018, 4, 1010.	1.5	12
8504	Competing endogenous RNA analysis reveals the regulatory potency of circRNA_036186 in HNSCC. <i>International Journal of Oncology</i> , 2018, 53, 1529-1543.	1.4	11
8505	Associations of Circulating Extracellular RNAs With Myocardial Remodeling and Heart Failure. <i>JAMA Cardiology</i> , 2018, 3, 871.	3.0	33
8506	Linking microbial co-occurrences to soil ecological processes across a woodland-grassland ecotone. <i>Ecology and Evolution</i> , 2018, 8, 8217-8230.	0.8	38

#	ARTICLE	IF	CITATIONS
8507	Induced Mutation Proves a Potential Target for TB Therapy: A Molecular Dynamics Study on LprG. <i>Cell Biochemistry and Biophysics</i> , 2018, 76, 345-356.	0.9	32
8508	Identification of Critical Genes and miRNAs Associated with the Development of Parkinson's Disease. <i>Journal of Molecular Neuroscience</i> , 2018, 65, 527-535.	1.1	12
8509	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. <i>EBioMedicine</i> , 2018, 34, 171-181.	2.7	32
8510	Insights into the structure and dynamics of lysyl oxidase propeptide, a flexible protein with numerous partners. <i>Scientific Reports</i> , 2018, 8, 11768.	1.6	39
8511	Temporal Proteomic Analysis of Pancreatic $\beta$ -Cells in Response to Lipotoxicity and Glucolipotoxicity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2119-2131.	2.5	25
8512	Transcriptome-referenced association study of clove shape traits in garlic. <i>DNA Research</i> , 2018, 25, 587-596.	1.5	31
8513	Identification of nine novel loci related to hematological traits in a Japanese population. <i>Physiological Genomics</i> , 2018, 50, 758-769.	1.0	5
8514	Dissecting LncRNA Roles in Renal Cell Carcinoma Metastasis and Characterizing Genomic Heterogeneity by Single-Cell RNA-seq. <i>Molecular Cancer Research</i> , 2018, 16, 1879-1888.	1.5	21
8515	Identification of a G2-like transcription factor, OsPHL3, functions as a negative regulator of flowering in rice by co-expression and reverse genetic analysis. <i>BMC Plant Biology</i> , 2018, 18, 157.	1.6	15
8516	GraphHi-C: graph-based visualization of Hi-C datasets. <i>BMC Research Notes</i> , 2018, 11, 418.	0.6	8
8517	Network analysis of inflammatory responses to sepsis by neutrophils and peripheral blood mononuclear cells. <i>PLoS ONE</i> , 2018, 13, e0201674.	1.1	22
8518	Gene network variation and alternative paths to convergent evolution in turtles. <i>Evolution &amp; Development</i> , 2018, 20, 172-185.	1.1	7
8519	Time-resolved proteome profiling of normal lung development. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L11-L24.	1.3	25
8520	Identification of Potential Prognostic Long Non-Coding RNA Biomarkers for Predicting Survival in Patients with Hepatocellular Carcinoma. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1854-1869.	1.1	37
8521	Genome-Wide Analysis of Prognostic lncRNAs, miRNAs, and mRNAs Forming a Competing Endogenous RNA Network in Hepatocellular Carcinoma. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1953-1967.	1.1	71
8522	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. <i>Microbiome</i> , 2018, 6, 138.	4.9	63
8523	Brain region-dependent gene networks associated with selective breeding for increased voluntary wheel-running behavior. <i>PLoS ONE</i> , 2018, 13, e0201773.	1.1	13
8524	Modeling Corticosteroid Pharmacogenomics and Proteomics in Rat Liver. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2018, 367, 168-183.	1.3	10



#	ARTICLE	IF	CITATIONS
8525	JQ1 is a potential therapeutic option for COPD patients with agrin overexpression. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 314, L690-L694.	1.3	4
8526	Genome-wide Identification and Characterization of Enhancers Across 10 Human Tissues. <i>International Journal of Biological Sciences</i> , 2018, 14, 1321-1332.	2.6	22
8527	A comprehensive analysis of <i>Candida albicans</i> phosphoproteome reveals dynamic changes in phosphoprotein abundance during hyphal morphogenesis. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9731-9743.	1.7	6
8528	Bioinformatics analysis of microarray data to reveal the pathogenesis of diffuse intrinsic pontine glioma. <i>Biological Research</i> , 2018, 51, 26.	1.5	23
8529	Circular RNA architecture and differentiation during leaf bud to young leaf development in tea ( <i>Camellia sinensis</i> ). <i>Planta</i> , 2018, 248, 1417-1429.	1.6	71
8530	In vitro study on role of ßF protein in avian reovirus pathogenesis. <i>Oncotarget</i> , 2018, 9, 19569-19583.	0.8	2
8531	Mutation of the Surface Layer Protein SlpB Has Pleiotropic Effects in the Probiotic <i>Propionibacterium freudenreichii</i> CIRM-BIA 129. <i>Frontiers in Microbiology</i> , 2018, 9, 1807.	1.5	10
8532	Molecular Networking-Based Metabolome and Bioactivity Analyses of Marine-Adapted Fungi Co-cultivated With Phytopathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 2072.	1.5	56
8533	NRF1 motif sequence-enriched genes involved in ER/PR +ve HER2 +ve breast cancer signaling pathways. <i>Breast Cancer Research and Treatment</i> , 2018, 172, 469-485.	1.1	18
8534	Effects of Anti-Integrin Treatment With Vedolizumab on Immune Pathways and Cytokines in Inflammatory Bowel Diseases. <i>Frontiers in Immunology</i> , 2018, 9, 1700.	2.2	38
8535	High Performance of Photosynthesis and Osmotic Adjustment Are Associated With Salt Tolerance Ability in Rice Carrying Drought Tolerance QTL: Physiological and Co-expression Network Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 1135.	1.7	58
8536	Ammonia determines transcriptional profile of microorganisms in anaerobic digestion. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 770-776.	0.8	18
8537	Time-resolved microbial guild responses to tidal cycling in a coastal acid-sulfate system. <i>Environmental Chemistry</i> , 2018, 15, 2.	0.7	5
8538	Development of an Integrated Visualization System for Phenotypic Character Networks. , 2018, , .		2
8539	Transcriptome response of the foundation plant <i>Spartina alterniflora</i> to the Deepwater Horizon oil spill. <i>Molecular Ecology</i> , 2018, 27, 2986-3000.	2.0	17
8540	RNA-seq analysis of aberrantly expressed long non-coding RNAs and mRNAs in a mouse model of ventilator-induced lung injury. <i>Molecular Medicine Reports</i> , 2018, 18, 882-892.	1.1	9
8541	Synthetic Lethality-based Identification of Targets for Anticancer Drugs in the Human Signaling Network. <i>Scientific Reports</i> , 2018, 8, 8440.	1.6	23
8542	Genome-Wide Expression Analysis Suggests Hypoxia-Triggered Hyper-Coagulation Leading to Venous Thrombosis at High Altitude. <i>Thrombosis and Haemostasis</i> , 2018, 118, 1279-1295.	1.8	29



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8543	Analysis of Gene Expression Changes in PHA-M Stimulated Lymphocytes – Unraveling PHA Activity as Prerequisite for Dicentric Chromosome Analysis. <i>Radiation Research</i> , 2018, 189, 579.	0.7	3
8544	Predicting protein lysine methylation sites by incorporating single-residue structural features into Chou's pseudo components. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 179, 31-38.	1.8	13
8545	Transcriptomics insights into the genetic regulation of root apical meristem exhaustion and determinate primary root growth in <i>Pachycereus pringlei</i> (Cactaceae). <i>Scientific Reports</i> , 2018, 8, 8529.	1.6	14
8546	Genome-wide screening differential long non-coding RNAs expression profiles discloses its roles involved in OHSS development. <i>Journal of Assisted Reproduction and Genetics</i> , 2018, 35, 1473-1482.	1.2	5
8547	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. <i>Molecular Cell</i> , 2018, 70, 854-867.e9.	4.5	408
8548	Transcriptomic and functional analyses unveil the role of long non-coding RNAs in anthocyanin biosynthesis during sea buckthorn fruit ripening. <i>DNA Research</i> , 2018, 25, 465-476.	1.5	114
8549	Epigenome-associated phenotypic acclimatization to ocean acidification in a reef-building coral. <i>Science Advances</i> , 2018, 4, eaar8028.	4.7	135
8550	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. <i>MSystems</i> , 2018, 3, .	1.7	96
8551	Expanding the horizons of microRNA bioinformatics. <i>Rna</i> , 2018, 24, 1005-1017.	1.6	27
8552	Bioinformatics analysis of microarray data to reveal the pathogenesis of brain ischemia. <i>Molecular Medicine Reports</i> , 2018, 18, 333-341.	1.1	6
8553	Urine metabolic fingerprinting can be used to predict the risk of metritis and highlight the pathobiology of the disease in dairy cows. <i>Metabolomics</i> , 2018, 14, 83.	1.4	22
8554	Genomic characterisation of an international <i>Pseudomonas aeruginosa</i> reference panel indicates that the two major groups draw upon distinct mobile gene pools. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	67
8555	Developmental Origin Governs CD8+ T Cell Fate Decisions during Infection. <i>Cell</i> , 2018, 174, 117-130.e14.	13.5	132
8556	MicroRNA alterations in iPSC-derived dopaminergic neurons from Parkinson disease patients. <i>Neurobiology of Aging</i> , 2018, 69, 283-291.	1.5	55
8557	G1P3 (IFI6), a mitochondrial localised antiapoptotic protein, promotes metastatic potential of breast cancer cells through mtROS. <i>British Journal of Cancer</i> , 2018, 119, 52-64.	2.9	53
8558	Interactions between metal binding viral proteins and human targets as revealed by network-based bioinformatics. <i>Journal of Inorganic Biochemistry</i> , 2018, 186, 157-161.	1.5	22
8560	Durum wheat ears perform better than the flag leaves under water stress: Gene expression and physiological evidence. <i>Environmental and Experimental Botany</i> , 2018, 153, 271-285.	2.0	52
8561	Loss of Trem2 in microglia leads to widespread disruption of cell coexpression networks in mouse brain. <i>Neurobiology of Aging</i> , 2018, 69, 151-166.	1.5	25

#	ARTICLE	IF	CITATIONS
8562	Prediction of novel target genes and pathways involved in bevacizumab-resistant colorectal cancer. PLoS ONE, 2018, 13, e0189582.	1.1	16
8563	A systematic approach to analyze the social determinants of cardiovascular disease. PLoS ONE, 2018, 13, e0190960.	1.1	29
8564	Genotype-by-environment interactions affecting heterosis in maize. PLoS ONE, 2018, 13, e0191321.	1.1	51
8565	Associations between sexual habits, menstrual hygiene practices, demographics and the vaginal microbiome as revealed by Bayesian network analysis. PLoS ONE, 2018, 13, e0191625.	1.1	92
8566	Shared and organism-specific host responses to childhood diarrheal diseases revealed by whole blood transcript profiling. PLoS ONE, 2018, 13, e0192082.	1.1	23
8567	Genome-wide profiling reveals functional diversification of $\hat{\alpha}$ FosB gene targets in the hippocampus of an Alzheimer's disease mouse model. PLoS ONE, 2018, 13, e0192508.	1.1	22
8568	Identification and characterization of microRNAs in the intestinal tissues of sheep ( <i>Ovis aries</i> ). PLoS ONE, 2018, 13, e0193371.	1.1	16
8569	TnSeq of <i>Mycobacterium tuberculosis</i> clinical isolates reveals strain-specific antibiotic liabilities. PLoS Pathogens, 2018, 14, e1006939.	2.1	78
8570	Reduction of antibiotic resistome and integron-integrase genes in laboratory-scale photobioreactors treating municipal wastewater. Water Research, 2018, 142, 363-372.	5.3	24
8571	Extracellular vesicles direct migration by synthesizing and releasing chemotactic signals. Journal of Cell Biology, 2018, 217, 2891-2910.	2.3	54
8572	Detection of multi-dimensional co-exclusion patterns in microbial communities. Bioinformatics, 2018, 34, 3695-3701.	1.8	4
8573	The <i>6xABRE</i> Synthetic Promoter Enables the Spatiotemporal Analysis of ABA-Mediated Transcriptional Regulation. Plant Physiology, 2018, 177, 1650-1665.	2.3	63
8574	Effects of secondary salinisation on macroinvertebrate functional traits in surface mining-contaminated streams, and recovery potential. Science of the Total Environment, 2018, 640-641, 1088-1097.	3.9	11
8575	Diversity, specificity, co-occurrence and hub taxa of the bacterial-fungal pollen microbiome. FEMS Microbiology Ecology, 2018, 94, .	1.3	68
8576	Prediction of Adipose Browning Capacity by Systematic Integration of Transcriptional Profiles. Cell Reports, 2018, 23, 3112-3125.	2.9	57
8577	Bacterial lineages putatively associated with the dissemination of antibiotic resistance genes in a full-scale urban wastewater treatment plant. Environment International, 2018, 118, 179-188.	4.8	93
8578	Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. Lecture Notes in Computer Science, 2018, , 501-513.	1.0	2
8579	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652

#	ARTICLE	IF	CITATIONS
8580	OmicsNet: A web-based tool for creation and visual analysis of biological networks in 3D space. <i>Nucleic Acids Research</i> , 2018, 46, W514-W522.	6.5	126
8581	Identification and analysis of key genes associated with ulcerative colitis based on DNA microarray data. <i>Medicine (United States)</i> , 2018, 97, e10658.	0.4	10
8582	Using Diagrams to Reason About Biological Mechanisms. <i>Lecture Notes in Computer Science</i> , 2018, , 264-279.	1.0	3
8583	Translating molecular advances in Down syndrome and Fragile X syndrome into therapies. <i>European Neuropsychopharmacology</i> , 2018, 28, 675-690.	0.3	14
8584	Differentiation of sow and mouse ovarian granulosa cells exposed to zearalenone in vitro using RNA-seq gene expression. <i>Toxicology and Applied Pharmacology</i> , 2018, 350, 78-90.	1.3	13
8585	Modeling Framework for Biogenic Methane Formation from Coal. <i>Energy &amp; Fuels</i> , 2018, 32, 8453-8461.	2.5	2
8586	Heterogeneity of interactions of microbial communities in regions of Taihu Lake with different nutrient loadings: A network analysis. <i>Scientific Reports</i> , 2018, 8, 8890.	1.6	40
8587	A seven-lncRNA signature predicts overall survival in esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2018, 8, 8823.	1.6	72
8588	Order-disorder transition of intrinsically disordered kinase inducible transactivation domain of CREB. <i>Journal of Chemical Physics</i> , 2018, 148, 225101.	1.2	5
8589	Gene expression profiling in human corticotroph tumours reveals distinct, neuroendocrine profiles. <i>Journal of Neuroendocrinology</i> , 2018, 30, e12628.	1.2	17
8590	A Rich Man, Poor Man Story of <i>S</i> -Adenosylmethionine and Cobalamin Revisited. <i>Annual Review of Biochemistry</i> , 2018, 87, 555-584.	5.0	52
8591	Functional characterization and genomic studies of a novel murine submandibular gland epithelial cell line. <i>PLoS ONE</i> , 2018, 13, e0192775.	1.1	7
8592	StudentViz: A Tool for Visualizing Students' Collaborations in a Social Learning Environment. <i>Lecture Notes in Educational Technology</i> , 2018, , 77-86.	0.5	0
8593	Single-Cell RNA-Seq Reveals Dynamic Early Embryonic-like Programs during Chemical Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 31-45.e7.	5.2	122
8594	Long non-coding RNA expression profile can predict early recurrence in hepatocellular carcinoma after curative resection. <i>Hepatology Research</i> , 2018, 48, 1140-1148.	1.8	56
8595	Stoichiometric balance of protein copy numbers is measurable and functionally significant in a protein-protein interaction network for yeast endocytosis. <i>PLoS Computational Biology</i> , 2018, 14, e1006022.	1.5	17
8596	Obesogenic diets alter metabolism in mice. <i>PLoS ONE</i> , 2018, 13, e0190632.	1.1	59
8597	miRACA: A database for miRNAs associated with cancers and age related disorders (ARD). <i>Frontiers in Biology</i> , 2018, 13, 36-50.	0.7	0

#	ARTICLE	IF	CITATIONS
8598	Dysbiosis in the Gut Bacterial Microbiome of Patients with Uveitis, an Inflammatory Disease of the Eye. Indian Journal of Microbiology, 2018, 58, 457-469.	1.5	118
8599	Circulating MicroRNAs: a Potential Biomarker for Cardiac Damage, Inflammatory Response, and Left Ventricular Function Recovery in Pediatric Viral Myocarditis. Journal of Cardiovascular Translational Research, 2018, 11, 319-328.	1.1	34
8600	Computational Aids for Assessing Bioactivities. , 2018, , 277-300.		4
8601	Isolation of mitotic chromosomes from vertebrate cells and characterization of their proteome by mass spectrometry. Methods in Cell Biology, 2018, 144, 329-348.	0.5	3
8602	FlyXCDBâ€”A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. Journal of Molecular Biology, 2018, 430, 3353-3411.	2.0	13
8603	GeNets: a unified web platform for network-based genomic analyses. Nature Methods, 2018, 15, 543-546.	9.0	62
8604	The Importance of Constraints and Control in Biological Mechanisms: Insights from Cancer Research. Philosophy of Science, 2018, 85, 573-593.	0.5	17
8606	Comparative Proteomics Analysis Reveals Trans Fatty Acid Isomers Activates Different Pathways in Human Umbilical Vein Endothelial Cell. Lipids, 2018, 53, 189-203.	0.7	1
8607	Metabolomic analysis of indolepyruvate decarboxylase pathway derivatives in the rhizobacterium Enterobacter cloacae. Rhizosphere, 2018, 6, 98-111.	1.4	8
8608	Genome wide association study reveals new candidate genes for resistance to nematodes in Creole goat. Small Ruminant Research, 2018, 166, 109-114.	0.6	12
8609	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. Journal of Cell Biology, 2018, 217, 2951-2974.	2.3	35
8610	A census of P. longumâ€™s phytochemicals and their network pharmacological evaluation for identifying novel drug-like molecules against various diseases, with a special focus on neurological disorders. PLoS ONE, 2018, 13, e0191006.	1.1	35
8611	Identification of ASB7 as ER stress responsive gene through a genome wide in silico screening for genes with ERSE. PLoS ONE, 2018, 13, e0194310.	1.1	7
8612	Metagenomic insights into the roles of <i>Proteobacteria</i> in the gastrointestinal microbiomes of healthy dogs and cats. MicrobiologyOpen, 2018, 7, e00677.	1.2	148
8613	A Proteomic Variant Approach (ProVarA) for Personalized Medicine of Inherited and Somatic Disease. Journal of Molecular Biology, 2018, 430, 2951-2973.	2.0	32
8614	Mapping biological process relationships and disease perturbations within a pathway network. Npj Systems Biology and Applications, 2018, 4, 22.	1.4	21
8615	Exploring the multi-drug resistance in Escherichia coli O157:H7 by gene interaction network: A systems biology approach. Genomics, 2019, 111, 958-965.	1.3	54
8616	A Survey of Social Network Analysis Techniques and their Applications to Socially Aware Networking. IEICE Transactions on Communications, 2019, E102.B, 17-39.	0.4	16

#	ARTICLE	IF	CITATIONS
8617	Gene co-expression network analysis for identifying genetic markers in Parkinson's disease - a three-way comparative approach. <i>Genomics</i> , 2019, 111, 819-830.	1.3	37
8618	A complex of the ubiquitin ligase TRIM32 and the deubiquitinase USP7 balances the level of c-Myc ubiquitination and thereby determines neural stem cell fate specification. <i>Cell Death and Differentiation</i> , 2019, 26, 728-740.	5.0	60
8619	Identification of key proteins and lncRNAs in hypertrophic cardiomyopathy by integrated network analysis. <i>Archives of Medical Science</i> , 2019, 15, 484-497.	0.4	14
8620	Potential role of RAB6C-AS1 long noncoding RNA in different cancers. <i>Journal of Cellular Physiology</i> , 2019, 234, 891-903.	2.0	12
8621	A brief history of bioinformatics. <i>Briefings in Bioinformatics</i> , 2019, 20, 1981-1996.	3.2	147
8622	Nine hub genes as the potential indicator for the clinical outcome of diabetic nephropathy. <i>Journal of Cellular Physiology</i> , 2019, 234, 1461-1468.	2.0	8
8623	Time based versus strain based myocardial performance indices in hypertrophic cardiomyopathy, the merging role of left atrial strain. <i>European Heart Journal Cardiovascular Imaging</i> , 2019, 20, 334-342.	0.5	12
8624	Effusion: prediction of protein function from sequence similarity networks. <i>Bioinformatics</i> , 2019, 35, 442-451.	1.8	12
8625	High-depth transcriptomic profiling reveals the temporal gene signature of human mesenchymal stem cells during chondrogenesis. <i>FASEB Journal</i> , 2019, 33, 358-372.	0.2	43
8626	Integration of miRNA weighted gene co-expression network and miRNA-mRNA co-expression analyses reveals potential regulatory functions of miRNAs in calf rumen development. <i>Genomics</i> , 2019, 111, 849-859.	1.3	25
8627	Comparative mRNA and miRNA expression in European mouflon ( <i>Ovis musimon</i> ) and sheep ( <i>Ovis aries</i> ) provides novel insights into the genetic mechanisms for female reproductive success. <i>Heredity</i> , 2019, 122, 172-186.	1.2	21
8628	Structural insights into pharmacophore-assisted <i>in silico</i> identification of protein-protein interaction inhibitors for inhibition of human toll-like receptor 4 myeloid differentiation factor-2 (hTLR4~MD-2) complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1968-1991.	2.0	12
8629	Variation in methane production over time and physiological state in sheep. <i>Animal Production Science</i> , 2019, 59, 441.	0.6	11
8630	Computational simulations assessment of mutations impact on streptokinase (SK) from a group G <i>Streptococci</i> with enhanced activity - insights into the functional roles of structural dynamics flexibility of SK and stabilization of SK-plasmin catalytic complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1944-1955.	2.0	6
8631	Proteomics Mass Spectrometry Data Analysis Tools. , 2019, , 84-95.		3
8632	Integrative Bioinformatics. , 2019, , 1092-1098.		0
8633	Biological Pathway Data Formats and Standards. , 2019, , 1063-1066.		0
8634	Biological Pathway Analysis. , 2019, , 1067-1070.		0

#	ARTICLE	IF	CITATIONS
8635	Severe Obstructive Sleep Apnea Is Associated with Alterations in the Nasal Microbiome and an Increase in Inflammation. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 99-109.	2.5	51
8636	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
8637	A proteomic insight into the MSP1 and flg22 induced signaling in <i>Oryza sativa</i> leaves. <i>Journal of Proteomics</i> , 2019, 196, 120-130.	1.2	31
8638	Celiac disease gene expression data can be used to classify biopsies along the Marsh score severity scale. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019, 34, 169-177.	1.4	10
8639	Transcriptome mining of non-BRCA1/A2 and BRCA1/A2 familial breast cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 575-583.	1.2	5
8640	Gene regulatory networks for lignin biosynthesis in switchgrass ( <i>Panicum virgatum</i> ). <i>Plant Biotechnology Journal</i> , 2019, 17, 580-593.	4.1	96
8641	Identification of a five-gene signature with prognostic value in colorectal cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 3829-3836.	2.0	22
8642	A Plasma-Derived Protein-Metabolite Multiplexed Panel for Early-Stage Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 372-379.	3.0	79
8643	Characteristics of microbial community indicate anthropogenic impact on the sediments along the Yangtze Estuary and its coastal area, China. <i>Science of the Total Environment</i> , 2019, 648, 306-314.	3.9	70
8644	A New Computational Approach to Identify Essential Genes in Bacterial Organisms Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , 2019, , 67-79.	0.5	2
8645	Metabolomic profiling reveals that natural biodiversity surrounding a banana crop may positively influence the nutritional/sensorial profile of ripe fruits. <i>Food Research International</i> , 2019, 124, 165-174.	2.9	13
8646	Computational resources associating diseases with genotypes, phenotypes and exposures. <i>Briefings in Bioinformatics</i> , 2019, 20, 2098-2115.	3.2	27
8647	Computational Pipelines and Workflows in Bioinformatics. , 2019, , 113-134.		0
8648	Quantitative proteomics using tandem mass tags in relation to the acute phase protein response in chicken challenged with <i>Escherichia coli</i> lipopolysaccharide endotoxin. <i>Journal of Proteomics</i> , 2019, 192, 64-77.	1.2	52
8649	The maternal-to-zygotic transition in bovine in vitro-fertilized embryos is associated with marked changes in small non-coding RNAs. <i>Biology of Reproduction</i> , 2019, 100, 331-350.	1.2	19
8650	Comprehensive review of hepatitis B virus-associated hepatocellular carcinoma research through text mining and big data analytics. <i>Biological Reviews</i> , 2019, 94, 353-367.	4.7	44
8651	Random walk with restart on multiplex and heterogeneous biological networks. <i>Bioinformatics</i> , 2019, 35, 497-505.	1.8	183
8652	MoIdentify: phenotype-driven module identification in metabolomics networks at different resolutions. <i>Bioinformatics</i> , 2019, 35, 532-534.	1.8	13

#	ARTICLE	IF	CITATIONS
8653	Transcriptome-wide association study and eQTL analysis to assess the genetic basis of bulb-yield traits in garlic ( <i>Allium sativum</i> ). <i>BMC Genomics</i> , 2019, 20, 657.	1.2	7
8654	Using Large Datasets to Understand Nanotechnology. <i>Advanced Materials</i> , 2019, 31, e1902798.	11.1	45
8655	A tissue-specific, injectable acellular gel for the treatment of chronic vocal fold scarring. <i>Acta Biomaterialia</i> , 2019, 99, 141-153.	4.1	13
8656	Genome-wide characterization of the AP2/ERF gene family in radish ( <i>Raphanus sativus</i> L.): Unveiling evolution and patterns in response to abiotic stresses. <i>Gene</i> , 2019, 718, 144048.	1.0	39
8657	Systems biology studies in <i>Pseudomonas aeruginosa</i> PA01 to understand their role in biofilm formation and multidrug efflux pumps. <i>Microbial Pathogenesis</i> , 2019, 136, 103668.	1.3	36
8658	The endosomal sorting adaptor HD-PTP is required for ephrin-B:EphB signalling in cellular collapse and spinal motor axon guidance. <i>Scientific Reports</i> , 2019, 9, 11945.	1.6	17
8659	A Map of the microRNA Regulatory Networks Identified by Experimentally Validated microRNA-Target Interactions in Five Domestic Animals: Cattle, Pig, Sheep, Dog, and Chicken. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 448-456.	1.0	5
8660	Multi-omics Analyses Reveal Synergistic Carbohydrate Metabolism in <i>Streptococcus mutans</i> - <i>Candida albicans</i> Mixed-Species Biofilms. <i>Infection and Immunity</i> , 2019, 87, .	1.0	71
8661	Integration of Gene Expression Profile Data to Verify Hub Genes of Patients with Stanford A Aortic Dissection. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	14
8662	Reproducibility of novel immune-inflammatory biomarkers over 4 months: an analysis with repeated measures design. <i>Biomarkers in Medicine</i> , 2019, 13, 639-648.	0.6	2
8663	Analysis of chickpea gene co-expression networks and pathways during heavy metal stress. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	2
8664	Molecular architecture of lineage allocation and tissue organization in early mouse embryo. <i>Nature</i> , 2019, 572, 528-532.	13.7	163
8665	Identification of CXCL13 as a potential biomarker in clear cell renal cell carcinoma via comprehensive bioinformatics analysis. <i>Biomedicine and Pharmacotherapy</i> , 2019, 118, 109264.	2.5	30
8666	Landscape of the Plasmodium Interactome Reveals Both Conserved and Species-Specific Functionality. <i>Cell Reports</i> , 2019, 28, 1635-1647.e5.	2.9	49
8667	Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea ( <i>Camellia sinensis</i> ) plantation soils. <i>Soil and Tillage Research</i> , 2019, 195, 104356.	2.6	117
8668	Potential therapeutic drugs for ischemic stroke based on bioinformatics analysis. <i>International Journal of Neuroscience</i> , 2019, 129, 1098-1102.	0.8	3
8669	Impact of Anthropogenic Organic Matter on the Distribution Patterns of Sediment Microbial Community from the Yangtze River, China. <i>Geomicrobiology Journal</i> , 2019, 36, 881-893.	1.0	9
8670	The Oral Mouse Microbiome Promotes Tumorigenesis in Oral Squamous Cell Carcinoma. <i>MSystems</i> , 2019, 4, .	1.7	50



#	ARTICLE	IF	CITATIONS
8671	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves' gastrointestinal microbiota. <i>PLoS ONE</i> , 2019, 14, e0220554.	1.1	61
8672	Altered expression of miRNAs and mRNAs reveals the potential regulatory role of miRNAs in the developmental process of early weaned goats. <i>PLoS ONE</i> , 2019, 14, e0220907.	1.1	21
8673	Small RNA profiling in <i>Pinus pinaster</i> reveals the transcriptome of developing seeds and highlights differences between zygotic and somatic embryos. <i>Scientific Reports</i> , 2019, 9, 11327.	1.6	28
8674	Identification of Fungal Communities Within the Tar Spot Complex of Corn in Michigan via Next-Generation Sequencing. <i>Phytobiomes Journal</i> , 2019, 3, 235-243.	1.4	28
8675	Long Non-Coding RNA Expression Levels Modulate Cell-Type-Specific Splicing Patterns by Altering Their Interaction Landscape with RNA-Binding Proteins. <i>Genes</i> , 2019, 10, 593.	1.0	16
8676	Remodeling of the <i>Caenorhabditis elegans</i> non-coding RNA transcriptome by heat shock. <i>Nucleic Acids Research</i> , 2019, 47, 9829-9841.	6.5	22
8677	A Long Noncoding RNA (lncRNA)-Associated Competing Endogenous RNA (ceRNA) Network Identifies Eight lncRNA Biomarkers in Patients with Osteoarthritis of the Knee. <i>Medical Science Monitor</i> , 2019, 25, 2058-2065.	0.5	39
8678	Gene Modules Co-regulated with Biosynthetic Gene Clusters for Allelopathy between Rice and Barnyardgrass. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3846.	1.8	9
8679	Cassava AGPase genes and their encoded proteins are different from those of other plants. <i>Planta</i> , 2019, 250, 1621-1635.	1.6	8
8680	Age- and Nicotine-Associated Gene Expression Changes in the Hippocampus of APP/PS1 Mice. <i>Journal of Molecular Neuroscience</i> , 2019, 69, 608-622.	1.1	12
8681	Crystal structures of AztD provide mechanistic insights into direct zinc transfer between proteins. <i>Communications Biology</i> , 2019, 2, 308.	2.0	7
8682	Integrative Systems Biology Resources and Approaches in Disease Analytics. , 0, , .		1
8683	A Systematic View Exploring the Role of Chloroplasts in Plant Abiotic Stress Responses. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	14
8684	Genome-wide identification, characterization, and expression profiling of SPX gene family in wheat. <i>International Journal of Biological Macromolecules</i> , 2019, 140, 17-32.	3.6	31
8685	Gene Coexpression Networks Reveal Key Drivers of Flavonoid Variation in Eleven Tea Cultivars ( <i>Camellia sinensis</i> ). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9967-9978.	2.4	20
8686	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019, 10, 3640.	5.8	75
8687	Systematic large-scale meta-analysis identifies miRNA-429/200a/b and miRNA-141/200c clusters as biomarkers for necrotizing enterocolitis in newborn. <i>Bioscience Reports</i> , 2019, 39, .	1.1	17
8688	Investigation into the underlying regulatory mechanisms shaping inflorescence architecture in <i>Chenopodium quinoa</i> . <i>BMC Genomics</i> , 2019, 20, 658.	1.2	16

#	ARTICLE	IF	CITATIONS
8689	Genome-wide analysis of long noncoding RNAs, microRNAs, and mRNAs forming a competing endogenous RNA network in repeated implantation failure. <i>Gene</i> , 2019, 720, 144056.	1.0	32
8690	An Insight Into the Molecular Mechanism of Berberine Towards Multiple Cancer Types Through Systems Pharmacology. <i>Frontiers in Pharmacology</i> , 2019, 10, 857.	1.6	34
8691	Identification and expression analysis of the GDSL esterase/lipase family genes, and the characterization of <i>SaGLIP8</i> in <i>Sedum alfredii</i> Hance under cadmium stress. <i>PeerJ</i> , 2019, 7, e6741.	0.9	18
8692	Co-expression network analysis identified key genes in association with mesenchymal stem cell osteogenic differentiation. <i>Cell and Tissue Research</i> , 2019, 378, 513-529.	1.5	16
8693	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	2.4	34
8694	Possible epigenetic regulatory effect of dysregulated circular RNAs in Alzheimer's disease model. <i>Scientific Reports</i> , 2019, 9, 11956.	1.6	16
8695	The Methodological Trends of Traditional Herbal Medicine Employing Network Pharmacology. <i>Biomolecules</i> , 2019, 9, 362.	1.8	108
8696	Identification of Key Genes and Pathways in Pancreatic Cancer Gene Expression Profile by Integrative Analysis. <i>Genes</i> , 2019, 10, 612.	1.0	22
8697	Exploring Chemical and Biological Space of Terpenoids. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3667-3678.	2.5	19
8698	Transcriptional alterations reveal <i>Bacillus amyloliquefaciens</i> -rice cooperation under salt stress. <i>Scientific Reports</i> , 2019, 9, 11912.	1.6	84
8699	Differential coexpression networks in bronchiolitis and emphysema phenotypes reveal heterogeneous mechanisms of chronic obstructive pulmonary disease. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 6989-6999.	1.6	14
8700	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
8701	Deciphering rhizosphere microbiome assembly of wild and modern common bean ( <i>Phaseolus vulgaris</i> ) in native and agricultural soils from Colombia. <i>Microbiome</i> , 2019, 7, 114.	4.9	140
8702	Identification and potential mechanisms of a 4-lncRNA signature that predicts prognosis in patients with laryngeal cancer. <i>Human Genomics</i> , 2019, 13, 36.	1.4	54
8703	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. <i>Cancer Cell</i> , 2019, 36, 194-209.e9.	7.7	184
8704	Comparative analysis of the gut microbial communities between two dominant amphipods from the Challenger Deep, Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 151, 103081.	0.6	16
8705	Moving from Empirical to Rational Vaccine Design in the "Omics" Era. <i>Vaccines</i> , 2019, 7, 89.	2.1	19
8706	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. <i>Genome Research</i> , 2019, 29, 1415-1428.	2.4	12

#	ARTICLE	IF	CITATIONS
8707	Novel Compound-Target Interactions Prediction for the Herbal Formula Hua-Yu-Qiang-Shen-Tong-Bi-Fang. <i>Chemical and Pharmaceutical Bulletin</i> , 2019, 67, 778-785.	0.6	10
8708	The Construction and Comprehensive Analysis of ceRNA Networks and Tumor-Infiltrating Immune Cells in Bone Metastatic Melanoma. <i>Frontiers in Genetics</i> , 2019, 10, 828.	1.1	26
8709	Integrated Analysis of miRNA and mRNA Endorses a Twenty miRNAs Signature for Colorectal Carcinoma. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4067.	1.8	32
8710	Characteristic genes in THP-1 derived macrophages infected with <i>Mycobacterium tuberculosis</i> H37Rv strain identified by integrating bioinformatics methods. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1243-1254.	1.8	7
8711	Identification of candidate genes and miRNAs associated with neuropathic pain induced by spared nerve injury. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1205-1218.	1.8	9
8712	TcMYB1, TcMYB4, and TcMYB8 participate in the regulation of lignan biosynthesis in <i>Taiwania cryptomerioides</i> Hayata. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	3
8713	A Species-Wide Inventory of NLR Genes and Alleles in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2019, 178, 1260-1272.e14.	13.5	265
8714	Structural insights into the binding mechanism of <i>Plasmodium falciparum</i> exported Hsp40-Hsp70 chaperone pair. <i>Computational Biology and Chemistry</i> , 2019, 83, 107099.	1.1	10
8715	The freeze-dried extracts of <i>Rotheca myricoides</i> (Hochst.) Steane & Mabb possess hypoglycemic, hypolipidemic and hypoinsulinemic on type 2 diabetes rat model. <i>Journal of Ethnopharmacology</i> , 2019, 244, 112077.	2.0	8
8716	Inference of the gene regulatory network acting downstream of <i>CROWN ROOTLESS1</i> in rice reveals a regulatory cascade linking genes involved in auxin signaling, crown root initiation, and root meristem specification and maintenance. <i>Plant Journal</i> , 2019, 100, 954-968.	2.8	13
8717	Identification of differentially expressed genes in hip cartilage with femoral head necrosis, based on genome-wide expression profiles. <i>Molecular Medicine Reports</i> , 2019, 20, 2073-2082.	1.1	2
8718	Transcriptome-based Discovery of AP2/ERF Transcription Factors and Expression Profiles Under Herbivore Stress Conditions in Bamboo ( <i>Bambusa emeiensis</i> ). <i>Journal of Plant Biology</i> , 2019, 62, 297-306.	0.9	6
8719	The cancer-associated, gain-of-function TP53 variant P152Lp53 activates multiple signaling pathways implicated in tumorigenesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 14081-14095.	1.6	5
8720	An integrated respiratory microbial gene catalogue to better understand the microbial aetiology of <i>Mycoplasma pneumoniae</i> pneumonia. <i>GigaScience</i> , 2019, 8, .	3.3	16
8721	Genome-wide association analysis of nutrient traits in the oyster <i>Crassostrea gigas</i> : genetic effect and interaction network. <i>BMC Genomics</i> , 2019, 20, 625.	1.2	31
8722	CNS cell type-specific gene profiling of P301S tau transgenic mice identifies genes dysregulated by progressive tau accumulation. <i>Journal of Biological Chemistry</i> , 2019, 294, 14149-14162.	1.6	10
8723	Key Genes Involved in Diabetic Nephropathy Investigated by Microarray Analysis. <i>Journal of Computational Biology</i> , 2019, 26, 1438-1447.	0.8	9
8724	In Silico Detection and Characterization of microRNAs and Their Target Genes in microRNA Microarray Datasets from Patients with Systemic Sclerosis-Interstitial Lung Disease. <i>DNA and Cell Biology</i> , 2019, 38, 933-944.	0.9	8

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8725	Competing Endogenous RNA Networks Underlying Anatomical and Physiological Characteristics of Poplar Wood in Acclimation to Low Nitrogen Availability. <i>Plant and Cell Physiology</i> , 2019, 60, 2478-2495.	1.5	26
8726	Evidence for shared molecular pathways of dysregulated decidualization in preeclampsia and endometrial disorders revealed by microarray data integration. <i>FASEB Journal</i> , 2019, 33, 11682-11695.	0.2	33
8727	Identification of long noncoding RNA RP11-169F17.1 and RP11-669N7.2 as novel prognostic biomarkers of stomach adenocarcinoma based on integrated bioinformatics analysis. <i>Epigenomics</i> , 2019, 11, 1307-1321.	1.0	12
8728	Comprehensive analysis of circRNA expression pattern and circRNA-mRNA-miRNA network in <i>Ctenopharyngodon idellus</i> kidney (CIK) cells after grass carp reovirus (GCRV) infection. <i>Aquaculture</i> , 2019, 512, 734349.	1.7	17
8729	A Genome-wide Functional Signature Ontology Map and Applications to Natural Product Mechanism of Action Discovery. <i>Cell Chemical Biology</i> , 2019, 26, 1380-1392.e6.	2.5	8
8730	Transcriptome Analysis Reveals New Insights into <i>MdBAK1</i> -Mediated Plant Growth in <i>Malus domestica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9757-9771.	2.4	9
8731	The transcription factor TCF-1 enforces commitment to the innate lymphoid cell lineage. <i>Nature Immunology</i> , 2019, 20, 1150-1160.	7.0	81
8732	(5R)-5-Hydroxytryptolide (LLDT-8) induces substantial epigenetic mediated immune response network changes in fibroblast-like synoviocytes from rheumatoid arthritis patients. <i>Scientific Reports</i> , 2019, 9, 11155.	1.6	16
8733	Fully Distributed AC Optimal Power Flow. <i>IEEE Access</i> , 2019, 7, 97594-97603.	2.6	10
8734	Bioinformatic validation identifies candidate key genes in diffuse large-B cell lymphoma. <i>Personalized Medicine</i> , 2019, 16, 313-323.	0.8	7
8735	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	1.3	15
8736	LOS2 gene plays a potential role in barley ( <i>Hordeum vulgare</i> L.) salinity tolerance as a hub gene. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	8
8737	Kaempferol attenuates neuroinflammation and blood brain barrier dysfunction to improve neurological deficits in cerebral ischemia/reperfusion rats. <i>Brain Research</i> , 2019, 1722, 146361.	1.1	69
8738	A systems pharmacology approach to investigate the mechanism of Oryeong-san formula for the treatment of hypertension. <i>Journal of Ethnopharmacology</i> , 2019, 244, 112129.	2.0	38
8739	Evaluating testosterone as a phenotypic integrator: From tissues to individuals to species. <i>Molecular and Cellular Endocrinology</i> , 2019, 496, 110531.	1.6	48
8740	Tempo of gene regulation in wild and cultivated <i>Vitis</i> species shows coordination between cold deacclimation and budbreak. <i>Plant Science</i> , 2019, 287, 110178.	1.7	27
8741	The impact of genetics and environment on the polar fraction metabolome of commercial <i>Brassica napus</i> seeds: a multi-site study. <i>Seed Science Research</i> , 2019, 29, 167-178.	0.8	4
8742	Cancerous inhibitor of protein phosphatase 2A (CIP2A) modifies energy metabolism via 5 <sup>α</sup> -AMP-activated protein kinase signalling in malignant cells. <i>Biochemical Journal</i> , 2019, 476, 2255-2269.	1.7	6

#	ARTICLE	IF	CITATIONS
8743	Efficacy of leflunomide combined with ligustrazine in the treatment of rheumatoid arthritis: prediction with network pharmacology and validation in a clinical trial. <i>Chinese Medicine</i> , 2019, 14, 26.	1.6	15
8744	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	3.8	66
8745	Circular RNA expression profiles in cisplatin-induced acute kidney injury in mice. <i>Epigenomics</i> , 2019, 11, 1191-1207.	1.0	19
8746	Epistatic Analysis of the Contribution of Rabs and Kifs to CATCHR Family Dependent Golgi Organization. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 126.	1.8	4
8747	Overexpression of Peroxidase Gene GsPRX9 Confers Salt Tolerance in Soybean. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3745.	1.8	53
8748	Natural Farming Improves Soil Quality and Alters Microbial Diversity in a Cabbage Field in Japan. <i>Sustainability</i> , 2019, 11, 3131.	1.6	26
8749	Identification of a thymus microRNA-mRNA regulatory network in Down syndrome. <i>Molecular Medicine Reports</i> , 2019, 20, 2063-2072.	1.1	3
8750	Taking insight into the gut microbiota of three spider species: No characteristic symbiont was found corresponding to the special feeding style of spiders. <i>Ecology and Evolution</i> , 2019, 9, 8146-8156.	0.8	19
8751	Identifying miltefosine-resistant key genes in protein-protein interactions network and experimental verification in Iranian <i>Leishmania major</i> . <i>Molecular Biology Reports</i> , 2019, 46, 5371-5388.	1.0	4
8752	RNA 5-Methylcytosine Facilitates the Maternal-to-Zygotic Transition by Preventing Maternal mRNA Decay. <i>Molecular Cell</i> , 2019, 75, 1188-1202.e11.	4.5	242
8753	CANPA: Computer-Assisted Natural Products Anticipation. <i>Analytical Chemistry</i> , 2019, 91, 11247-11252.	3.2	29
8754	Impact of sea level change on coastal soil organic matter, priming effects and prokaryotic community assembly. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	15
8755	Time Series Genome-Centric Analysis Unveils Bacterial Response to Operational Disturbance in Activated Sludge. <i>MSystems</i> , 2019, 4, .	1.7	23
8756	Genome-wide transcriptomic analysis of a desert willow, <i>Salix psammophila</i> , reveals the function of hub genes SpMDP1 and SpWRKY33 in drought tolerance. <i>BMC Plant Biology</i> , 2019, 19, 356.	1.6	11
8757	Morphological Characteristics and Comparative Transcriptome Analysis of Three Different Phenotypes of <i>Pristella maxillaris</i> . <i>Frontiers in Genetics</i> , 2019, 10, 698.	1.1	14
8758	Comparative Transcriptomics Identify Key Hypothalamic Circular RNAs that Participate in Sheep ( <i>Ovis</i> ) Tj ETQq1 1 0.784314 r/gBT /Ov	1.0	34
8759	Integrated bioinformatics analysis to identify 15 hub genes in breast cancer. <i>Oncology Letters</i> , 2019, 18, 1023-1034.	0.8	16
8760	Prognostic significance of contactin 3 expression and associated genes in glioblastoma multiforme. <i>Oncology Letters</i> , 2019, 18, 1863-1871.	0.8	5

#	ARTICLE	IF	CITATIONS
8761	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019, 20, 663.	1.2	19
8762	Genetic variants of the <i>oppA</i> gene are involved in metabolic regulation of surfactin in <i>Bacillus subtilis</i> . <i>Microbial Cell Factories</i> , 2019, 18, 141.	1.9	9
8763	The occurrence of <i>Listeria monocytogenes</i> is associated with built environment microbiota in three tree fruit processing facilities. <i>Microbiome</i> , 2019, 7, 115.	4.9	61
8764	Co-Expression Network Analysis Revealed That the <i>ATP5G1</i> Gene Is Associated With Major Depressive Disorder. <i>Frontiers in Genetics</i> , 2019, 10, 703.	1.1	13
8765	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>Cell Reports</i> , 2019, 28, 2048-2063.e8.	2.9	68
8766	Physiological and proteomic response of <i>Escherichia coli</i> O157:H7 to a bioprotective lactic acid bacterium in a meat environment. <i>Food Research International</i> , 2019, 125, 108622.	2.9	9
8767	Comparative Transcriptomic Analysis Reveals Regulatory Mechanisms of Theanine Synthesis in Tea ( <i>Camellia sinensis</i> ) and Oil Tea ( <i>Camellia oleifera</i> ) Plants. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 10235-10244.	2.4	15
8768	Cocaine induces differential circular RNA expression in striatum. <i>Translational Psychiatry</i> , 2019, 9, 199.	2.4	23
8769	Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. <i>Npj Genomic Medicine</i> , 2019, 4, 19.	1.7	163
8770	Modular structure in <i>C. elegans</i> neural network and its response to external localized stimuli. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2019, 533, 122051.	1.2	13
8771	High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes. <i>Nature Communications</i> , 2019, 10, 3120.	5.8	202
8772	Integrated analyses of microRNA-29 family and the related combination biomarkers demonstrate their widespread influence on risk, recurrence, metastasis and survival outcome in colorectal cancer. <i>Cancer Cell International</i> , 2019, 19, 181.	1.8	14
8773	Prognostic lncRNAs, miRNAs, and mRNAs Form a Competing Endogenous RNA Network in Colon Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 712.	1.3	40
8774	Proteomic Analysis of Breast Cancer Resistance to the Anticancer Drug RH1 Reveals the Importance of Cancer Stem Cells. <i>Cancers</i> , 2019, 11, 972.	1.7	4
8775	Genome-Wide Analysis and Expression Profiling of the Heat Shock Factor Gene Family in <i>Phyllostachys edulis</i> during Development and in Response to Abiotic Stresses. <i>Forests</i> , 2019, 10, 100.	0.9	15
8776	Understanding the Role of the WRKY Gene Family under Stress Conditions in Pigeonpea ( <i>Cajanus cajan</i> ) Tj ETQq1 1.0.784314.rgBT /Ov	1.6	20
8777	Integrated Transcriptomic and Proteomic Analysis of Red Blood Cells from Rainbow Trout Challenged with VHSV Point Towards Novel Immunomodulant Targets. <i>Vaccines</i> , 2019, 7, 63.	2.1	13
8778	Bioinformatics analysis of a long non-coding RNA and mRNA regulation network in rats with middle cerebral artery occlusion based on RNA sequencing. <i>Molecular Medicine Reports</i> , 2019, 20, 417-432.	1.1	10



#	ARTICLE	IF	CITATIONS
8779	Identification of critical genes associated with human osteosarcoma metastasis based on integrated gene expression profiling. <i>Molecular Medicine Reports</i> , 2019, 20, 915-930.	1.1	25
8780	Moonlighting Proteins and Cardiopathy in the Spatial Response of MCF7 Breast Cancer Cells to Tamoxifen. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1900029.	0.8	3
8781	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. <i>Medical Oncology</i> , 2019, 36, 73.	1.2	19
8782	Prioritizing chemicals of ecological concern in Great Lakes tributaries using high-throughput screening data and adverse outcome pathways. <i>Science of the Total Environment</i> , 2019, 686, 995-1009.	3.9	70
8783	Mass Spectral Similarity Networking and Gas-Phase Fragmentation Reactions in the Structural Analysis of Flavonoid Glycoconjugates. <i>Analytical Chemistry</i> , 2019, 91, 10413-10423.	3.2	36
8784	BRCA2 abrogation triggers innate immune responses potentiated by treatment with PARP inhibitors. <i>Nature Communications</i> , 2019, 10, 3143.	5.8	141
8785	Silencing of RAD51AP1 suppresses epithelial-mesenchymal transition and metastasis in non-small cell lung cancer. <i>Thoracic Cancer</i> , 2019, 10, 1748-1763.	0.8	16
8786	Grapevine comparative early transcriptomic profiling suggests that <i>Flavescence dorée</i> phytoplasma represses plant responses induced by vector feeding in susceptible varieties. <i>BMC Genomics</i> , 2019, 20, 526.	1.2	22
8787	Clinicohistopathological implications of MMP/VEGF expression in retinoblastoma: a combined meta-analysis and bioinformatics analysis. <i>Journal of Translational Medicine</i> , 2019, 17, 226.	1.8	12
8788	Proteome profiling of low grade serous ovarian cancer. <i>Journal of Ovarian Research</i> , 2019, 12, 64.	1.3	10
8789	Exploring the Molecular Mechanism of the Drug-Treated Breast Cancer Based on Gene Expression Microarray. <i>Biomolecules</i> , 2019, 9, 282.	1.8	15
8790	Discovering and Constructing ceRNA-miRNA-Target Gene Regulatory Networks during Anther Development in Maize. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3480.	1.8	43
8791	Integration of Metabolite Profiling and Transcriptome Analysis Reveals Genes Related to Volatile Terpenoid Metabolism in Finger Citron ( <i>C. medica</i> var. <i>sarcodactylis</i> ). <i>Molecules</i> , 2019, 24, 2564.	1.7	39
8792	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71.	2.4	29
8793	Traditional Chinese Medicine-Based Subtyping of Early-Stage Type 2 Diabetes Using Plasma Metabolomics Combined with Ultra-Weak Photon Emission. <i>Engineering</i> , 2019, 5, 916-923.	3.2	9
8794	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019, 13, 2800-2816.	4.4	125
8795	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. <i>Scientific Reports</i> , 2019, 9, 9807.	1.6	10
8796	Transcriptome profiling of <i>Puccinellia tenuiflora</i> during seed germination under a long-term saline-alkali stress. <i>BMC Genomics</i> , 2019, 20, 589.	1.2	34



#	ARTICLE	IF	CITATIONS
8797	A comprehensive expression analysis of the expansin gene family in potato ( <i>Solanum tuberosum</i> ) discloses stress-responsive expansin-like B genes for drought and heat tolerances. <i>PLoS ONE</i> , 2019, 14, e0219837.	1.1	37
8798	Identification and validation of a prognostic four-genes signature for hepatocellular carcinoma: integrated ceRNA network analysis. <i>Hepatology International</i> , 2019, 13, 618-630.	1.9	44
8799	Identification of candidate disease genes in patients with common variable immunodeficiency. <i>Quantitative Biology</i> , 2019, 7, 190-201.	0.3	2
8800	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019, 16, 737-742.	9.0	67
8801	Spatiotemporal Gene Coexpression and Regulation in Mouse Cardiomyocytes of Early Cardiac Morphogenesis. <i>Journal of the American Heart Association</i> , 2019, 8, e012941.	1.6	12
8802	Screening key lncRNAs for human lung adenocarcinoma based on machine learning and weighted gene co-expression network analysis. <i>Cancer Biomarkers</i> , 2019, 25, 313-324.	0.8	28
8803	Identification and characterization of sexual dimorphism-linked gene expression profile in hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 937-952.	1.2	10
8804	New SDC function prediction based on protein-protein interaction using bioinformatics tools. <i>Computational Biology and Chemistry</i> , 2019, 83, 107087.	1.1	10
8805	Comparative analysis of shrimp ( <i>Penaeus vannamei</i> ) miRNAs expression profiles during WSSV infection under experimental conditions and in pond culture. <i>Fish and Shellfish Immunology</i> , 2019, 93, 288-295.	1.6	17
8806	Integrative multi-omic analysis identifies new drivers and pathways in molecularly distinct subtypes of ALS. <i>Scientific Reports</i> , 2019, 9, 9968.	1.6	28
8807	NAPS update: network analysis of molecular dynamics data and protein-nucleic acid complexes. <i>Nucleic Acids Research</i> , 2019, 47, W462-W470.	6.5	45
8808	Global proteomic analyses define an environmentally contingent Hsp90 interactome and reveal chaperone-dependent regulation of stress granule proteins and the R2TP complex in a fungal pathogen. <i>PLoS Biology</i> , 2019, 17, e3000358.	2.6	34
8809	Identification of key candidate genes for pancreatic cancer by bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 451-458.	0.8	4
8810	Candidate genes and pathways associated with brain metastasis from lung cancer compared with lymph node metastasis. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 1276-1284.	0.8	1
8811	Identification of a novel lncRNA GABPB1-IT1 that is downregulated and predicts a poor prognosis in non-small cell lung cancer. <i>Oncology Letters</i> , 2019, 18, 838-845.	0.8	4
8812	Predicting the survival of patients with lung adenocarcinoma using a four-gene prognosis risk model. <i>Oncology Letters</i> , 2019, 18, 535-544.	0.8	9
8813	Investigation of differentially expressed genes in nasopharyngeal carcinoma by integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 916-926.	0.8	4
8814	Metabolomic Analysis Identifies Alterations of Amino Acid Metabolome Signatures in the Postmortem Brain of Alzheimer's Disease. <i>Experimental Neurobiology</i> , 2019, 28, 376-389.	0.7	26

#	ARTICLE	IF	CITATIONS
8815	Non-coding RNA Transcription in Tetrahymena Meiotic Nuclei Requires Dedicated Mediator Complex-Associated Proteins. <i>Current Biology</i> , 2019, 29, 2359-2370.e5.	1.8	9
8816	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	2.0	24
8817	Proteomic study of the membrane components of signalling cascades of <i>Botrytis cinerea</i> controlled by phosphorylation. <i>Scientific Reports</i> , 2019, 9, 9860.	1.6	13
8818	Low gut microbiota diversity and dietary magnesium intake are associated with the development of PPI-induced hypomagnesemia. <i>FASEB Journal</i> , 2019, 33, 11235-11246.	0.2	32
8819	Comparative proteomic analysis of Tibetan pig spermatozoa at high and low altitudes. <i>BMC Genomics</i> , 2019, 20, 569.	1.2	14
8820	<i>Caenorhabditis elegans</i> hub genes that respond to amyloid beta are homologs of genes involved in human Alzheimer's disease. <i>PLoS ONE</i> , 2019, 14, e0219486.	1.1	16
8821	Genome-Wide Identification of Circular RNAs Revealed the Dominant Intergenic Region Circularization Model in <i>Apostichopus japonicus</i> . <i>Frontiers in Genetics</i> , 2019, 10, 603.	1.1	16
8822	Head Start Immunity: Characterizing the Early Protection of C Strain Vaccine Against Subsequent Classical Swine Fever Virus Infection. <i>Frontiers in Immunology</i> , 2019, 10, 1584.	2.2	9
8823	Comprehensive Gene Expression Analysis in NMIBC Using RNA-seq Reveals New Therapy Strategies. <i>Frontiers in Oncology</i> , 2019, 9, 523.	1.3	11
8824	Circular RNA Signature in Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2019, 10, 3361-3372.	1.2	57
8825	Changes in saliva of dogs with canine leishmaniosis: A proteomic approach. <i>Veterinary Parasitology</i> , 2019, 272, 44-52.	0.7	19
8826	Elicited and pre-existing anti-Neu5Gc antibodies differentially affect human endothelial cells transcriptome. <i>Xenotransplantation</i> , 2019, 26, e12535.	1.6	12
8827	Genome-wide identification of lncRNAs as novel prognosis biomarkers of glioma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19518-19528.	1.2	32
8828	Purification, characterization, and application of a high activity 3-ketosteroid-1-dehydrogenase from <i>Mycobacterium neoaurum</i> DSM 1381. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6605-6616.	1.7	16
8829	An Asymmetric Reductase That Intercepts Acyclic Imino Acids Produced <i>in Situ</i> by a Partner Oxidase. <i>Journal of the American Chemical Society</i> , 2019, 141, 12258-12267.	6.6	5
8830	iOmicsPASS: network-based integration of multiomics data for predictive subnetwork discovery. <i>Npj Systems Biology and Applications</i> , 2019, 5, 22.	1.4	79
8831	Multi-level immune response network in mild-moderate Chronic Obstructive Pulmonary Disease (COPD). <i>Respiratory Research</i> , 2019, 20, 152.	1.4	34
8832	Quantitative and Comparative Analysis of Global Patterns of (Microtubule) Cytoskeleton Organization with CytoskeletonAnalyzer2D. <i>Methods in Molecular Biology</i> , 2019, 1992, 151-171.	0.4	1

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8833	Revealing synergistic mechanism of multiple components in <i>Stauntonia brachyanthera</i> Hand.-Mazz. for gout by virtual screening and system pharmacological approach. <i>Bioorganic Chemistry</i> , 2019, 91, 103118.	2.0	1
8834	Vitamin D (1,25-(OH) <sub>2</sub> D <sub>3</sub> ) regulates the gene expression through competing endogenous RNAs networks in high glucose-treated endothelial progenitor cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 193, 105425.	1.2	11
8835	Lamellarin Sulfates from the Pacific Tunicate <i>Didemnum ternerratum</i> . <i>Journal of Natural Products</i> , 2019, 82, 2000-2008.	1.5	29
8836	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019, 5, 810-821.	4.7	132
8837	APE1 and NPM1 protect cancer cells from platinum compounds cytotoxicity and their expression pattern has a prognostic value in TNBC. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 309.	3.5	28
8838	Co-expression analysis reveals dysregulated miRNAs and miRNA-mRNA interactions in the development of contrast-induced acute kidney injury. <i>PLoS ONE</i> , 2019, 14, e0218574.	1.1	9
8839	Identification and analysis of genes associated with head and neck squamous cell carcinoma by integrated bioinformatics methods. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e857.	0.6	27
8840	An effective drug sensitizing agent increases gefitinib treatment by down regulating PI3K/Akt/mTOR pathway and up regulating autophagy in non-small cell lung cancer. <i>Biomedicine and Pharmacotherapy</i> , 2019, 118, 109169.	2.5	28
8841	Mapping human microbiome drug metabolism by gut bacteria and their genes. <i>Nature</i> , 2019, 570, 462-467.	13.7	666
8842	Understanding the Mechanistic Contribution of Herbal Extracts in Compound Kushen Injection With Transcriptome Analysis. <i>Frontiers in Oncology</i> , 2019, 9, 632.	1.3	22
8843	Determining the endocrine disruption potential of industrial chemicals using an integrative approach: Public databases, in vitro exposure, and modeling receptor interactions. <i>Environment International</i> , 2019, 131, 104969.	4.8	22
8844	Development and use of a Cytoscape app for GRNCOP2. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 177, 211-218.	2.6	2
8845	Protective effects and network analysis of natural compounds obtained from <i>Radix dipsaci</i> , <i>Eucommiae cortex</i> , and <i>Rhizoma drynariae</i> against RANKL-induced osteoclastogenesis in vitro. <i>Journal of Ethnopharmacology</i> , 2019, 244, 112074.	2.0	14
8846	MicroRNAs fingerprint of bicuspid aortic valve. <i>Journal of Molecular and Cellular Cardiology</i> , 2019, 134, 98-106.	0.9	25
8847	PPAR expression, muscle size, and metabolic rates across the Gray catbird's annual cycle are greatest in preparation for fall migration. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	23
8848	An Apple a Day: Which Bacteria Do We Eat With Organic and Conventional Apples?. <i>Frontiers in Microbiology</i> , 2019, 10, 1629.	1.5	87
8849	High Constitutive Cytokine Release by Primary Human Acute Myeloid Leukemia Cells Is Associated with a Specific Intercellular Communication Phenotype. <i>Journal of Clinical Medicine</i> , 2019, 8, 970.	1.0	26
8850	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. <i>Cell Host and Microbe</i> , 2019, 26, 86-99.e7.	5.1	42

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8851	Phenolics lie at the centre of functional versatility in the responses of two phytochemically diverse tropical trees to canopy thinning. <i>Journal of Experimental Botany</i> , 2019, 70, 5853-5864.	2.4	8
8852	Metagenomic Functional Shifts to Plant Induced Environmental Changes. <i>Frontiers in Microbiology</i> , 2019, 10, 1682.	1.5	28
8853	The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. <i>Methods in Molecular Biology</i> , 2019, 1910, 271-308.	0.4	4
8854	Network analysis of dynamically important residues in protein structures mediating ligand-binding conformational changes. <i>European Biophysics Journal</i> , 2019, 48, 559-568.	1.2	9
8855	A C19MC-LIN28A-MYCN Oncogenic Circuit Driven by Hijacked Super-enhancers Is a Distinct Therapeutic Vulnerability in ETMRs: A Lethal Brain Tumor. <i>Cancer Cell</i> , 2019, 36, 51-67.e7.	7.7	69
8856	Plant Networks as Traits and Hypotheses: Moving Beyond Description. <i>Trends in Plant Science</i> , 2019, 24, 840-852.	4.3	43
8857	Transcriptomic and Gas Chromatography-Mass Spectrometry Metabolomic Profiling Analysis of the Epidermis Provides Insights into Cuticular Wax Regulation in Developing 'Yuluxiang' Pear Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8319-8331.	2.4	15
8858	Changes in saliva proteins in two conditions of compromised welfare in pigs: An experimental induced stress by nose snaring and lameness. <i>Research in Veterinary Science</i> , 2019, 125, 227-234.	0.9	16
8859	Mechanistic Insights into Specific G Protein Interactions with Adenosine Receptors. <i>Journal of Physical Chemistry B</i> , 2019, 123, 6462-6473.	1.2	80
8860	Characterization and Crystal Structure of a Nonheme Diiron Monooxygenase Involved in Platensimycin and Platencin Biosynthesis. <i>Journal of the American Chemical Society</i> , 2019, 141, 12406-12412.	6.6	23
8861	IRF1 is critical for the TNF-driven interferon response in rheumatoid fibroblast-like synoviocytes. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-11.	3.2	49
8862	MicroRNA-351 eases insulin resistance and liver gluconeogenesis via the PI3K/AKT pathway by inhibiting FLOT2 in mice of gestational diabetes mellitus. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5895-5906.	1.6	55
8863	Widespread Translational Control of Fibrosis in the Human Heart by RNA-Binding Proteins. <i>Circulation</i> , 2019, 140, 937-951.	1.6	95
8864	Microarray analysis of infectious bronchitis virus infection of chicken primary dendritic cells. <i>BMC Genomics</i> , 2019, 20, 557.	1.2	30
8865	Transcriptional Analysis of the Early Ripening of 'Kyoho' Grape in Response to the Treatment of Riboflavin. <i>Genes</i> , 2019, 10, 514.	1.0	11
8866	Potential Role of Rainbow Trout Erythrocytes as Mediators in the Immune Response Induced by a DNA Vaccine in Fish. <i>Vaccines</i> , 2019, 7, 60.	2.1	12
8867	Exploration of the hub genes and miRNAs in lung adenocarcinoma. <i>Oncology Letters</i> , 2019, 18, 1713-1722.	0.8	4
8868	Molecular Dynamics Simulations Study on the Resistant Mechanism of Insects to Imidacloprid due to Y151E and R81T Mutations in nAChRs. <i>Molecular Informatics</i> , 2019, 38, 1800125.	1.4	4

#	ARTICLE	IF	CITATIONS
8869	Oncogene Amplification in Growth Factor Signaling Pathways Renders Cancers Dependent on Membrane Lipid Remodeling. <i>Cell Metabolism</i> , 2019, 30, 525-538.e8.	7.2	130
8870	Are bacteria responsible for aroma deterioration upon storage of the black truffle <i>Tuber aestivum</i> : A microbiome and volatilome study. <i>Food Microbiology</i> , 2019, 84, 103251.	2.1	32
8871	Plasma Cells Are Obligate Effectors of Enhanced Myelopoiesis in Aging Bone Marrow. <i>Immunity</i> , 2019, 51, 351-366.e6.	6.6	76
8872	Drivers and ecological consequences of dominance in periurban phytoplankton communities using networks approaches. <i>Water Research</i> , 2019, 163, 114893.	5.3	52
8873	Taxonomic features and comparisons of the gut microbiome from two edible fungus-farming termites ( <i>Macrotermes falciger</i> ; <i>M. natalensis</i> ) harvested in the Vhembe district of Limpopo, South Africa. <i>BMC Microbiology</i> , 2019, 19, 164.	1.3	17
8874	MolNetEnhancer: Enhanced Molecular Networks by Integrating Metabolome Mining and Annotation Tools. <i>Metabolites</i> , 2019, 9, 144.	1.3	245
8875	Analysis of university workplace building surfaces reveals usage-specific chemical signatures. <i>Building and Environment</i> , 2019, 162, 106289.	3.0	6
8876	Long-read sequencing identifies GGC repeat expansions in NOTCH2NLC associated with neuronal intranuclear inclusion disease. <i>Nature Genetics</i> , 2019, 51, 1215-1221.	9.4	328
8877	Temporal map of the pig polytrauma plasma proteome with fluid resuscitation and intravenous vitamin C treatment. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 1827-1837.	1.9	8
8878	Amazon fish bacterial communities show structural convergence along widespread hydrochemical gradients. <i>Molecular Ecology</i> , 2019, 28, 3612-3626.	2.0	27
8879	Facultative Anaerobes Shape Multispecies Biofilms Composed of Meat Processing Surface Bacteria and <i>Escherichia coli</i> O157:H7 or <i>Salmonella enterica</i> Serovar Typhimurium. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
8880	Identification of Key Genes and Candidate Pathways in Human Autosomal Dominant Polycystic Kidney Disease by Bioinformatics Analysis. <i>Kidney and Blood Pressure Research</i> , 2019, 44, 533-552.	0.9	14
8881	T-type calcium channels drive the proliferation of androgen receptor negative prostate cancer cells. <i>Prostate</i> , 2019, 79, 1580-1586.	1.2	14
8882	Identification of gene co-expression modules and hub genes associated with lymph node metastasis of papillary thyroid cancer. <i>Endocrine</i> , 2019, 66, 573-584.	1.1	35
8883	Integrating Gene and Protein Expression Reveals Perturbed Functional Networks in Alzheimer's Disease. <i>Cell Reports</i> , 2019, 28, 1103-1116.e4.	2.9	67
8884	Passage and community changes of filterable bacteria during microfiltration of a surface water supply. <i>Environment International</i> , 2019, 131, 104998.	4.8	16
8885	The plastisphere in marine ecosystem hosts potential specific microbial degraders including <i>Alcanivorax borkumensis</i> as a key player for the low-density polyethylene degradation. <i>Journal of Hazardous Materials</i> , 2019, 380, 120899.	6.5	231
8886	Insights about multi-targeting and synergistic neuromodulators in Ayurvedic herbs against epilepsy: integrated computational studies on drug-target and protein-protein interaction networks. <i>Scientific Reports</i> , 2019, 9, 10565.	1.6	31

#	ARTICLE	IF	CITATIONS
8887	Systems biology and network pharmacology of frailty reveal novel epigenetic targets and mechanisms. <i>Scientific Reports</i> , 2019, 9, 10593.	1.6	6
8888	Genome and transcriptome evolve separately in recently hybridized <i>Trichosporon</i> fungi. <i>Communications Biology</i> , 2019, 2, 263.	2.0	9
8889	Magnesium transporter 1 (MAGT1) deficiency causes selective defects in N-linked glycosylation and expression of immune-response genes. <i>Journal of Biological Chemistry</i> , 2019, 294, 13638-13656.	1.6	57
8890	Targeted ITS1 sequencing unravels the mycodiversity of deep-sea sediments from the Gulf of Mexico. <i>Environmental Microbiology</i> , 2019, 21, 4046-4061.	1.8	19
8891	Salinity drives meiofaunal community structure dynamics across the Baltic ecosystem. <i>Molecular Ecology</i> , 2019, 28, 3813-3829.	2.0	31
8892	The association between pneumococcal vaccination, ethnicity, and the nasopharyngeal microbiota of children in Fiji. <i>Microbiome</i> , 2019, 7, 106.	4.9	11
8893	N-terminal $\beta$ -strand underpins biochemical specialization of an ATG8 isoform. <i>PLoS Biology</i> , 2019, 17, e3000373.	2.6	47
8894	miRNA-Gene Regulatory Network in Gnotobiotic Mice Stimulated by Dysbiotic Gut Microbiota Transplanted From a Genetically Obese Child. <i>Frontiers in Microbiology</i> , 2019, 10, 1517.	1.5	8
8895	Temporal Variation in the Microbiome of <i>Acropora</i> Coral Species Does Not Reflect Seasonality. <i>Frontiers in Microbiology</i> , 2019, 10, 1775.	1.5	29
8896	Meta-Analysis of Gene Expression and Identification of Biological Regulatory Mechanisms in Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2019, 13, 633.	1.4	43
8897	Inactivation of Prostaglandin E2 as a Mechanism for UGT2B17-Mediated Adverse Effects in Chronic Lymphocytic Leukemia. <i>Frontiers in Oncology</i> , 2019, 9, 606.	1.3	12
8898	A Transcriptomic Model of Postnatal Cardiac Effects of Prenatal Maternal Cortisol Excess in Sheep. <i>Frontiers in Physiology</i> , 2019, 10, 816.	1.3	5
8899	Proteomic Data Integration Highlights Central Actors Involved in Einkorn ( <i>Triticum monococcum</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T Science, 2019, 10, 832.	1.7	2
8900	Co-Expression Network Analysis Identified Gene Signatures in Osteosarcoma as a Predictive Tool for Lung Metastasis and Survival. <i>Journal of Cancer</i> , 2019, 10, 3706-3716.	1.2	49
8901	Transcriptome profiling-based identification of prognostic subtypes and multi-omics signatures of glioblastoma. <i>Scientific Reports</i> , 2019, 9, 10555.	1.6	26
8902	Systematic analysis of the lysine succinylome in the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>BMC Genomics</i> , 2019, 20, 585.	1.2	17
8903	Identification and Application of Gene Expression Signatures Associated with Lifespan Extension. <i>Cell Metabolism</i> , 2019, 30, 573-593.e8.	7.2	113
8904	Computational systems pharmacology reveals an antiplatelet and neuroprotective mechanism of Deng-Zhan-Xi-Xin injection in the treatment of ischemic stroke. <i>Pharmacological Research</i> , 2019, 147, 104365.	3.1	59



#	ARTICLE	IF	CITATIONS
8905	Charge-Mediated Pyrin Oligomerization Nucleates Antiviral IFI16 Sensing of Herpesvirus DNA. <i>MBio</i> , 2019, 10, .	1.8	25
8906	MicroRNA-203 Acts as a Potent Suppressor in Septic Shock by Alleviating Lung Injury via Inhibition of VNN1. <i>Kidney and Blood Pressure Research</i> , 2019, 44, 565-582.	0.9	23
8907	Quantitative proteomics reveals TMOD1-related proteins associated with water balance regulation. <i>PLoS ONE</i> , 2019, 14, e0219932.	1.1	5
8908	&lt;p&gt;Gene expression profiling reveals candidate biomarkers and probable molecular mechanism in diabetic peripheral neuropathy&lt;/p&gt;. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 1213-1223.	1.1	13
8909	Tunicamycin Sensitivity-Suppression by High Gene Dosage Reveals New Functions of the Yeast Hog1 MAP Kinase. <i>Cells</i> , 2019, 8, 710.	1.8	7
8910	Targeting HIV/HCV Coinfection Using a Machine Learning-Based Multiple Quantitative Structure-Activity Relationships (Multiple QSAR) Method. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3572.	1.8	26
8911	A Paranigral VTA Nociceptin Circuit that Constrains Motivation for Reward. <i>Cell</i> , 2019, 178, 653-671.e19.	13.5	76
8912	Transcriptomes in rat sciatic nerves at different stages of experimental autoimmune neuritis determined by RNA sequencing. <i>Clinical and Experimental Immunology</i> , 2019, 198, 184-197.	1.1	1
8913	MicroRNAâ€transcriptome networks in whole blood and monocytes of women undergoing preterm labour. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 6835-6845.	1.6	17
8914	Systematic identification of long noncoding <scp>RNA</scp>s expressed during lightâ€induced anthocyanin accumulation in apple fruit. <i>Plant Journal</i> , 2019, 100, 572-590.	2.8	91
8915	Genomic Evidence for Simultaneous Optimization of Transcription and Translation through Codon Variants in the <i>pmoCAB</i> Operon of Type Ia Methanotrophs. <i>MSystems</i> , 2019, 4, .	1.7	7
8916	Flower bud proteome reveals modulation of sex-biased proteins potentially associated with sex expression and modification in dioecious <i>Coccinia grandis</i> . <i>BMC Plant Biology</i> , 2019, 19, 330.	1.6	10
8917	Analysis of gene expression in rheumatoid arthritis and related conditions offers insights into sex-bias, gene biotypes and co-expression patterns. <i>PLoS ONE</i> , 2019, 14, e0219698.	1.1	12
8918	Uncovering mechanisms of global ocean change effects on the Dungeness crab ( <i>Cancer magister</i> ) through metabolomics analysis. <i>Scientific Reports</i> , 2019, 9, 10717.	1.6	19
8919	Molecular complexity of the major urinary protein system of the Norway rat, <i>Rattus norvegicus</i> . <i>Scientific Reports</i> , 2019, 9, 10757.	1.6	14
8920	The global motion affecting electron transfer in <i>Plasmodium falciparum</i> type II NADH dehydrogenases: a novel non-competitive mechanism for quinoline ketone derivative inhibitors. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 18105-18118.	1.3	9
8921	Comparative Genomics of Marine Sponge-Derived <i>Streptomyces</i> spp. Isolates SM17 and SM18 With Their Closest Terrestrial Relatives Provides Novel Insights Into Environmental Niche Adaptations and Secondary Metabolite Biosynthesis Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1713.	1.5	25
8922	Decoding Wheat Endosphereâ€Rhizosphere Microbiomes in <i>Rhizoctonia solani</i> â€Infested Soils Challenged by <i>Streptomyces</i> Biocontrol Agents. <i>Frontiers in Plant Science</i> , 2019, 10, 1038.	1.7	46



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8923	Evolutionary and Comparative Expression Analyses of TCP Transcription Factor Gene Family in Land Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3591.	1.8	41
8924	Identification of Biomarkers Related to Neuropathic Pain Induced by Peripheral Nerve Injury. <i>Journal of Molecular Neuroscience</i> , 2019, 69, 505-515.	1.1	6
8925	Glutathione deficiency-elicited reprogramming of hepatic metabolism protects against alcohol-induced steatosis. <i>Free Radical Biology and Medicine</i> , 2019, 143, 127-139.	1.3	18
8926	Genome-wide analysis of multi-view data of miRNA-seq to identify miRNA biomarkers for stomach cancer. <i>Journal of Biomedical Informatics</i> , 2019, 97, 103254.	2.5	6
8927	m1A Regulated Genes Modulate PI3K/AKT/mTOR and ErbB Pathways in Gastrointestinal Cancer. <i>Translational Oncology</i> , 2019, 12, 1323-1333.	1.7	102
8928	Genetic variation across RNA metabolism and cell death gene networks is implicated in the semantic variant of primary progressive aphasia. <i>Scientific Reports</i> , 2019, 9, 10854.	1.6	9
8929	Identifying potential drug targets in hepatocellular carcinoma based on network analysis and one-class support vector machine. <i>Scientific Reports</i> , 2019, 9, 10442.	1.6	17
8930	Enhancement of using combined packing materials on the removal of mixed sulfur compounds in a biotrickling filter and analysis of microbial communities. <i>BMC Biotechnology</i> , 2019, 19, 52.	1.7	12
8931	Modulation of posterior intestinal mucosal proteome in rainbow trout ( <i>Oncorhynchus mykiss</i> ) after <i>Yersinia ruckeri</i> infection. <i>Veterinary Research</i> , 2019, 50, 54.	1.1	12
8932	Integrated identification of key genes and pathways in Alzheimer's disease via comprehensive bioinformatical analyses. <i>Hereditas</i> , 2019, 156, 25.	0.5	32
8933	Microbial Community Structures and Important Associations Between Soil Nutrients and the Responses of Specific Taxa to Rice-Frog Cultivation. <i>Frontiers in Microbiology</i> , 2019, 10, 1752.	1.5	31
8934	Hyphenated chromatography detection and compound-target-disease investigation on herb-pair Chuanxiong Rhizoma - Xiangfu Rhizoma. <i>Journal of Ethnopharmacology</i> , 2019, 243, 112125.	2.0	8
8935	Viruses as key reservoirs of antibiotic resistance genes in the environment. <i>ISME Journal</i> , 2019, 13, 2856-2867.	4.4	88
8936	Transcriptional Profiling Reveals a Time-of-Day-Specific Role of REVEILLE 4/8 in Regulating the First Wave of Heat Shock-Induced Gene Expression in Arabidopsis. <i>Plant Cell</i> , 2019, 31, 2353-2369.	3.1	79
8937	Molecular Evolution and Functional Analysis of Rubredoxin-Like Proteins in Plants. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	7
8938	The Seasonal Dynamics and the Influence of Human Activities on Campus Outdoor Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1579.	1.5	7
8939	Downregulation of microRNA-196a inhibits stem cell self-renewal ability and stemness in non-small-cell lung cancer through upregulating GPX3 expression. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 115, 105571.	1.2	20
8940	Humanized yeast genetic interaction mapping predicts synthetic lethal interactions of FBXW7 in breast cancer. <i>BMC Medical Genomics</i> , 2019, 12, 112.	0.7	10

#	ARTICLE	IF	CITATIONS
8941	<p>Construction and validation of a seven-microRNA signature as a prognostic tool for lung squamous cell carcinoma</p>. Cancer Management and Research, 2019, Volume 11, 5701-5709.	0.9	10
8942	<p>mRNAs expression profiles of high glucose-induced memory in human umbilical vein endothelial cells</p>. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2019, Volume 12, 1249-1261.	1.1	5
8943	<p>Characterization of NDM-5- and CTX-M-55-coproducing <em>Escherichia coli</em> GSH8M-2 isolated from the effluent of a wastewater treatment plant in Tokyo Bay</p>. Infection and Drug Resistance, 2019, Volume 12, 2243-2249.	1.1	25
8944	<p>Evaluation of $\beta$ -synuclein and apolipoprotein E as potential biomarkers in cerebrospinal fluid to monitor pharmacotherapeutic efficacy in dopamine dictated disease states of Parkinson's disease and schizophrenia</p>. Neuropsychiatric Disease and Treatment, 2019, Volume 15, 2073-2085.	1.0	4
8945	<p>The prognostic value of LINC01296 in pan-cancers and the molecular regulatory mechanism in hepatocellular carcinoma: a comprehensive study based on data mining, bioinformatics, and in vitro validation</p>. OncoTargets and Therapy, 2019, Volume 12, 5861-5885.	1.0	4
8946	Vineyard Soil Microbiome Composition Related to Rotundone Concentration in Australian Cool Climate 'Peppery' Shiraz Grapes. Frontiers in Microbiology, 2019, 10, 1607.	1.5	40
8947	Variations in Soil Functional Fungal Community Structure Associated With Pure and Mixed Plantations in Typical Temperate Forests of China. Frontiers in Microbiology, 2019, 10, 1636.	1.5	46
8948	Investigation of Precise Molecular Mechanistic Action of Tobacco-Associated Carcinogen 'NNK' Induced Carcinogenesis: A System Biology Approach. Genes, 2019, 10, 564.	1.0	7
8949	DNA Methylation Module Network-Based Prognosis and Molecular Typing of Cancer. Genes, 2019, 10, 571.	1.0	16
8950	New Discorhabdin Alkaloids from the Antarctic Deep-Sea Sponge Latrunculia biformis. Marine Drugs, 2019, 17, 439.	2.2	27
8951	Rare Angiogenin and Ribonuclease 4 variants associated with amyotrophic lateral sclerosis exhibit loss-of-function: a comprehensive in silico study. Metabolic Brain Disease, 2019, 34, 1661-1677.	1.4	7
8952	The newly proposed TACK and DPANN archaea detected in the production waters from a high-temperature petroleum reservoir. International Biodeterioration and Biodegradation, 2019, 143, 104729.	1.9	11
8953	Development of a Chimeric Model to Study and Manipulate Human Microglia In Vivo. Neuron, 2019, 103, 1016-1033.e10.	3.8	218
8954	Distinct immune response profile during rhipicephalus (boophilus) microplus infestations of guzerat dairy herd according to the maternal lineage ancestry (mitochondrial DNA). Veterinary Parasitology, 2019, 273, 36-44.	0.7	0
8955	Enterotype-based Analysis of Gut Microbiota along the Conventional Adenoma-Carcinoma Colorectal Cancer Pathway. Scientific Reports, 2019, 9, 10923.	1.6	46
8956	A bioinformatic analysis identifies circadian expression of splicing factors and time-dependent alternative splicing events in the HD-MY-Z cell line. Scientific Reports, 2019, 9, 11062.	1.6	11
8957	Trypanosoma brucei ribonuclease H2A is an essential R-loop processing enzyme whose loss causes DNA damage during transcription initiation and antigenic variation. Nucleic Acids Research, 2019, 47, 9180-9197.	6.5	32
8958	Systems Network Genomic Analysis Reveals Cardioprotective Effect of MURC/Cavin4 Deletion Against Ischemia/Reperfusion Injury. Journal of the American Heart Association, 2019, 8, e012047.	1.6	10

#	ARTICLE	IF	CITATIONS
8959	Prediction of regulatory long intergenic non-coding RNAs acting in trans through base-pairing interactions. <i>BMC Genomics</i> , 2019, 20, 601.	1.2	23
8960	Equine arteritis virus long-term persistence is orchestrated by CD8+ T lymphocyte transcription factors, inhibitory receptors, and the CXCL16/CXCR6 axis. <i>PLoS Pathogens</i> , 2019, 15, e1007950.	2.1	20
8961	Machine Learning Classifiers for Endometriosis Using Transcriptomics and Methylomics Data. <i>Frontiers in Genetics</i> , 2019, 10, 766.	1.1	32
8962	Physiological and Transcriptomic Changes during the Early Phases of Adventitious Root Formation in Mulberry Stem Hardwood Cuttings. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3707.	1.8	20
8963	Identification of driver genes and key pathways of prolactinoma predicts the therapeutic effect of genipin. <i>Molecular Medicine Reports</i> , 2019, 20, 2712-2724.	1.1	3
8964	Profiling and functional analysis of differentially expressed circular RNAs in high glucose-induced human umbilical vein endothelial cells. <i>FEBS Open Bio</i> , 2019, 9, 1640-1651.	1.0	28
8965	TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. <i>GigaScience</i> , 2019, 8, .	3.3	6
8966	Prediction of hub genes associated with intramuscular fat content in Nelore cattle. <i>BMC Genomics</i> , 2019, 20, 520.	1.2	24
8967	Enteropathogenic <i>Escherichia coli</i> remodels host endosomes to promote endocytic turnover and breakdown of surface polarity. <i>PLoS Pathogens</i> , 2019, 15, e1007851.	2.1	16
8968	Interplay of transcriptional signaling by progesterone, cyclic AMP, and inflammation in myometrial cells: implications for the control of human parturition. <i>Molecular Human Reproduction</i> , 2019, 25, 408-422.	1.3	21
8969	Improving risk stratification in heart failure with preserved ejection fraction by combining two validated risk scores. <i>Open Heart</i> , 2019, 6, e000961.	0.9	13
8970	Comprehensive dissection of transcript and metabolite shifts during seed germination and post-germination stages in poplar. <i>BMC Plant Biology</i> , 2019, 19, 279.	1.6	16
8971	Identification of Key Genes and Circular RNAs in Human Gastric Cancer. <i>Medical Science Monitor</i> , 2019, 25, 2488-2504.	0.5	40
8972	Co-expression Network Analysis Elucidated a Core Module in Association With Prognosis of Non-functioning Non-invasive Human Pituitary Adenoma. <i>Frontiers in Endocrinology</i> , 2019, 10, 361.	1.5	23
8973	mTOR Signaling Pathway Regulates Sperm Quality in Older Men. <i>Cells</i> , 2019, 8, 629.	1.8	18
8974	Identification of potential key genes and pathways predicting pathogenesis and prognosis for triple-negative breast cancer. <i>Cancer Cell International</i> , 2019, 19, 172.	1.8	31
8975	Distribution and co-occurrence of antibiotic and metal resistance genes in biofilms of an anthropogenically impacted stream. <i>Science of the Total Environment</i> , 2019, 688, 437-449.	3.9	40
8976	Comparative mechanisms of PAH toxicity by benzo[a]pyrene and dibenzo[def,p]chrysene in primary human bronchial epithelial cells cultured at air-liquid interface. <i>Toxicology and Applied Pharmacology</i> , 2019, 379, 114644.	1.3	27

#	ARTICLE	IF	CITATIONS
8977	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019, 10, 2889.	5.8	84
8978	Deep transcriptome analysis using RNA-Seq suggests novel insights into molecular aspects of fat-tail metabolism in sheep. <i>Scientific Reports</i> , 2019, 9, 9203.	1.6	34
8979	NOTCH Activation Promotes Valve Formation by Regulating the Endocardial Secretome. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1782-1795.	2.5	18
8980	Biological molecular layer classification of muscle-invasive bladder cancer opens new treatment opportunities. <i>BMC Cancer</i> , 2019, 19, 636.	1.1	15
8981	Gene expression signature of atypical breast hyperplasia and regulation by SFRP1. <i>Breast Cancer Research</i> , 2019, 21, 76.	2.2	19
8982	Differential genetic and functional background in inflammatory bowel disease phenotypes of a Greek population: a systems bioinformatics approach. <i>Gut Pathogens</i> , 2019, 11, 31.	1.6	12
8983	MiR-30e-5p and MiR-15a-5p Expressions in Plasma and Urine of Type 1 Diabetic Patients With Diabetic Kidney Disease. <i>Frontiers in Genetics</i> , 2019, 10, 563.	1.1	29
8984	Transcriptome analysis of rice-seedling roots under soil salt stress using RNA-Seq method. <i>Plant Biotechnology Reports</i> , 2019, 13, 567-578.	0.9	37
8985	Common and distinct transcriptional signatures of mammalian embryonic lethality. <i>Nature Communications</i> , 2019, 10, 2792.	5.8	16
8986	SPX4 Acts on PHR1-Dependent and -Independent Regulation of Shoot Phosphorus Status in Arabidopsis. <i>Plant Physiology</i> , 2019, 181, 332-352.	2.3	54
8987	The construction and analysis of the aberrant lncRNA-miRNA-mRNA network in non-small cell lung cancer. <i>Journal of Thoracic Disease</i> , 2019, 11, 1772-1778.	0.6	43
8988	Lineage-Specific Evolved MicroRNAs Regulating NB-LRR Defense Genes in Triticeae. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3128.	1.8	8
8989	Screening key genes and signaling pathways in colorectal cancer by integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1259-1269.	1.1	28
8990	Clustered microRNAs hsa-miR-221-3p/hsa-miR-222-3p and their targeted genes might be prognostic predictors for hepatocellular carcinoma. <i>Journal of Cancer</i> , 2019, 10, 2520-2533.	1.2	33
8991	Genomic ecology of Marine Group II, the most common marine planktonic Archaea across the surface ocean. <i>MicrobiologyOpen</i> , 2019, 8, e00852.	1.2	27
8992	Composting swine carcasses with nitrogen transformation microbial strains: Succession of microbial community and nitrogen functional genes. <i>Science of the Total Environment</i> , 2019, 688, 555-566.	3.9	50
8993	Computational Systems Pharmacology-Target Mapping for Fentanyl-Laced Cocaine Overdose. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3486-3499.	1.7	19
8995	Flowers and climate change: a metabolic perspective. <i>New Phytologist</i> , 2019, 224, 1425-1441.	3.5	90

#	ARTICLE	IF	CITATIONS
8996	Cooperation Between the Inflammation and Coagulation Systems Promotes the Survival of Circulating Tumor Cells in Renal Cell Carcinoma Patients. <i>Frontiers in Oncology</i> , 2019, 9, 504.	1.3	31
8997	Significantly dysregulated genes in osteoarthritic labrum cells identified through gene expression profiling. <i>Molecular Medicine Reports</i> , 2019, 20, 1716-1724.	1.1	2
8998	DNA methylation profiling identifies potentially significant epigenetically regulated genes in glioblastoma multiforme. <i>Oncology Letters</i> , 2019, 18, 1679-1688.	0.8	8
8999	Small Nucleolar RNA 71A Promotes Lung Cancer Cell Proliferation, Migration and Invasion via MAPK/ERK Pathway. <i>Journal of Cancer</i> , 2019, 10, 2261-2275.	1.2	24
9000	Identification and functional prediction of lncRNAs in response to PEG and ABA treatment in cassava. <i>Environmental and Experimental Botany</i> , 2019, 166, 103809.	2.0	12
9001	Systematic analysis of lysine acetylome reveals potential functions of lysine acetylation in <i>Shewanella baltica</i> , the specific spoilage organism of aquatic products. <i>Journal of Proteomics</i> , 2019, 205, 103419.	1.2	22
9002	Identification of an early cell fate regulator by detecting dynamics in transcriptional heterogeneity and co-regulation during astrocyte differentiation. <i>Npj Systems Biology and Applications</i> , 2019, 5, 18.	1.4	10
9003	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multi-enrichment Approach. <i>Journal of Infectious Diseases</i> , 2019, 220, 1312-1324.	1.9	13
9004	Digital gene expression analyses of mammary glands from meat ewes naturally infected with clinical mastitis. <i>Royal Society Open Science</i> , 2019, 6, 181604.	1.1	8
9005	Global gene expression reveals an increase of HMGB1 and APEX1 proteins and their involvement in oxidative stress, apoptosis and inflammation pathways among beta-thalassaemia intermedia and major phenotypes. <i>British Journal of Haematology</i> , 2019, 186, 608-619.	1.2	7
9006	Sequence-based GWAS, network and pathway analyses reveal genes co-associated with milk cheese-making properties and milk composition in MontbÃ©liarde cows. <i>Genetics Selection Evolution</i> , 2019, 51, 34.	1.2	46
9007	NFBTA: A Potent Cytotoxic Agent against Glioblastoma. <i>Molecules</i> , 2019, 24, 2411.	1.7	19
9008	Genome-wide identification of a competing endogenous RNA network in cholangiocarcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 18995-19003.	1.2	15
9009	Integrated analysis identifying new lncRNA markers revealed in ceRNA network for tumor recurrence in papillary thyroid carcinoma and build of nomogram. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19673-19683.	1.2	23
9010	Compositional response of <i>Phaseolus vulgaris</i> rhizomicrobiome to a changing soil environment is regulated by long-distance plant signaling. <i>Plant and Soil</i> , 2019, 442, 257-269.	1.8	4
9011	Interaction of rat $10^9$ nicotinic acetylcholine receptor with $10^9$ -conotoxin RglA and Vc1.1: Insights from docking, molecular dynamics and binding free energy contributions. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 92, 55-64.	1.3	1
9012	Myc targeted CDK18 promotes ATR and homologous recombination to mediate PARP inhibitor resistance in glioblastoma. <i>Nature Communications</i> , 2019, 10, 2910.	5.8	77
9013	Label propagation defines signaling networks associated with recurrently mutated cancer genes. <i>Scientific Reports</i> , 2019, 9, 9401.	1.6	1

#	ARTICLE	IF	CITATIONS
9014	Comprehensive Analysis of Core Genes and Potential Mechanisms in Rectal Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 1262-1277.	0.8	15
9015	Expression Analysis and Regulation Network Identification of the CONSTANS-Like Gene Family in Moso Bamboo ( <i>Phyllostachys edulis</i> ) Under Photoperiod Treatments. <i>DNA and Cell Biology</i> , 2019, 38, 607-626.	0.9	5
9016	A T164S mutation in the dengue virus NS1 protein is associated with greater disease severity in mice. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	32
9017	Comparative Analysis of Microfluidics Thrombus Formation in Multiple Genetically Modified Mice: Link to Thrombosis and Hemostasis. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 99.	1.1	12
9018	Upper tract urothelial carcinoma has a luminal-papillary T-cell depleted contexture and activated FGFR3 signaling. <i>Nature Communications</i> , 2019, 10, 2977.	5.8	140
9019	The water depth-dependent co-occurrence patterns of marine bacteria in shallow and dynamic Southern Coast, Korea. <i>Scientific Reports</i> , 2019, 9, 9176.	1.6	33
9020	Overexpression of miR-101 May Target DUSP1 to Promote the Cartilage Degradation in Rheumatoid Arthritis. <i>Journal of Computational Biology</i> , 2019, 26, 1067-1079.	0.8	4
9021	An Integrative Computational Approach for a Prioritization of Key Transcription Regulators Associated With Nanomaterial-Induced Toxicity. <i>Toxicological Sciences</i> , 2019, 171, 303-314.	1.4	10
9022	Transcriptome profiling of longissimus thoracis muscles identifies highly connected differentially expressed genes in meat type sheep of India. <i>PLoS ONE</i> , 2019, 14, e0217461.	1.1	21
9023	Genome-wide association studies for heat stress response in <i>Bos taurus</i> × <i>Bos indicus</i> crossbred cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8148-8158.	1.4	31
9024	Contrasting Gene Expression Profiles of Monocytes and Lymphocytes From Peste-Des-Petits-Ruminants Virus Infected Goats. <i>Frontiers in Immunology</i> , 2019, 10, 1463.	2.2	16
9025	Distinct niche partitioning of marine and freshwater microbes during colonisation. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	4
9026	Hydrothermal vent protistan distribution along the Mariana arc suggests vent endemics may be rare and novel. <i>Environmental Microbiology</i> , 2019, 21, 3796-3815.	1.8	23
9027	Utilising network pharmacology to explore the underlying mechanism of Wumei Pill in treating pancreatic neoplasms. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 158.	3.7	80
9028	Land Use Change and Water Quality Use for Irrigation Alters Drylands Soil Fungal Community in the Mezquital Valley, Mexico. <i>Frontiers in Microbiology</i> , 2019, 10, 1220.	1.5	15
9029	Raw Material Regulates Flavor Formation via Driving Microbiota in Chinese Liquor Fermentation. <i>Frontiers in Microbiology</i> , 2019, 10, 1520.	1.5	40
9030	Assessing Specialized Metabolite Diversity in the Cosmopolitan Plant Genus <i>Euphorbia</i> L.. <i>Frontiers in Plant Science</i> , 2019, 10, 846.	1.7	40
9031	Global Dynamics in Protein Disorder during Maize Seed Development. <i>Genes</i> , 2019, 10, 502.	1.0	4



#	ARTICLE	IF	CITATIONS
9032	CDC20 and its downstream genes: potential prognosis factors of osteosarcoma. <i>International Journal of Clinical Oncology</i> , 2019, 24, 1479-1489.	1.0	11
9033	Assessing interactions, predicting function, and increasing degradation potential of a PAH-degrading bacterial consortium by effect of an inoculant strain. <i>Environmental Science and Pollution Research</i> , 2019, 26, 25932-25944.	2.7	4
9034	Leveraging New Definitions of the LxVP SLiM To Discover Novel Calcineurin Regulators and Substrates. <i>ACS Chemical Biology</i> , 2019, 14, 2672-2682.	1.6	17
9035	The TWIST1-centered competing endogenous RNA network promotes proliferation, invasion, and migration of lung adenocarcinoma. <i>Oncogenesis</i> , 2019, 8, 62.	2.1	18
9036	Regulatory Crosstalk of Doxorubicin, Estradiol and TNF $\alpha$ Combined Treatment in Breast Cancer-derived Cell Lines. <i>Scientific Reports</i> , 2019, 9, 15172.	1.6	2
9037	Gene and lncRNA co-expression network analysis reveals novel ceRNA network for triple-negative breast cancer. <i>Scientific Reports</i> , 2019, 9, 15122.	1.6	29
9038	Interactive exploration of heterogeneous biological networks with Biomine Explorer. <i>Bioinformatics</i> , 2019, 35, 5385-5388.	1.8	8
9039	<i>Aggregatibacter actinomycetemcomitans</i> colonization and persistence in a primate model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22307-22313.	3.3	13
9040	ACAT1 and Metabolism-Related Pathways Are Essential for the Progression of Clear Cell Renal Cell Carcinoma (ccRCC), as Determined by Co-expression Network Analysis. <i>Frontiers in Oncology</i> , 2019, 9, 957.	1.3	45
9041	A Co-Expression Network in Hexaploid Wheat Reveals Mostly Balanced Expression and Lack of Significant Gene Loss of Homeologous Meiotic Genes Upon Polyploidization. <i>Frontiers in Plant Science</i> , 2019, 10, 1325.	1.7	24
9042	Understanding how long-term organic amendments increase soil phosphatase activities: Insight into phoD- and phoC-harboring functional microbial populations. <i>Soil Biology and Biochemistry</i> , 2019, 139, 107632.	4.2	110
9043	Genomic analysis of the four ecologically distinct cactus host populations of <i>Drosophila mojavensis</i> . <i>BMC Genomics</i> , 2019, 20, 732.	1.2	17
9044	C3orf70 Is Involved in Neural and Neurobehavioral Development. <i>Pharmaceuticals</i> , 2019, 12, 156.	1.7	8
9045	Explore prognostic marker of colorectal cancer based on ceRNA network. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19358-19370.	1.2	10
9046	Identification of messenger and long noncoding RNAs associated with gallbladder cancer via gene expression profile analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19377-19387.	1.2	15
9047	ER-shaping atlastin proteins act as central hubs to promote flavivirus replication and virion assembly. <i>Nature Microbiology</i> , 2019, 4, 2416-2429.	5.9	59
9048	Transcriptomic analysis reveals potential genes involved in tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Scientific Reports</i> , 2019, 9, 14929.	1.6	45
9049	Integrated analysis of co-expression and ceRNA network identifies five lncRNAs as prognostic markers for breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 8410-8419.	1.6	53



#	ARTICLE	IF	CITATIONS
9050	How and Why Men and Women Differ in Their Microbiomes: Medical Ecology and Network Analyses of the Microgenderome. <i>Advanced Science</i> , 2019, 6, 1902054.	5.6	70
9051	Underlying mechanisms of reproductive toxicity caused by multigenerational exposure of 2, bromo-4, 6-dinitroaniline (BDNA) to Zebrafish ( <i>Danio rerio</i> ) at environmental relevant levels. <i>Aquatic Toxicology</i> , 2019, 216, 105285.	1.9	16
9052	Deciphering bacterial and fungal endophyte communities in leaves of two maple trees with green islands. <i>Scientific Reports</i> , 2019, 9, 14183.	1.6	25
9053	Acute systemic inflammatory response to lipopolysaccharide stimulation in pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2019, 20, 728.	1.2	10
9054	<p>Construction And Analysis Of The Time-Evolving Pain-Related Brain Network Using Literature Mining</p>. <i>Journal of Pain Research</i> , 2019, Volume 12, 2891-2903.	0.8	2
9055	Arsenic Response of Three Altiplanic <i>Exiguobacterium</i> Strains With Different Tolerance Levels Against the Metalloid Species: A Proteomics Study. <i>Frontiers in Microbiology</i> , 2019, 10, 2161.	1.5	20
9056	Diazotroph Diversity and Nitrogen Fixation in Summer Active Perennial Grasses in a Mediterranean Region Agricultural Soil. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 115.	1.6	34
9057	The central bacterial community in <i>Pericarpium Citri Reticulatae</i> "Chachiensis"™. <i>Food Research International</i> , 2019, 125, 108624.	2.9	13
9058	Genome-Wide Investigation of the NAC Gene Family and Its Potential Association with the Secondary Cell Wall in Moso Bamboo. <i>Biomolecules</i> , 2019, 9, 609.	1.8	19
9059	Biological Network Approaches and Applications in Rare Disease Studies. <i>Genes</i> , 2019, 10, 797.	1.0	30
9060	Identification of miRNAs Involved in <i>Bacillus velezensis</i> FZB42-Activated Induced Systemic Resistance in Maize. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5057.	1.8	15
9061	Effects of 1, 3-dioleoyl-2-palmitoylglycerol and its plant-oil formula on the toddler fecal microbiota during <i>in vitro</i> fermentation. <i>CYTA - Journal of Food</i> , 2019, 17, 850-863.	0.9	2
9062	Exploring novel herbicidin analogues by transcriptional regulator overexpression and MS/MS molecular networking. <i>Microbial Cell Factories</i> , 2019, 18, 175.	1.9	14
9063	Machine learning of human plasma lipidomes for obesity estimation in a large population cohort. <i>PLoS Biology</i> , 2019, 17, e3000443.	2.6	51
9064	An integrated epigenome and transcriptome analysis identifies PAX2 as a master regulator of drug resistance in high grade pancreatic ductal adenocarcinoma. <i>PLoS ONE</i> , 2019, 14, e0223554.	1.1	7
9065	Identification of SPP1 as an Extracellular Matrix Signature for Metastatic Castration-Resistant Prostate Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 924.	1.3	33
9066	Biosynthetic metabolomes of cysteinylâ€containing immunoresolvents. <i>FASEB Journal</i> , 2019, 33, 13794-13807.	0.2	20
9067	Gut microbiome diversity is associated with sleep physiology in humans. <i>PLoS ONE</i> , 2019, 14, e0222394.	1.1	175

#	ARTICLE	IF	CITATIONS
9068	Common Nodes of Virus-Host Interaction Revealed Through an Integrated Network Analysis. <i>Frontiers in Immunology</i> , 2019, 10, 2186.	2.2	67
9069	Trichostatin A, a Histone Deacetylase Inhibitor, Alleviates Eosinophilic Meningitis Induced by <i>Angiostrongylus cantonensis</i> Infection in Mice. <i>Frontiers in Microbiology</i> , 2019, 10, 2280.	1.5	7
9070	Bioinformatic Identification of miR-622 Key Target Genes and Experimental Validation of the miR-622-RNF8 Axis in Breast Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1114.	1.3	20
9071	Spatiotemporal dynamics of multidrug resistant bacteria on intensive care unit surfaces. <i>Nature Communications</i> , 2019, 10, 4569.	5.8	39
9072	Zinc binding proteome of a phytopathogen <i>Xanthomonas translucens</i> pv. <i>undulosa</i> . <i>Royal Society Open Science</i> , 2019, 6, 190369.	1.1	10
9073	Illuminating biological pathways for drug targeting in head and neck squamous cell carcinoma. <i>PLoS ONE</i> , 2019, 14, e0223639.	1.1	2
9074	Bioinformatic Exploration of Metal-Binding Proteome of Zoonotic Pathogen <i>Orientia tsutsugamushi</i> . <i>Frontiers in Genetics</i> , 2019, 10, 797.	1.1	12
9075	N6-methyladenosine mRNA marking promotes selective translation of regulons required for human erythropoiesis. <i>Nature Communications</i> , 2019, 10, 4596.	5.8	42
9076	Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. <i>Acta Neuropathologica Communications</i> , 2019, 7, 150.	2.4	40
9077	Deciphering the Pharmacological Mechanisms of the Huayu-Qiangshen-Tongbi Formula Through Integrating Network Pharmacology and In Vitro Pharmacological Investigation. <i>Frontiers in Pharmacology</i> , 2019, 10, 1065.	1.6	22
9078	Convolutional neural network model to predict causal risk factors that share complex regulatory features. <i>Nucleic Acids Research</i> , 2019, 47, e146-e146.	6.5	6
9079	MicroRNAs and Epigenetics Strategies to Reverse Breast Cancer. <i>Cells</i> , 2019, 8, 1214.	1.8	75
9080	Tri- and Diterpenoids from <i>Stillingia loranthacea</i> as Inhibitors of Zika Virus Replication. <i>Journal of Natural Products</i> , 2019, 82, 2721-2730.	1.5	12
9081	A one-step tRNA-CRISPR system for genome-wide genetic interaction mapping in mammalian cells. <i>Scientific Reports</i> , 2019, 9, 14499.	1.6	7
9082	Understanding the binding specificities of mRNA targets by the mammalian Quaking protein. <i>Nucleic Acids Research</i> , 2019, 47, 10564-10579.	6.5	8
9083	Hi-C guided assemblies reveal conserved regulatory topologies on X and autosomes despite extensive genome shuffling. <i>Genes and Development</i> , 2019, 33, 1591-1612.	2.7	43
9084	Endocrine and local signaling interact to regulate spermatogenesis in zebrafish: Follicle-stimulating hormone, retinoic acid and androgens. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	13
9085	Identification of potential biomarkers and pathways in ulcerative colitis with combined public mRNA and miRNA expression microarray data analysis. <i>Journal of Gastrointestinal Oncology</i> , 2019, 10, 847-858.	0.6	11

#	ARTICLE	IF	CITATIONS
9086	A High-Content Screening Approach to Identify MicroRNAs Against Head and Neck Cancer Cell Survival and EMT in an Inflammatory Microenvironment. <i>Frontiers in Oncology</i> , 2019, 9, 1100.	1.3	9
9087	Investigating the Multi-Target Pharmacological Mechanism of <i>Hedyotis diffusa</i> Willd Acting on Prostate Cancer: A Network Pharmacology Approach. <i>Biomolecules</i> , 2019, 9, 591.	1.8	41
9088	Transcriptomic analysis on the promoter regions discover gene networks involving mastitis in cattle. <i>Microbial Pathogenesis</i> , 2019, 137, 103801.	1.3	9
9089	Genetic interaction networks mediate individual statin drug response in <i>Saccharomyces cerevisiae</i> . <i>Npj Systems Biology and Applications</i> , 2019, 5, 35.	1.4	11
9090	Computational methods for NMR and MS for structure elucidation II: database resources and advanced methods. <i>Physical Sciences Reviews</i> , 2019, 4, .	0.8	6
9091	Cardiac and Skeletal Muscle Transcriptome Response to Heat Stress in Kenyan Chicken Ecotypes Adapted to Low and High Altitudes Reveal Differences in Thermal Tolerance and Stress Response. <i>Frontiers in Genetics</i> , 2019, 10, 993.	1.1	27
9092	Characterization of Distinct CyanoHABs-Related Modules in Microbial Recurrent Association Network. <i>Frontiers in Microbiology</i> , 2019, 10, 1637.	1.5	33
9093	&p&gt;Cerebrospinal Fluid Proteomics For Identification Of $\alpha$ 2-Macroglobulin As A Potential Biomarker To Monitor Pharmacological Therapeutic Efficacy In Dopamine Dictated Disease States Of Parkinsonâ€™s Disease And Schizophrenia&lt;p&gt;. <i>Neuropsychiatric Disease and Treatment</i> , 2019, Volume 15, 2853-2867.	1.0	14
9094	Integrative Analysis Reveals Across-Cancer Expression Patterns and Clinical Relevance of Ribonucleotide Reductase in Human Cancers. <i>Frontiers in Oncology</i> , 2019, 9, 956.	1.3	13
9095	Transcriptome-Enabled Network Inference Revealed the GmCOL1 Feed-Forward Loop and Its Roles in Photoperiodic Flowering of Soybean. <i>Frontiers in Plant Science</i> , 2019, 10, 1221.	1.7	20
9096	Association of Lipidomic Profiles With Progression of Carotid Artery Atherosclerosis in HIV Infection. <i>JAMA Cardiology</i> , 2019, 4, 1239.	3.0	26
9097	<i>MIR155HG</i> is a prognostic biomarker and associated with immune infiltration and immune checkpoint molecules expression in multiple cancers. <i>Cancer Medicine</i> , 2019, 8, 7161-7173.	1.3	97
9098	Analysis of new retrogenes provides insight into dog adaptive evolution. <i>Ecology and Evolution</i> , 2019, 9, 11185-11197.	0.8	6
9099	Analysis of miRNAâ€mRNA regulatory network revealed key genes induced by aflatoxin B1 exposure in primary human hepatocytes. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e971.	0.6	13
9100	Comparative transcriptomic analysis reveals beneficial effect of dietary mulberry leaves on the muscle quality of finishing pigs. <i>Veterinary Medicine and Science</i> , 2019, 5, 526-535.	0.6	13
9101	Signal Integration and Transcriptional Regulation of the Inflammatory Response Mediated by the GM-/M-CSF Signaling Axis in Human Monocytes. <i>Cell Reports</i> , 2019, 29, 860-872.e5.	2.9	29
9102	Identification of Key Hydroxymethylated Genes and Transcription Factors Associated with Alpha-Fetoprotein-Negative Hepatocellular Carcinoma. <i>DNA and Cell Biology</i> , 2019, 38, 1346-1356.	0.9	9
9103	Compound Dynamics and Combinatorial Patterns of Amino Acid Repeats Encode a System of Evolutionary and Developmental Markers. <i>Genome Biology and Evolution</i> , 2019, 11, 3159-3178.	1.1	9

#	ARTICLE	IF	CITATIONS
9104	Lysine acetylation contributes to development, aflatoxin biosynthesis and pathogenicity in <i>Aspergillus flavus</i> . <i>Environmental Microbiology</i> , 2019, 21, 4792-4807.	1.8	27
9105	Genome-wide transcriptional adaptation to salt stress in <i>Populus</i> . <i>BMC Plant Biology</i> , 2019, 19, 367.	1.6	32
9106	Application Communities Detection in Network. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 31.	1.3	1
9107	Investigating the Protective Effect of Cross Saponins of <i>Tribulus terrestris</i> Fruit against Ischemic Stroke in Rat Using Metabolomics and Network Pharmacology. <i>Metabolites</i> , 2019, 9, 240.	1.3	22
9108	The receptor-like kinase NIK1 targets FLS2/BAK1 immune complex and inversely modulates antiviral and antibacterial immunity. <i>Nature Communications</i> , 2019, 10, 4996.	5.8	59
9109	Making multi-omics data accessible to researchers. <i>Scientific Data</i> , 2019, 6, 251.	2.4	107
9110	Co-expression of synaptic genes in the sponge <i>Amphimedon queenslandica</i> uncovers ancient neural submodules. <i>Scientific Reports</i> , 2019, 9, 15781.	1.6	11
9111	<i>C. elegans</i> protein interaction network analysis probes RNAi validated pro-longevity effect of <i>nhr-6</i> , a human homolog of tumor suppressor <i>Nr4a1</i> . <i>Scientific Reports</i> , 2019, 9, 15711.	1.6	7
9112	Exploring gene networks in two sunflower lines with contrasting leaf senescence phenotype using a system biology approach. <i>BMC Plant Biology</i> , 2019, 19, 446.	1.6	10
9113	Analysis of prognosis, genome, microbiome, and microbial metabolome in different sites of colorectal cancer. <i>Journal of Translational Medicine</i> , 2019, 17, 353.	1.8	29
9114	Bioconversion of coal to methane by microbial communities from soil and from an opencast mine in the Xilingol grassland of northeast China. <i>Biotechnology for Biofuels</i> , 2019, 12, 236.	6.2	33
9115	Breast Milk Supply of MicroRNA Associated with Leptin and Adiponectin Is Affected by Maternal Overweight/Obesity and Influences Infancy BMI. <i>Nutrients</i> , 2019, 11, 2589.	1.7	40
9116	Transcriptome analysis of roots from resistant and susceptible rice varieties infected with <i>Hirschmanniella mucronata</i> . <i>FEBS Open Bio</i> , 2019, 9, 1968-1982.	1.0	7
9117	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	0.8	18
9118	G-quadruplexes Sequester Free Heme in Living Cells. <i>Cell Chemical Biology</i> , 2019, 26, 1681-1691.e5.	2.5	58
9119	Mechanistic insights into autocrine and paracrine roles of endothelial GABA signaling in the embryonic forebrain. <i>Scientific Reports</i> , 2019, 9, 16256.	1.6	9
9120	Data Integration in Poplar: Omics Layers and Integration Strategies. <i>Frontiers in Genetics</i> , 2019, 10, 874.	1.1	15
9121	Two Receptors, Two Isoforms, Two Cancers: Comprehensive Analysis of KIT and TrkA Expression in Neuroblastoma and Acute Myeloid Leukemia. <i>Frontiers in Oncology</i> , 2019, 9, 1046.	1.3	23

#	ARTICLE	IF	CITATIONS
9122	Deciphering Underlying Drivers of Disease Suppressiveness Against Pathogenic <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2535.	1.5	38
9123	Activation of RAW264.7 macrophages by active fraction of <i>Albizia julibrissin</i> saponin via Ca <sup>2+</sup> -ERK1/2-CREB-lncRNA pathways. <i>International Immunopharmacology</i> , 2019, 77, 105955.	1.7	9
9124	DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1981-1982.	1.8	2
9125	CancerTracer: a curated database for inpatient tumor heterogeneity. <i>Nucleic Acids Research</i> , 2019, 48, D797-D806.	6.5	9
9126	Assessing Chemical-Induced Liver Injury In Vivo From In Vitro Gene Expression Data in the Rat: The Case of Thioacetamide Toxicity. <i>Frontiers in Genetics</i> , 2019, 10, 1233.	1.1	14
9127	Transcriptome Analysis Implicates Involvement of Long Noncoding RNAs in Cytoplasmic Male Sterility and Fertility Restoration in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5530.	1.8	11
9128	Fast Detection of Two Smenamide Family Members Using Molecular Networking. <i>Marine Drugs</i> , 2019, 17, 618.	2.2	16
9129	MicroRNA-425-5p Expression Affects BRAF/RAS/MAPK Pathways In Colorectal Cancers. <i>International Journal of Medical Sciences</i> , 2019, 16, 1480-1491.	1.1	35
9130	A systems biology approach to identify the key targets of curcumin and capsaicin that downregulate pro-inflammatory pathways in human monocytes. <i>Computational Biology and Chemistry</i> , 2019, 83, 107162.	1.1	4
9131	PCuAC domains from methane-oxidizing bacteria use a histidine brace to bind copper. <i>Journal of Biological Chemistry</i> , 2019, 294, 16351-16363.	1.6	11
9132	SIGNOR 2.0, the SIGNaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	6.5	160
9133	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. <i>Science</i> , 2019, 366, 606-612.	6.0	621
9134	Meta-Analysis of Polymyositis and Dermatomyositis Microarray Data Reveals Novel Genetic Biomarkers. <i>Genes</i> , 2019, 10, 864.	1.0	6
9135	Py3plex toolkit for visualization and analysis of multilayer networks. <i>Applied Network Science</i> , 2019, 4, .	0.8	14
9136	Poly(ADP-Ribose) Polymerase-1 inhibition potentiates cell death and phosphorylation of DNA damage response proteins in oxidative stressed retinal cells. <i>Experimental Eye Research</i> , 2019, 188, 107790.	1.2	6
9137	Role of alternative splicing signatures in the prognosis of glioblastoma. <i>Cancer Medicine</i> , 2019, 8, 7623-7636.	1.3	20
9138	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
9139	Exploration of the antibiotic resistome in a wastewater treatment plant by a nine-year longitudinal metagenomic study. <i>Environment International</i> , 2019, 133, 105270.	4.8	85

#	ARTICLE	IF	CITATIONS
9140	Multimiomics analysis of tolerant interaction of potato with potato virus Y. <i>Scientific Data</i> , 2019, 6, 250.	2.4	11
9141	TSEA-DB: a trait-tissue association map for human complex traits and diseases. <i>Nucleic Acids Research</i> , 2019, 48, D1022-D1030.	6.5	23
9142	SourceSet: A graphical model approach to identify primary genes in perturbed biological pathways. <i>PLoS Computational Biology</i> , 2019, 15, e1007357.	1.5	4
9143	In silico assessment of human Calprotectin subunits (S100A8/A9) in presence of sodium and calcium ions using Molecular Dynamics simulation approach. <i>PLoS ONE</i> , 2019, 14, e0224095.	1.1	9
9144	Integrative proteomic and phosphoproteomic profiling of prostate cell lines. <i>PLoS ONE</i> , 2019, 14, e0224148.	1.1	14
9145	Identification of Prognostic and Metastatic Alternative Splicing Signatures in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 270.	2.0	55
9146	The Regulation of Ruminal Short-Chain Fatty Acids on the Functions of Rumen Barriers. <i>Frontiers in Physiology</i> , 2019, 10, 1305.	1.3	33
9147	Dissecting the Genome-Wide Evolution and Function of R2R3-MYB Transcription Factor Family in <i>Rosa chinensis</i> . <i>Genes</i> , 2019, 10, 823.	1.0	14
9148	Disclosing the Mechanism of Spontaneous Aggregation and Template-Induced Misfolding of the Key Hexapeptide (PHF6) of Tau Protein Based on Molecular Dynamics Simulation. <i>ACS Chemical Neuroscience</i> , 2019, 10, 4810-4823.	1.7	27
9149	The Empusa code generator and its application to GBOL, an extendable ontology for genome annotation. <i>Scientific Data</i> , 2019, 6, 254.	2.4	13
9150	Links of Extracellular Enzyme Activities, Microbial Metabolism, and Community Composition in the River-Impacted Coastal Waters. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 3507-3520.	1.3	12
9151	Chemotherapy-induced neuroinflammation is associated with disrupted colonic and bacterial homeostasis in female mice. <i>Scientific Reports</i> , 2019, 9, 16490.	1.6	84
9152	Prognostic values and prospective pathway signaling of MicroRNA-182 in ovarian cancer: a study based on gene expression omnibus (GEO) and bioinformatics analysis. <i>Journal of Ovarian Research</i> , 2019, 12, 106.	1.3	18
9153	Targeting Epithelial Mesenchymal Plasticity in Pancreatic Cancer: A Compendium of Preclinical Discovery in a Heterogeneous Disease. <i>Cancers</i> , 2019, 11, 1745.	1.7	6
9154	Evaluation of the Anti-Diabetic Activity of Some Common Herbs and Spices: Providing New Insights with Inverse Virtual Screening. <i>Molecules</i> , 2019, 24, 4030.	1.7	60
9155	Diagnostic and prognostic biomarkers of Human Leukocyte Antigen complex for hepatitis B virus-related hepatocellular carcinoma. <i>Journal of Cancer</i> , 2019, 10, 5173-5190.	1.2	10
9156	Comprehensive investigation of alternative splicing and development of a prognostic risk score for prostate cancer based on six-gene signatures. <i>Journal of Cancer</i> , 2019, 10, 5585-5596.	1.2	23
9157	Rapid Identification of Protein-Protein Interactions in Plants. <i>Current Protocols in Plant Biology</i> , 2019, 4, e20099.	2.8	22



#	ARTICLE	IF	CITATIONS
9158	Species-wide Metabolic Interaction Network for Understanding Natural Lignocellulose Digestion in Termite Gut Microbiota. <i>Scientific Reports</i> , 2019, 9, 16329.	1.6	28
9159	Long non-coding RNAs and latent HIV "A" search for novel targets for latency reversal. <i>PLoS ONE</i> , 2019, 14, e0224879.	1.1	24
9160	Combined Therapy Sensitivity Index Based on a 13-Gene Signature Predicts Prognosis for IDH Wild-type and MGMT Promoter Unmethylated Glioblastoma Patients. <i>Journal of Cancer</i> , 2019, 10, 5536-5548.	1.2	10
9161	Identification of key regulators in prostate cancer from gene expression datasets of patients. <i>Scientific Reports</i> , 2019, 9, 16420.	1.6	19
9162	Accelerated evolution of oligodendrocytes in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24334-24342.	3.3	43
9163	Integrated Network Analysis Reveals FOXM1 and MYBL2 as Key Regulators of Cell Proliferation in Non-small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1011.	1.3	54
9164	Duplication 2p16 is associated with perisylvian polymicrogyria. <i>American Journal of Medical Genetics, Part A</i> , 2019, 179, 2343-2356.	0.7	1
9165	System-level responses to cisplatin in pro-apoptotic stages of breast cancer MCF-7 cell line. <i>Computational Biology and Chemistry</i> , 2019, 83, 107155.	1.1	7
9166	Dissecting primate early post-implantation development using long-term in vitro embryo culture. <i>Science</i> , 2019, 366, .	6.0	137
9167	Enhancing PLP-Binding Capacity of Class-III $\alpha$ -Transaminase by Single Residue Substitution. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 282.	2.0	16
9168	Mining Public Toxicogenomic Data Reveals Insights and Challenges in Delineating Liver Steatosis Adverse Outcome Pathways. <i>Frontiers in Genetics</i> , 2019, 10, 1007.	1.1	14
9169	Heat-Shock Protein 90 Controls the Expression of Cell-Cycle Genes by Stabilizing Metazoan-Specific Host-Cell Factor HCFC1. <i>Cell Reports</i> , 2019, 29, 1645-1659.e9.	2.9	22
9170	Cox-LASSO Analysis Reveals a Ten-lncRNA Signature to Predict Outcomes in Patients with High-Grade Serous Ovarian Cancer. <i>DNA and Cell Biology</i> , 2019, 38, 1519-1528.	0.9	14
9171	Transcriptome analysis of two inflorescence branching mutants reveals cytokinin is an important regulator in controlling inflorescence architecture in the woody plant <i>Jatropha curcas</i> . <i>BMC Plant Biology</i> , 2019, 19, 468.	1.6	11
9172	Systems genomics approaches provide new insights into <i>Arabidopsis thaliana</i> root growth regulation under combinatorial mineral nutrient limitation. <i>PLoS Genetics</i> , 2019, 15, e1008392.	1.5	46
9173	Networking the Blue Economy in Seychelles: pioneers, resistance, and the power of influence. <i>Journal of Political Ecology</i> , 2019, 26, .	0.4	15
9174	First Insights on the Presence of the Unfolded Protein Response in Human Spermatozoa. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5518.	1.8	16
9175	A New Strategy for Identifying Mechanisms of Drug-drug Interaction Using Transcriptome Analysis: Compound Kushen Injection as a Proof of Principle. <i>Scientific Reports</i> , 2019, 9, 15889.	1.6	4



#	ARTICLE	IF	CITATIONS
9176	Enzymatic Reconstitution and Biosynthetic Investigation of the Bacterial Carbazole Neocarazostatin A. <i>Journal of Organic Chemistry</i> , 2019, 84, 16323-16328.	1.7	12
9177	Biclustering-based association rule mining approach for predicting cancer-associated protein interactions. <i>IET Systems Biology</i> , 2019, 13, 234-242.	0.8	7
9178	<i>Didelphis albiventris</i> : an overview of unprecedented transcriptome sequencing of the white-eared opossum. <i>BMC Genomics</i> , 2019, 20, 866.	1.2	0
9179	Integrated analysis of gene modulation profile identifies pathogenic factors and pathways in the liver of diabetic mice. <i>Journal of Diabetes and Metabolic Disorders</i> , 2019, 18, 471-485.	0.8	1
9180	Investigation of Proteomic and Phosphoproteomic Responses to Signaling Network Perturbations Reveals Functional Pathway Organizations in Yeast. <i>Cell Reports</i> , 2019, 29, 2092-2104.e4.	2.9	41
9181	From expression footprints to causal pathways: contextualizing large signaling networks with CARNIVAL. <i>Npj Systems Biology and Applications</i> , 2019, 5, 40.	1.4	96
9182	Membrane associated proteins of two <i>Trichomonas gallinae</i> clones vary with the virulence. <i>PLoS ONE</i> , 2019, 14, e0224032.	1.1	8
9183	The Construction and Analysis of ceRNA Network and Patterns of Immune Infiltration in Mesothelioma With Bone Metastasis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 257.	2.0	26
9184	Microbiome Response to Hot Water Treatment and Potential Synergy With Biological Control on Stored Apples. <i>Frontiers in Microbiology</i> , 2019, 10, 2502.	1.5	50
9185	Comparative Genomics and Metabolomics Analyses of Clavulanic Acid-Producing <i>Streptomyces</i> Species Provides Insight Into Specialized Metabolism. <i>Frontiers in Microbiology</i> , 2019, 10, 2550.	1.5	20
9186	Taxonomically Informed Scoring Enhances Confidence in Natural Products Annotation. <i>Frontiers in Plant Science</i> , 2019, 10, 1329.	1.7	84
9187	Comparative co-expression network analysis extracts the <i>SlHSP70</i> gene affecting to shoot elongation of tomato. <i>Plant Biotechnology</i> , 2019, 36, 143-153.	0.5	8
9188	Network Reconstruction and Significant Pathway Extraction Using Phosphoproteomic Data from Cancer Cells. <i>Proteomics</i> , 2019, 19, 1800450.	1.3	5
9189	Potential therapeutic drugs for ischemic stroke and stress disorder: A bioinformatics analysis. <i>Informatics in Medicine Unlocked</i> , 2019, 17, 100259.	1.9	4
9190	Ants reign over a distinct microbiome in forest soil. <i>Soil Biology and Biochemistry</i> , 2019, 139, 107529.	4.2	11
9191	Transcriptome analysis reveals that cyclophosphamide induces premature ovarian failure by blocking cholesterol biosynthesis pathway. <i>Life Sciences</i> , 2019, 239, 116999.	2.0	10
9192	Drivers of Î±-Sheet Formation in Transthyretin under Amyloidogenic Conditions. <i>Biochemistry</i> , 2019, 58, 4408-4423.	1.2	12
9193	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161

#	ARTICLE	IF	CITATIONS
9194	GenGraph: a python module for the simple generation and manipulation of genome graphs. <i>BMC Bioinformatics</i> , 2019, 20, 519.	1.2	4
9195	Identification of CBL and CIPK gene families and functional characterization of CaCIPK1 under <i>Phytophthora capsici</i> in pepper ( <i>Capsicum annuum</i> L.). <i>BMC Genomics</i> , 2019, 20, 775.	1.2	57
9196	Long non-coding RNA HCP5 serves as a ceRNA sponging miR-17-5p and miR-27a/b to regulate the pathogenesis of childhood obesity via the MAPK signaling pathway. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2019, 32, 1327-1339.	0.4	19
9197	Regulation of microRNAs in coronary atherosclerotic plaque. <i>Epigenomics</i> , 2019, 11, 1387-1397.	1.0	16
9198	Sleep Deprivation Alters the Pituitary Stress Transcriptome in Male and Female Mice. <i>Frontiers in Endocrinology</i> , 2019, 10, 676.	1.5	7
9199	Assessing the Impact of Sample Heterogeneity on Transcriptome Analysis of Human Diseases Using MDP Webtool. <i>Frontiers in Genetics</i> , 2019, 10, 971.	1.1	17
9200	Eukaryote Genes Are More Likely than Prokaryote Genes to Be Composites. <i>Genes</i> , 2019, 10, 648.	1.0	2
9201	Analytic Correlation Filtration: A New Tool to Reduce Analytical Complexity of Metabolomic Datasets. <i>Metabolites</i> , 2019, 9, 250.	1.3	5
9202	Insights into the genome structure of four acetogenic bacteria with specific reference to the Wood–Ljungdahl pathway. <i>MicrobiologyOpen</i> , 2019, 8, e938.	1.2	16
9203	Elucidation of a sialic acid metabolism pathway in mucus-foraging <i>Ruminococcus gnavus</i> unravels mechanisms of bacterial adaptation to the gut. <i>Nature Microbiology</i> , 2019, 4, 2393-2404.	5.9	83
9204	An Integrated Graph Regularized Non-Negative Matrix Factorization Model for Gene Co-Expression Network Analysis. <i>IEEE Access</i> , 2019, 7, 126594-126602.	2.6	9
9205	Voluntary exercise normalizes the proteomic landscape in muscle and brain and improves the phenotype of progeroid mice. <i>Aging Cell</i> , 2019, 18, e13029.	3.0	25
9206	Network Pharmacology Reveals the Molecular Mechanism of Cuyuxunxi Prescription in Promoting Wound Healing in Patients with Anal Fistula. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-9.	0.5	15
9207	Leveraging User-Friendly Network Approaches to Extract Knowledge From High-Throughput Omics Datasets. <i>Frontiers in Genetics</i> , 2019, 10, 1120.	1.1	11
9208	Complementary DNA/RNA-Based Profiling: Characterization of Corrosive Microbial Communities and Their Functional Profiles in an Oil Production Facility. <i>Frontiers in Microbiology</i> , 2019, 10, 2587.	1.5	20
9209	Transcription Factor and miRNA Interplays Can Manifest the Survival of ccRCC Patients. <i>Cancers</i> , 2019, 11, 1668.	1.7	46
9210	Metabolomic, transcriptomic and genetic integrative analysis reveals important roles of adenosine diphosphate in haemostasis and platelet activation in non-small cell lung cancer. <i>Molecular Oncology</i> , 2019, 13, 2406-2421.	2.1	24
9211	Logical modelling reveals the PDC-PDK interaction as the regulatory switch driving metabolic flexibility at the cellular level. <i>Genes and Nutrition</i> , 2019, 14, 27.	1.2	9

#	ARTICLE	IF	CITATIONS
9212	Identification of differentially expressed genes and pathways between intramuscular and abdominal fat-derived preadipocyte differentiation of chickens in vitro. <i>BMC Genomics</i> , 2019, 20, 743.	1.2	42
9213	Gene Cascade Finder: A tool for identification of gene cascades and its application in <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2019, 14, e0215187.	1.1	5
9214	Transcriptomic Responses in the Livers and Jejunal Mucosa of Pigs under Different Feeding Frequencies. <i>Animals</i> , 2019, 9, 675.	1.0	4
9215	Enhanced Exopolysaccharide Production by <i>Lactobacillus rhamnosus</i> in Co-Culture with <i>Saccharomyces cerevisiae</i> . <i>Applied Sciences (Switzerland)</i> , 2019, 9, 4026.	1.3	27
9216	Integrated Analysis of microRNA and mRNA Expression Profiles: An Attempt to Disentangle the Complex Interaction Network in Attention Deficit Hyperactivity Disorder. <i>Brain Sciences</i> , 2019, 9, 288.	1.1	22
9217	Genome-Wide Analysis of NAC Gene Family in <i>Betula pendula</i> . <i>Forests</i> , 2019, 10, 741.	0.9	44
9218	The Impact of Moyamoya Disease and RNF213 Mutations on the Spectrum of Plasma Protein and MicroRNA. <i>Journal of Clinical Medicine</i> , 2019, 8, 1648.	1.0	7
9219	Identification of biomarkers associated with diagnosis and prognosis of colorectal cancer patients based on integrated bioinformatics analysis. <i>Gene</i> , 2019, 692, 119-125.	1.0	121
9220	Breaking the paradigm: Dr Insight empowers signature-free, enhanced drug repurposing. <i>Bioinformatics</i> , 2019, 35, 2818-2826.	1.8	36
9221	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. <i>Nature Communications</i> , 2019, 10, 4788.	5.8	59
9222	Insights into replicative senescence of human testicular peritubular cells. <i>Scientific Reports</i> , 2019, 9, 15052.	1.6	33
9224	Transcriptome Analyses of FY Mutants Reveal Its Role in mRNA Alternative Polyadenylation. <i>Plant Cell</i> , 2019, 31, 2332-2352.	3.1	36
9225	Developmental stages and gut microenvironments influence gut microbiota dynamics in the invasive beetle <i>Popillia japonica</i> Newman (Coleoptera: Scarabaeidae). <i>Environmental Microbiology</i> , 2019, 21, 4343-4359.	1.8	42
9226	Elevated hsa-miR-590-3p expression downregulates HMGB2 expression and contributes to the severity of IgA nephropathy. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 7299-7309.	1.6	11
9227	BRK phosphorylates SMAD4 for proteasomal degradation and inhibits tumor suppressor FRK to control SNAIL, SLUG, and metastatic potential. <i>Science Advances</i> , 2019, 5, eaaw3113.	4.7	16
9228	Nipah Virus-Like Particle Egress Is Modulated by Cytoskeletal and Vesicular Trafficking Pathways: a Validated Particle Proteomics Analysis. <i>MSystems</i> , 2019, 4, .	1.7	11
9229	Potential molecular mechanism of ACE gene at different time points in STEMI patients based on genome-wide microarray dataset. <i>Lipids in Health and Disease</i> , 2019, 18, 184.	1.2	3
9230	Comprehensive analysis of non-small-cell lung cancer microarray datasets identifies several prognostic biomarkers. <i>Future Oncology</i> , 2019, 15, 3135-3148.	1.1	2

#	ARTICLE	IF	CITATIONS
9231	Cross-Species Gene Expression Analysis Reveals Gene Modules Implicated in Human Osteosarcoma. <i>Frontiers in Genetics</i> , 2019, 10, 697.	1.1	14
9232	Diversity and Co-Occurrence Patterns of Soil Bacterial and Fungal Communities of Chinese Cordyceps Habitats at Shergyla Mountain, Tibet: Implications for the Occurrence. <i>Microorganisms</i> , 2019, 7, 284.	1.6	14
9233	Comprehensive analysis of differentially expressed profiles and reconstruction of a competing endogenous RNA network in papillary renal cell carcinoma. <i>Molecular Medicine Reports</i> , 2019, 19, 4685-4696.	1.1	11
9234	Biosynthesis of GDP-glycerol-1-phosphate-mannose for the Capsular Polysaccharide of <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2019, 58, 3893-3902.	1.2	20
9235	Comprehensive analysis of the lysine acetylome in <i>Aeromonas hydrophila</i> reveals cross-talk between lysine acetylation and succinylation in LuxS. <i>Emerging Microbes and Infections</i> , 2019, 8, 1229-1239.	3.0	27
9236	Therapeutic Effect of Ecdysterone Combine Paeonol Oral Cavity Direct Administered on Radiation-Induced Oral Mucositis in Rats. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3800.	1.8	6
9237	Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. <i>Sustainability</i> , 2019, 11, 4428.	1.6	24
9238	Effect of cold stress on gene expression and functional pathways in maize root system. <i>Grassland Science</i> , 2019, 65, 249-256.	0.6	4
9239	A vaccine-induced gene expression signature correlates with protection against SIV and HIV in multiple trials. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	26
9240	Identification of Genes and Pathways Associated with Acne Using Integrated Bioinformatics Methods. <i>Dermatology</i> , 2019, 235, 445-455.	0.9	14
9241	The Inhibitory Effect of Cordycepin on the Proliferation of MCF-7 Breast Cancer Cells, and Its Mechanism: An Investigation Using Network Pharmacology-Based Analysis. <i>Biomolecules</i> , 2019, 9, 414.	1.8	31
9242	Identification of Msp1-Induced Signaling Components in Rice Leaves by Integrated Proteomic and Phosphoproteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4135.	1.8	30
9243	Identification of aberrantly methylated differentially expressed genes in glioblastoma multiforme and their association with patient survival. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 2140-2152.	0.8	13
9244	Comparative Transcriptomic and Proteomic Analyses Identify Key Genes Associated With Milk Fat Traits in Chinese Holstein Cows. <i>Frontiers in Genetics</i> , 2019, 10, 672.	1.1	13
9245	Proteomics profiling of plasma exosomes in epithelial ovarian cancer: A potential role in the coagulation cascade, diagnosis and prognosis. <i>International Journal of Oncology</i> , 2019, 54, 1719-1733.	1.4	78
9246	Surface water extracts impair gene profiles and differentiation in human mesenchymal stem cells. <i>Environment International</i> , 2019, 132, 104823.	4.8	2
9247	Network Analysis for the Digital Humanities: Principles, Problems, Extensions. <i>Isis</i> , 2019, 110, 538-554.	0.1	12
9248	Evidence for a non-canonical JAK/STAT signaling pathway in the synthesis of the brain's major ion channels and neurotransmitter receptors. <i>BMC Genomics</i> , 2019, 20, 677.	1.2	25

#	ARTICLE	IF	CITATIONS
9249	DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	17
9250	Identification and in Silico Characterization of GT Factors Involved in Phytohormone and Abiotic Stresses Responses in <i>Brachypodium distachyon</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4115.	1.8	1
9251	FoxOs could play an important role during influenza A viruses infection via microarray analysis based on GEO database. <i>Infection, Genetics and Evolution</i> , 2019, 75, 104009.	1.0	6
9252	Current status of clinical proteogenomics in lung cancer. <i>Expert Review of Proteomics</i> , 2019, 16, 761-772.	1.3	27
9253	Jacob's Ladder: The User Implications of Leveraging Graph Pivots. , 2019, , .		1
9254	Neural crest related gene transcript regulation by valproic acid analogues in the cardiac embryonic stem cell test. <i>Reproductive Toxicology</i> , 2019, 90, 44-52.	1.3	10
9255	Via. , 2019, , .		5
9256	Next-generation sequencing predicts interaction network between miRNA and target genes in lipoteichoic acid-stimulated human neutrophils. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1436-1446.	1.8	4
9257	RITAN: rapid integration of term annotation and network resources. <i>PeerJ</i> , 2019, 7, e6994.	0.9	17
9258	Identification of microRNA-181 as a promising biomarker for predicting the poor survival in colorectal cancer. <i>Cancer Medicine</i> , 2019, 8, 5995-6009.	1.3	15
9259	The persistence of antimicrobial resistance and related environmental factors in abandoned and working swine feedlots. <i>Environmental Pollution</i> , 2019, 255, 113116.	3.7	14
9261	In silico evidence of de novo interactions between ribosomal and Epstein - Barr virus proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 34.	1.0	3
9262	MiR-190a potentially ameliorates postoperative cognitive dysfunction by regulating Tiam1. <i>BMC Genomics</i> , 2019, 20, 670.	1.2	17
9263	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. <i>PLoS ONE</i> , 2019, 14, e0221444.	1.1	1
9264	Hamiltonian energy as an efficient approach to identify the significant key regulators in biological networks. <i>PLoS ONE</i> , 2019, 14, e0221463.	1.1	2
9265	In silico studies reveal RSc1154 and RhIE as temperature-related pathogenic proteins of <i>Ralstonia solanacearum</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	0
9266	The Evolution of Tau Phosphorylation and Interactions. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 256.	1.7	59
9267	Alterations in the Ocular Surface Fungal Microbiome in Fungal Keratitis Patients. <i>Microorganisms</i> , 2019, 7, 309.	1.6	43

#	ARTICLE	IF	CITATIONS
9268	Prognostic value of ATAD3 gene cluster expression in hepatocellular carcinoma. <i>Oncology Letters</i> , 2019, 18, 1304-1310.	0.8	11
9269	Biochemical and structural characterization of a highly active branched-chain amino acid aminotransferase from <i>Pseudomonas</i> sp. for efficient biosynthesis of chiral amino acids. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8051-8062.	1.7	7
9270	Proteomic and Interactome Approaches Reveal PAK4, PHB-2, and 14-3-3 $\beta$ as Targets of Overactivated Cdc42 in Cellular Responses to Genomic Instability. <i>Journal of Proteome Research</i> , 2019, 18, 3597-3614.	1.8	10
9271	Genome-wide profiling of DNA methylome and transcriptome in peripheral blood monocytes for major depression: A Monozygotic Discordant Twin Study. <i>Translational Psychiatry</i> , 2019, 9, 215.	2.4	49
9272	Differential transcriptome dynamics during the onset of conceptus elongation and between female and male porcine embryos. <i>BMC Genomics</i> , 2019, 20, 679.	1.2	11
9273	Mitochondrial genomic variation drives differential nuclear gene expression in discrete regions of <i>Drosophila</i> gene and protein interaction networks. <i>BMC Genomics</i> , 2019, 20, 691.	1.2	15
9274	Constructing Human Proteoform Families Using Intact-Mass and Top-Down Proteomics with a Multi-Protease Global Post-Translational Modification Discovery Database. <i>Journal of Proteome Research</i> , 2019, 18, 3671-3680.	1.8	21
9275	Space Station conditions are selective but do not alter microbial characteristics relevant to human health. <i>Nature Communications</i> , 2019, 10, 3990.	5.8	79
9276	A systems biology approach towards the identification of candidate therapeutic genes and potential biomarkers for Parkinson's disease. <i>PLoS ONE</i> , 2019, 14, e0220995.	1.1	17
9277	Identification of Hub Genes and Key Pathways Associated With Bipolar Disorder Based on Weighted Gene Co-expression Network Analysis. <i>Frontiers in Physiology</i> , 2019, 10, 1081.	1.3	90
9278	A Radiogenomic Approach for Decoding Molecular Mechanisms Underlying Tumor Progression in Prostate Cancer. <i>Cancers</i> , 2019, 11, 1293.	1.7	19
9279	A Coordinated Response at The Transcriptome and Interactome Level is Required to Ensure Uropathogenic <i>Escherichia coli</i> Survival during Bacteremia. <i>Microorganisms</i> , 2019, 7, 292.	1.6	5
9280	Antibiotics-Driven Gut Microbiome Perturbation Alters Immunity to Vaccines in Humans. <i>Cell</i> , 2019, 178, 1313-1328.e13.	13.5	402
9281	Proteomics of Melanoma Response to Immunotherapy Reveals Mitochondrial Dependence. <i>Cell</i> , 2019, 179, 236-250.e18.	13.5	206
9282	Identification of putative miRNA biomarkers in early rheumatoid arthritis by genome-wide microarray profiling: A pilot study. <i>Gene</i> , 2019, 720, 144081.	1.0	22
9283	Resin tapping transcriptome in adult slash pine ( <i>Pinus elliottii</i> var. <i>elliottii</i> ). <i>Industrial Crops and Products</i> , 2019, 139, 111545.	2.5	20
9284	Global expression profiling of cognitive level and decline in middle-aged monozygotic twins. <i>Neurobiology of Aging</i> , 2019, 84, 141-147.	1.5	10
9285	Rapid metabolic shifts occur during the transition between hunger and satiety in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2019, 10, 4052.	5.8	40



#	ARTICLE	IF	CITATIONS
9286	Logical Architecture of Water Distribution Networks. , 2019, , .		3
9287	Comprehensive analysis of long noncoding RNA (lncRNA)-chromatin interactions reveals lncRNA functions dependent on binding diverse regulatory elements. <i>Journal of Biological Chemistry</i> , 2019, 294, 15613-15622.	1.6	32
9288	Polyubiquitin Chains Linked by Lysine Residue 48 (K48) Selectively Target Oxidized Proteins<i>In Vivo</i>. <i>Antioxidants and Redox Signaling</i> , 2019, 31, 1133-1149.	2.5	22
9289	Identifying Hepatocellular Carcinoma Driver Genes by Integrative Pathway Crosstalk and Protein Interaction Network. <i>DNA and Cell Biology</i> , 2019, 38, 1112-1124.	0.9	8
9290	Hypoxic exosomes facilitate angiogenesis and metastasis in esophageal squamous cell carcinoma through altering the phenotype and transcriptome of endothelial cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 389.	3.5	87
9291	Conservation and divergence of protein pathways in the vertebrate heart. <i>PLoS Biology</i> , 2019, 17, e3000437.	2.6	18
9292	Genome-wide investigation of the clinical implications and molecular mechanism of long noncoding RNA LINC00668 and protein-coding genes in hepatocellular carcinoma. <i>International Journal of Oncology</i> , 2019, 55, 860-878.	1.4	13
9293	Analysis of clinical significance and prospective molecular mechanism of main elements of the JAK/STAT pathway in hepatocellular carcinoma. <i>International Journal of Oncology</i> , 2019, 55, 805-822.	1.4	12
9294	Crosstalk between microRNAs, the putative target genes and the lncRNA network in metabolic diseases. <i>Molecular Medicine Reports</i> , 2019, 20, 3543-3554.	1.1	10
9295	Butyrate mediated regulation of RNA binding proteins in the post-transcriptional regulation of inflammatory gene expression. <i>Cellular Signalling</i> , 2019, 64, 109410.	1.7	18
9296	Exploring the effect of aplidin on low molecular weight protein tyrosine phosphatase by molecular docking and molecular dynamic simulation study. <i>Computational Biology and Chemistry</i> , 2019, 83, 107123.	1.1	0
9297	Systems pharmacology dissection of action mechanisms of <i>Dipsaci Radix</i> for osteoporosis. <i>Life Sciences</i> , 2019, 235, 116820.	2.0	27
9298	Network-guided analysis of hippocampal proteome identifies novel proteins that colocalize with A $\beta$ in a mice model of early-stage Alzheimer's disease. <i>Neurobiology of Disease</i> , 2019, 132, 104603.	2.1	13
9299	Systems Pharmacological Approach to Investigate the Mechanism of <i>Hericium erinaceus</i> for Alzheimer's Disease. <i>Digital Chinese Medicine</i> , 2019, 2, 7-18.	0.5	3
9300	A mutated rabbit defensin NP-1 produced by <i>Chlorella ellipsoidea</i> can improve the growth performance of broiler chickens. <i>Scientific Reports</i> , 2019, 9, 12778.	1.6	2
9301	Predicting Soybean Yield and Sudden Death Syndrome Development Using At-Planting Risk Factors. <i>Phytopathology</i> , 2019, 109, 1710-1719.	1.1	8
9302	Differential dynamics of microbial community networks help identify microorganisms interacting with residue-borne pathogens: the case of <i>Zymoseptoria tritici</i> in wheat. <i>Microbiome</i> , 2019, 7, 125.	4.9	41
9303	Diagnostic and prognostic value of mRNA expression of phospholipase C $\beta$ family genes in hepatitis B virus-associated hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 41, 2855-2875.	1.2	10



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9304	De novo transcriptome assembly for four species of crustose coralline algae and analysis of unique orthologous genes. <i>Scientific Reports</i> , 2019, 9, 12611.	1.6	10
9305	A putative mechanism of the Sodium/Iodide Symporter regulation during repetitive administration of stable Iodide described by a Systems Biology approach. <i>BIO Web of Conferences</i> , 2019, 14, 05008.	0.1	0
9306	Mechanisms of early- and late-feathering in Qingyuan partridge chickens. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 1172-1181.	0.5	1
9307	<i>P4HB</i> , a Novel Hypoxia Target Gene Related to Gastric Cancer Invasion and Metastasis. <i>BioMed Research International</i> , 2019, 2019, 1-13.	0.9	35
9308	Significance of circulating microRNAs in diabetes mellitus type 2 and platelet reactivity: bioinformatic analysis and review. <i>Cardiovascular Diabetology</i> , 2019, 18, 113.	2.7	111
9309	Integration analysis for novel lncRNA markers predicting tumor recurrence in human colon adenocarcinoma. <i>Journal of Translational Medicine</i> , 2019, 17, 299.	1.8	18
9310	Identification of modules and functional analysis in CRC subtypes by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2019, 14, e0221772.	1.1	6
9311	Phenotype-Specific Therapeutic Effect of <i>Rhodiola wallichiana</i> var. <i>cholaensis</i> Combined with Dexamethasone on Experimental Murine Asthma and Its Comprehensive Pharmacological Mechanism. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4216.	1.8	7
9312	Cyclin-CDK Complexes are Key Controllers of Capacitation-Dependent Actin Dynamics in Mammalian Spermatozoa. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4236.	1.8	7
9313	Single Stranded DNA Viruses Associated with Capybara Faeces Sampled in Brazil. <i>Viruses</i> , 2019, 11, 710.	1.5	36
9314	The regulatory role of microRNA-mRNA co-expression in hepatitis B virus-associated acute liver failure. <i>Annals of Hepatology</i> , 2019, 18, 883-892.	0.6	6
9315	A Structure-Informed Atlas of Human-Virus Interactions. <i>Cell</i> , 2019, 178, 1526-1541.e16.	13.5	108
9316	MicroRNA-124 alleviates the lung injury in mice with septic shock through inhibiting the activation of the MAPK signaling pathway by downregulating MAPK14. <i>International Immunopharmacology</i> , 2019, 76, 105835.	1.7	32
9317	Proteomic, gene and metabolite characterization reveal the uptake and toxicity mechanisms of cadmium sulfide quantum dots in soybean plants. <i>Environmental Science: Nano</i> , 2019, 6, 3010-3026.	2.2	37
9318	Global Transcriptome and Co-Expression Network Analysis Reveal Contrasting Response of Japonica and Indica Rice Cultivar to $\gamma$ Radiation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4358.	1.8	6
9319	<i>Orthosipon stamineus</i> extract exerts inhibition of bacterial adhesion and chaperon-usher system of uropathogenic <i>Escherichia coli</i> —a transcriptomic study. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8571-8584.	1.7	12
9320	Differential expression of novel MicroRNAs from developing fetal heart of <i>Gallus gallus domesticus</i> implies a role in cardiac development. <i>Molecular and Cellular Biochemistry</i> , 2019, 462, 157-165.	1.4	1
9321	Stress-glucocorticoid-TSC22D3 axis compromises therapy-induced antitumor immunity. <i>Nature Medicine</i> , 2019, 25, 1428-1441.	15.2	185

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9322	Cytoscape Automation: empowering workflow-based network analysis. <i>Genome Biology</i> , 2019, 20, 185.	3.8	888
9323	The Role of MicroRNAs in Early Chondrogenesis of Human Induced Pluripotent Stem Cells (hiPSCs). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4371.	1.8	21
9324	Expression profile of tRNA-derived fragments and their potential roles in human varicose veins. <i>Molecular Medicine Reports</i> , 2019, 20, 3191-3201.	1.1	4
9325	Upregulation of MAPK10, TUBB2B and RASL11B may contribute to the development of neuroblastoma. <i>Molecular Medicine Reports</i> , 2019, 20, 3475-3486.	1.1	4
9326	Genome Investigation of a Cariogenic Pathogen with Implications in Cardiovascular Diseases. <i>Indian Journal of Microbiology</i> , 2019, 59, 451-459.	1.5	0
9327	Interrogating Mutant Allele Expression via Customized Reference Genomes to Define Influential Cancer Mutations. <i>Scientific Reports</i> , 2019, 9, 12766.	1.6	5
9328	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019, 294, 15973-15986.	1.6	118
9329	CSF1R inhibitor JNJ-40346527 attenuates microglial proliferation and neurodegeneration in P301S mice. <i>Brain</i> , 2019, 142, 3243-3264.	3.7	156
9330	Identification and Classification of Differentially Expressed Genes and Network Meta-Analysis Reveals Potential Molecular Signatures Associated With Tuberculosis. <i>Frontiers in Genetics</i> , 2019, 10, 932.	1.1	26
9331	Comprehensive Analysis of a Competing Endogenous RNA Network Identifies Seven-lncRNA Signature as a Prognostic Biomarker for Melanoma. <i>Frontiers in Oncology</i> , 2019, 9, 935.	1.3	40
9332	Network Analysis Reveals Seasonal Patterns of Bacterial Community Networks in Lake Taihu under Aquaculture Conditions. <i>Water (Switzerland)</i> , 2019, 11, 1868.	1.2	13
9333	AML Subtype Is a Major Determinant of the Association between Prognostic Gene Expression Signatures and Their Clinical Significance. <i>Cell Reports</i> , 2019, 28, 2866-2877.e5.	2.9	10
9334	New insights into the heat responses of grape leaves via combined phosphoproteomic and acetylproteomic analyses. <i>Horticulture Research</i> , 2019, 6, 100.	2.9	20
9335	Antarctic food web architecture under varying dynamics of sea ice cover. <i>Scientific Reports</i> , 2019, 9, 12454.	1.6	28
9336	Comparative adipose transcriptome analysis digs out genes related to fat deposition in two pig breeds. <i>Scientific Reports</i> , 2019, 9, 12925.	1.6	41
9337	pathCHEMO, a generalizable computational framework uncovers molecular pathways of chemoresistance in lung adenocarcinoma. <i>Communications Biology</i> , 2019, 2, 334.	2.0	10
9338	Origins and Evolution of the $\alpha$ -L-Fucosidases: From Bacteria to Metazoans. <i>Frontiers in Microbiology</i> , 2019, 10, 1756.	1.5	15
9339	The Genomics of <i>Streptococcus Pneumoniae</i> Carriage Isolates from UK Children and Their Household Contacts, Pre-PCV7 to Post-PCV13. <i>Genes</i> , 2019, 10, 687.	1.0	16

#	ARTICLE	IF	CITATIONS
9340	Identification of Long Non-Coding RNAs and the Regulatory Network Responsive to Arbuscular Mycorrhizal Fungi Colonization in Maize Roots. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4491.	1.8	22
9341	NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. <i>Scientific Reports</i> , 2019, 9, 12970.	1.6	12
9342	Possible Molecular Mechanisms for the Roles of MicroRNA-21 Played in Lung Cancer. <i>Technology in Cancer Research and Treatment</i> , 2019, 18, 153303381987513.	0.8	7
9343	Chemical Diversity in a Stingless Bee-Plant Symbiosis. <i>ACS Omega</i> , 2019, 4, 15208-15214.	1.6	3
9344	B cells sustain inflammation and predict response to immune checkpoint blockade in human melanoma. <i>Nature Communications</i> , 2019, 10, 4186.	5.8	236
9345	Exome Sequencing Reveals Immune Genes as Susceptibility Modifiers in Individuals with $\alpha$ 1-Antitrypsin Deficiency. <i>Scientific Reports</i> , 2019, 9, 13088.	1.6	7
9346	Fibrogenic Activity of MECP2 Is Regulated by Phosphorylation in Hepatic Stellate Cells. <i>Gastroenterology</i> , 2019, 157, 1398-1412.e9.	0.6	27
9347	Adaption of human antibody $\gamma$ and $\kappa$ light chain architectures to CDR repertoires. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 109-127.	1.0	12
9348	Evolutionary flexibility in flooding response circuitry in angiosperms. <i>Science</i> , 2019, 365, 1291-1295.	6.0	101
9349	Comparative study of excretory-secretory proteins released by <i>Schistosoma mansoni</i> -resistant, susceptible and naïve <i>Biomphalaria glabrata</i> . <i>Parasites and Vectors</i> , 2019, 12, 452.	1.0	19
9350	Wikipedia network analysis of cancer interactions and world influence. <i>PLoS ONE</i> , 2019, 14, e0222508.	1.1	9
9351	Age-Related Alterations in Immune Contexture Are Associated with Aggressiveness in Rhabdomyosarcoma. <i>Cancers</i> , 2019, 11, 1380.	1.7	15
9352	Sequence and Structural Analysis of AA9 and AA10 LPMOs: An Insight into the Basis of Substrate Specificity and Regioselectivity. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4594.	1.8	15
9353	Fruit metabolic and transcriptional programs differentiate among Andean tomato ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	15
9354	Microbial Interaction Network Inference in Microfluidic Droplets. <i>Cell Systems</i> , 2019, 9, 229-242.e4.	2.9	91
9355	Construction of a Competitive Endogenous RNA Network and Identification of Potential Regulatory Axis in Gastric Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 912.	1.3	24
9356	Distinct Gut Microbiota Composition and Functional Category in Children With Cerebral Palsy and Epilepsy. <i>Frontiers in Pediatrics</i> , 2019, 7, 394.	0.9	46
9357	Transcriptomic Signatures of Experimental Alkaloid Consumption in a Poison Frog. <i>Genes</i> , 2019, 10, 733.	1.0	12

#	ARTICLE	IF	CITATIONS
9358	Visual exploration of microbiome data. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	2
9359	Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6.	5.1	62
9361	Predicting gene regulatory interactions based on spatial gene expression data and deep learning. <i>PLoS Computational Biology</i> , 2019, 15, e1007324.	1.5	42
9362	Dramatic Remodeling of the Gut Microbiome Around Parturition and Its Relationship With Host Serum Metabolic Changes in Sows. <i>Frontiers in Microbiology</i> , 2019, 10, 2123.	1.5	22
9363	Identification of novel genes associated with duck OASL in response to influenza A virus. <i>Journal of Integrative Agriculture</i> , 2019, 18, 1451-1459.	1.7	2
9364	Determination of the Gene Regulatory Network of a Genome-Reduced Bacterium Highlights Alternative Regulation Independent of Transcription Factors. <i>Cell Systems</i> , 2019, 9, 143-158.e13.	2.9	36
9365	Integrating network pharmacology and bioinformatics analysis to explore the mechanism of Yupingfengsan in treating lung adenocarcinoma. <i>European Journal of Integrative Medicine</i> , 2019, 31, 100967.	0.8	5
9366	Turbidity matters: differential effect of a 2,4-D formulation on the structure of microbial communities from clear and turbid freshwater systems. <i>Heliyon</i> , 2019, 5, e02221.	1.4	8
9367	Comparing progression molecular mechanisms between lung adenocarcinoma and lung squamous cell carcinoma based on genetic and epigenetic networks: big data mining and genome-wide systems identification. <i>Oncotarget</i> , 2019, 10, 3760-3806.	0.8	12
9368	MAPK1B, PACS2 and AHCYL1 are regulated by miR-34A/B/C and miR-449 in neuroplasticity following traumatic spinal cord injury in rats: Preliminary explorative results from microarray data. <i>Molecular Medicine Reports</i> , 2019, 20, 3011-3018.	1.1	2
9369	Detection of de novo genetic variants in Mayer-Rokitansky-Kuster-Hauser syndrome by whole genome sequencing. <i>European Journal of Obstetrics and Gynecology and Reproductive Biology: X</i> , 2019, 4, 100089.	0.6	12
9370	Landscape of Enhancer-Enhancer Cooperative Regulation during Human Cardiac Commitment. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 840-851.	2.3	11
9371	Dynamic methylome of internal mRNA N7-methylguanosine and its regulatory role in translation. <i>Cell Research</i> , 2019, 29, 927-941.	5.7	154
9372	Utilizing Whole <i>Fusobacterium</i> Genomes To Identify, Correct, and Characterize Potential Virulence Protein Families. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	28
9373	An Integrated Approach for Efficient Multi-Omics Joint Analysis. , 2019, 2019, 619-625.		1
9374	Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, <i>Astatotilapia burtoni</i> . <i>BMC Genomics</i> , 2019, 20, 699.	1.2	10
9375	Effect of hyperoside on cervical cancer cells and transcriptome analysis of differentially expressed genes. <i>Cancer Cell International</i> , 2019, 19, 235.	1.8	24
9376	Prognostic significance of TOP2A in non-small cell lung cancer revealed by bioinformatic analysis. <i>Cancer Cell International</i> , 2019, 19, 239.	1.8	35

#	ARTICLE	IF	CITATIONS
9377	Dietary Bioactive Lipid Compounds Rich in Menthol Alter Interactions Among Members of Ruminal Microbiota in Sheep. <i>Frontiers in Microbiology</i> , 2019, 10, 2038.	1.5	18
9378	Reconstruction and Analysis of Gene Networks of Human Neurotransmitter Systems Reveal Genes with Contentious Manifestation for Anxiety, Depression, and Intellectual Disabilities. <i>Genes</i> , 2019, 10, 699.	1.0	5
9379	VcFT-induced mobile florigenic signals in transgenic and transgrafted blueberries. <i>Horticulture Research</i> , 2019, 6, 105.	2.9	25
9380	Identification of key modules and prognostic markers in adrenocortical carcinoma by weighted gene co-expression network analysis. <i>Oncology Letters</i> , 2019, 18, 3673-3681.	0.8	11
9381	Proteogenomic Network Analysis of Context-Specific KRAS Signaling in Mouse-to-Human Cross-Species Translation. <i>Cell Systems</i> , 2019, 9, 258-270.e6.	2.9	44
9382	Gene networks underlying the early regulation of <i>Paraburkholderia phytofirmans</i> PsJN induced systemic resistance in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2019, 14, e0221358.	1.1	34
9383	A Network Pharmacology Study of the Multi-Targeting Profile of an Antiarrhythmic Chinese Medicine Xin Su Ning. <i>Frontiers in Pharmacology</i> , 2019, 10, 1138.	1.6	16
9384	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	1.7	13
9385	Evaluating Socio-Ecological Interactions for the Management of Protected Urban Green Spaces. <i>Frontiers in Environmental Science</i> , 2019, 7, .	1.5	7
9386	Bioactivation of Napabucasin Triggers Reactive Oxygen Species-Mediated Cancer Cell Death. <i>Clinical Cancer Research</i> , 2019, 25, 7162-7174.	3.2	46
9387	Plasmacytoid DCs From Patients With Sjögren's Syndrome Are Transcriptionally Primed for Enhanced Pro-inflammatory Cytokine Production. <i>Frontiers in Immunology</i> , 2019, 10, 2096.	2.2	48
9388	Lysine Propionylation is a Widespread Post-Translational Modification Involved in Regulation of Photosynthesis and Metabolism in Cyanobacteria. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4792.	1.8	12
9389	Identification of Microbial Profiles in Heavy-Metal-Contaminated Soil from Full-Length 16S rRNA Reads Sequenced by a PacBio System. <i>Microorganisms</i> , 2019, 7, 357.	1.6	18
9390	A combined molecular biology and network pharmacology approach to investigate the multi-target mechanisms of Chaihu Shugan San on Alzheimer's disease. <i>Biomedicine and Pharmacotherapy</i> , 2019, 120, 109370.	2.5	57
9391	A retinal-binding protein mediates olfactory attraction in the migratory locusts. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 114, 103214.	1.2	2
9392	Resolving a clinical tuberculosis outbreak using palaeogenomic genome reconstruction methodologies. <i>Tuberculosis</i> , 2019, 119, 101865.	0.8	1
9393	Global transcriptional regulation of STAT3- and MYC-mediated sepsis-induced ARDS. <i>Therapeutic Advances in Respiratory Disease</i> , 2019, 13, 175346661987984.	1.0	35
9394	Transcriptome analysis of <i>Plasmodium berghei</i> during exo-erythrocytic development. <i>Malaria Journal</i> , 2019, 18, 330.	0.8	46

#	ARTICLE	IF	CITATIONS
9395	<p>Roundabout signaling pathway involved in the pathogenesis of COPD by integrative bioinformatics analysis</p>. International Journal of COPD, 2019, Volume 14, 2145-2162.	0.9	18
9396	<p>MicroRNA-424 regulates cisplatin resistance of gastric cancer by targeting SMURF1 based on GEO database and primary validation in human gastric cancer tissues</p>. OncoTargets and Therapy, 2019, Volume 12, 7623-7636.	1.0	30
9397	<p>TNF-like ligand 1A is associated with progression and prognosis of human gastric cancer</p>. OncoTargets and Therapy, 2019, Volume 12, 7715-7723.	1.0	2
9398	Understanding the Modus Operandi of MicroRNA Regulatory Clusters. Cells, 2019, 8, 1103.	1.8	11
9399	Identification of Alternatively-Activated Pathways between Primary Breast Cancer and Liver Metastatic Cancer Using Microarray Data. Genes, 2019, 10, 753.	1.0	12
9400	Marine Natural Products and Drug Resistance in Latent Tuberculosis. Marine Drugs, 2019, 17, 549.	2.2	13
9401	Genome profiling revealed the activation of IL2RG/JAK3/STAT5 in peripheral Tâ€cell lymphoma expressing the ITKâ€SYK fusion gene. International Journal of Oncology, 2019, 55, 1077-1089.	1.4	8
9402	Diversity of vaginal microbiome and metabolome during genital infections. Scientific Reports, 2019, 9, 14095.	1.6	210
9403	MABE 2.0. , 2019, , .		3
9404	Mapping Interactome Networks of DNAJC11, a Novel Mitochondrial Protein Causing Neuromuscular Pathology in Mice. Journal of Proteome Research, 2019, 18, 3896-3912.	1.8	6
9405	Multilayered Control of Protein Turnover by TORC1 and Atg1. Cell Reports, 2019, 28, 3486-3496.e6.	2.9	87
9406	RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. Scientific Reports, 2019, 9, 13917.	1.6	60
9407	Expression Profiling of Blood microRNAs 885, 361, and 17 in the Patients with the Parkinsonâ€™s disease: Integrating Interaction Data to Uncover the Possible Triggering Age-Related Mechanisms. Scientific Reports, 2019, 9, 13759.	1.6	21
9408	LurR is a regulator of the central lactate oxidation pathway in sulfate-reducing Desulfovibrio species. PLoS ONE, 2019, 14, e0214960.	1.1	3
9409	Genetic Characteristic and RNA-Seq Analysis in Transparent Mutant of Carpâ€™Goldfish Nucleocytoplasmic Hybrid. Genes, 2019, 10, 704.	1.0	4
9410	Genome-Wide Analysis of Cotton Auxin Early Response Gene Families and Their Roles in Somatic Embryogenesis. Genes, 2019, 10, 730.	1.0	18
9411	High-fat diet feeding and palmitic acid increase CRC growth in Î²2AR-dependent manner. Cell Death and Disease, 2019, 10, 711.	2.7	33
9412	Genome Mining Coupled with OSMAC-Based Cultivation Reveal Differential Production of Surugamide A by the Marine Sponge Isolate Streptomyces sp. SM17 When Compared to Its Terrestrial Relative S. albidoflavus J1074. Microorganisms, 2019, 7, 394.	1.6	21



#	ARTICLE	IF	CITATIONS
9413	The EFI Web Resource for Genomic Enzymology Tools: Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic Pathways. <i>Biochemistry</i> , 2019, 58, 4169-4182.	1.2	441
9415	Genome-Wide Methylation Profiling in Canine Mammary Tumor Reveals miRNA Candidates Associated with Human Breast Cancer. <i>Cancers</i> , 2019, 11, 1466.	1.7	16
9416	Causality Detection Methods Applied to the Investigation of Malaria Epidemics. <i>Entropy</i> , 2019, 21, 784.	1.1	9
9417	Identification of potential key genes in esophageal adenocarcinoma using bioinformatics. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 3291-3298.	0.8	10
9418	Comparative modulation of lncRNAs in wild-type and rag1-heterozygous mutant zebrafish exposed to immune challenge with spring viraemia of carp virus (SVCV). <i>Scientific Reports</i> , 2019, 9, 14174.	1.6	36
9419	Identification and analysis of survival-associated ceRNA triplets in prostate adenocarcinoma. <i>Oncology Letters</i> , 2019, 18, 4040-4047.	0.8	4
9420	A novel approach based on metabolomics coupled with network pharmacology to explain the effect mechanisms of Danggui Buxue Tang in anaemia. <i>Chinese Journal of Natural Medicines</i> , 2019, 17, 275-290.	0.7	18
9421	MTA1 coregulator regulates LDHA expression and function in breast cancer. <i>Biochemical and Biophysical Research Communications</i> , 2019, 520, 54-59.	1.0	18
9422	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	13.5	65
9423	Construction and analysis of a diabetic nephropathy related protein-protein interaction network reveals nine critical and functionally associated genes. <i>Computational Biology and Chemistry</i> , 2019, 83, 107115.	1.1	1
9424	The spatial binding model of the pioneer factor Oct4 with its target genes during cell reprogramming. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1226-1233.	1.9	23
9425	Niche-Specific Factors Dynamically Regulate Sebaceous Gland Stem Cells in the Skin. <i>Developmental Cell</i> , 2019, 51, 326-340.e4.	3.1	32
9426	Time course analysis of immunity-related gene expression in the sea cucumber <i>Apostichopus japonicus</i> during exposure to thermal and hypoxic stress. <i>Fish and Shellfish Immunology</i> , 2019, 95, 383-390.	1.6	21
9427	The <i>Salix psammophila</i> SpRLCK1 involved in drought and salt tolerance. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 222-233.	2.8	11
9428	Transcriptome Sequencing of Peripheral Blood Mononuclear Cells from Elite Controller-Long Term Non Progressors. <i>Scientific Reports</i> , 2019, 9, 14265.	1.6	29
9429	Widespread cis-regulatory convergence between the extinct Tasmanian tiger and gray wolf. <i>Genome Research</i> , 2019, 29, 1648-1658.	2.4	18
9430	LGP2 binds to PACT to regulate RIG-I and MDA5-mediated antiviral responses. <i>Science Signaling</i> , 2019, 12, .	1.6	51
9431	Microarray-based analysis of COL11A1 and TWIST1 as important differentially expressed pathogenic genes between left and right-sided colon cancer. <i>Molecular Medicine Reports</i> , 2019, 20, 4202-4214.	1.1	6



#	ARTICLE	IF	CITATIONS
9432	Metabolomics using Fourier transform mass spectrometry. , 2019, , 325-356.		2
9433	Comparative analysis of midgut bacterial community under <i>Vibrio splendidus</i> infection in <i>Apostichopus japonicus</i> with hindgut as a reference. <i>Aquaculture</i> , 2019, 513, 734427.	1.7	15
9434	Modulation of Caspase-3 activity using a redox active vitamin K3 analogue, plumbagin, as a novel strategy for radioprotection. <i>Free Radical Biology and Medicine</i> , 2019, 143, 560-572.	1.3	14
9435	Sockeye salmon demonstrate robust yet distinct transcriptomic kidney responses to rhabdovirus (IHNV) exposure and infection. <i>Fish and Shellfish Immunology</i> , 2019, 94, 525-538.	1.6	13
9436	Interleukin 22 disrupts pancreatic function in newborn mice expressing IL-23. <i>Nature Communications</i> , 2019, 10, 4517.	5.8	8
9437	Insights into sucrose pathway of chicory stems by integrative transcriptomic and metabolic analyses. <i>Phytochemistry</i> , 2019, 167, 112086.	1.4	2
9438	Signal flow control of complex signaling networks. <i>Scientific Reports</i> , 2019, 9, 14289.	1.6	6
9439	Expression of microRNA in human retinal pigment epithelial cells following infection with Zaire ebolavirus. <i>BMC Research Notes</i> , 2019, 12, 639.	0.6	10
9440	Plasma Metabolic Signature and Abnormalities in HIV-Infected Individuals on Long-Term Successful Antiretroviral Therapy. <i>Metabolites</i> , 2019, 9, 210.	1.3	46
9441	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. <i>Cell Reports</i> , 2019, 29, 495-510.e6.	2.9	66
9442	Refinements of LC-MS/MS Spectral Counting Statistics Improve Quantification of Low Abundance Proteins. <i>Scientific Reports</i> , 2019, 9, 13653.	1.6	23
9443	Association study reveals Th17, Treg, and Th2 loci related to resistance to <i>Haemonchus contortus</i> in Florida Native sheep1. <i>Journal of Animal Science</i> , 2019, 97, 4428-4444.	0.2	14
9444	A Transcriptome Analysis Identifies Biological Pathways and Candidate Genes for Feed Efficiency in DLY Pigs. <i>Genes</i> , 2019, 10, 725.	1.0	10
9446	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. <i>Nature Genetics</i> , 2019, 51, 1429-1433.	9.4	76
9447	A framework for the investigation of rare genetic disorders in neuropsychiatry. <i>Nature Medicine</i> , 2019, 25, 1477-1487.	15.2	90
9448	Analysis of cardiovascular disease-related NF- $\kappa$ B-regulated genes and microRNAs in TNF $\alpha$ -treated primary mouse vascular endothelial cells. <i>Journal of Zhejiang University: Science B</i> , 2019, 20, 803-815.	1.3	8
9449	Proteomic Analysis Reveals a Biofilm-Like Behavior of Planktonic Aggregates of <i>Staphylococcus epidermidis</i> Grown Under Environmental Pressure/Stress. <i>Frontiers in Microbiology</i> , 2019, 10, 1909.	1.5	14
9450	Xiaoerfupi alleviates the symptoms of functional dyspepsia by regulating the HTR3A and c-FOS. <i>Biomedicine and Pharmacotherapy</i> , 2019, 120, 109442.	2.5	13

#	ARTICLE	IF	CITATIONS
9451	The RNA-mediated estrogen receptor $\hat{\pm}$ interactome of hormone-dependent human breast cancer cell nuclei. <i>Scientific Data</i> , 2019, 6, 173.	2.4	18
9452	Identification and validation of four hub genes involved in the plaque deterioration of atherosclerosis. <i>Aging</i> , 2019, 11, 6469-6489.	1.4	13
9453	&lt;p&gt;A network pharmacology approach to explore active compounds and pharmacological mechanisms of epimedium for treatment of premature ovarian insufficiency&lt;p&gt;. <i>Drug Design, Development and Therapy</i> , 2019, Volume 13, 2997-3007.	2.0	35
9454	Non-volatile pungent compounds isolated from <i>Zingiber officinale</i> and their mechanisms of action. <i>Food and Function</i> , 2019, 10, 1203-1211.	2.1	14
9455	De Novo Assembly and Discovery of Genes That Involved in Drought Tolerance in the Common Vetch. <i>International Journal of Molecular Sciences</i> , 2019, 20, 328.	1.8	20
9456	Pericardial fluid: an underrated molecular library of heart conditions and a potential vehicle for cardiac therapy. <i>Basic Research in Cardiology</i> , 2019, 114, 10.	2.5	31
9457	<i>Omics.</i> , 2019, , 375-400.		0
9458	Downregulated lncRNA-MIAT confers protection against erectile dysfunction by downregulating lipoprotein lipase via activation of miR-328a-5p in diabetic rats. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 1226-1240.	1.8	15
9459	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	2.9	33
9460	Disclosing the Template-Induced Misfolding Mechanism of Tau Protein by Studying the Dissociation of the Boundary Chain from the Formed Tau Fibril Based on a Steered Molecular Dynamics Simulation. <i>ACS Chemical Neuroscience</i> , 2019, 10, 1854-1865.	1.7	14
9461	Untargeted metabolomic profiling reveals multiple pathway perturbations and new clinical biomarkers in urea cycle disorders. <i>Genetics in Medicine</i> , 2019, 21, 1977-1986.	1.1	47
9462	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. <i>Nature Protocols</i> , 2019, 14, 482-517.	5.5	1,172
9463	Low mutation and neoantigen burden and fewer effector tumor infiltrating lymphocytes correlate with breast cancer metastasization to lymph nodes. <i>Scientific Reports</i> , 2019, 9, 253.	1.6	18
9464	Uncoupling of transcriptomic and cytological differentiation in mouse spermatocytes with impaired meiosis. <i>Molecular Biology of the Cell</i> , 2019, 30, 717-728.	0.9	10
9465	Protein and metabolite composition of <i>Arabidopsis</i> stress granules. <i>New Phytologist</i> , 2019, 222, 1420-1433.	3.5	103
9466	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	2.3	34
9467	Integrative Analyses of Genes Associated with Subcutaneous Insulin Resistance. <i>Biomolecules</i> , 2019, 9, 37.	1.8	14
9468	Weighted gene co-expression network analysis for identifying hub genes in association with prognosis in Wilms tumor. <i>Molecular Medicine Reports</i> , 2019, 19, 2041-2050.	1.1	13

#	ARTICLE	IF	CITATIONS
9469	GCâ€“MS metabolic profiling reveals fructose-2,6-bisphosphate regulates branched chain amino acid metabolism in the heart during fasting. <i>Metabolomics</i> , 2019, 15, 18.	1.4	18
9470	A Six-Gene-Based Prognostic Model Predicts Survival in Head and Neck Squamous Cell Carcinoma Patients. <i>Journal of Maxillofacial and Oral Surgery</i> , 2019, 18, 320-327.	0.6	1
9471	Differential expression of a set of microRNA genes reveals the potential mechanism of papillary thyroid carcinoma. <i>Annales D'Endocrinologie</i> , 2019, 80, 77-83.	0.6	1
9472	DOF2.1 Controls Cytokinin-Dependent Vascular Cell Proliferation Downstream of TMO5/LHW. <i>Current Biology</i> , 2019, 29, 520-529.e6.	1.8	80
9473	Genome-wide association study and protein network analysis for understanding candidate genes involved in root development at the rapeseed seedling stage. <i>Plant Physiology and Biochemistry</i> , 2019, 137, 42-52.	2.8	15
9474	Expression analysis of lung miRNAs responding to ovine VM virus infection by RNA-seq. <i>BMC Genomics</i> , 2019, 20, 62.	1.2	16
9475	Prenatal Bisphenol A Exposure in Mice Induces Multitissue Multiomics Disruptions Linking to Cardiometabolic Disorders. <i>Endocrinology</i> , 2019, 160, 409-429.	1.4	35
9476	Bioinformatics analysis of sex differences in arrhythmogenic right ventricular cardiomyopathy. <i>Molecular Medicine Reports</i> , 2019, 19, 2238-2244.	1.1	6
9477	Biogeography and Diversity of Freshwater Bacteria on a River Catchment Scale. <i>Microbial Ecology</i> , 2019, 78, 324-335.	1.4	7
9478	CALD1, CNN1, and TAGLN identified as potential prognostic molecular markers of bladder cancer by bioinformatics analysis. <i>Medicine (United States)</i> , 2019, 98, e13847.	0.4	33
9479	High Throughput mRNA Sequencing Reveals Potential Therapeutic Targets of Tao-Hong-Si-Wu Decoction in Experimental Middle Cerebral Artery Occlusion. <i>Frontiers in Pharmacology</i> , 2018, 9, 1570.	1.6	17
9480	Proteomic Analysis of Cyclic Ketamine Compounds Ability to Induce Neural Differentiation in Human Adult Mesenchymal Stem Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 523.	1.8	9
9481	Global Transcriptional Insights of Pollen-Pistil Interactions Commencing Self-Incompatibility and Fertilization in Tea [ <i>Camellia sinensis</i> (L.) O. Kuntze]. <i>International Journal of Molecular Sciences</i> , 2019, 20, 539.	1.8	34
9482	Secondary analysis of existing microarray data reveals potential gene drivers of cutaneous squamous cell carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 15270-15278.	2.0	14
9483	A detailed image of rutin underlying intracellular signaling pathways in human SW480 colorectal cancer cells based on miRNAsâ€“lncRNAsâ€“mRNAsâ€“TFs interactions. <i>Journal of Cellular Physiology</i> , 2019, 234, 15570-15580.	2.0	30
9484	Muscle wasting in patients with endâ€“stage renal disease or earlyâ€“stage lung cancer: common mechanisms at work. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2019, 10, 323-337.	2.9	30
9485	A Hierarchical Regulatory Landscape during the Multiple Stages of EMT. <i>Developmental Cell</i> , 2019, 48, 539-553.e6.	3.1	67
9486	Loss of function dysbiosis associated with antibiotics and high fat, high sugar diet. <i>ISME Journal</i> , 2019, 13, 1379-1390.	4.4	29

#	ARTICLE	IF	CITATIONS
9487	Identification of a 26-lncRNAs Risk Model for Predicting Overall Survival of Cervical Squamous Cell Carcinoma Based on Integrated Bioinformatics Analysis. <i>DNA and Cell Biology</i> , 2019, 38, 322-332.	0.9	25
9488	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	2.4	258
9489	Dynamic expression and functional analysis of circRNA in granulosa cells during follicular development in chicken. <i>BMC Genomics</i> , 2019, 20, 96.	1.2	59
9490	Enterobacteriaceae dominate the core microbiome and contribute to the resistome of arugula ( <i>Eruca</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	4.9	84
9491	An integrated transcriptional analysis of the developing human retina. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	75
9492	Integrative Analysis of Transcriptome and GWAS Data to Identify the Hub Genes Associated With Milk Yield Trait in Buffalo. <i>Frontiers in Genetics</i> , 2019, 10, 36.	1.1	52
9493	Insights into the substrate binding specificity of quorum-quenching acylase PvdQ. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 88, 104-120.	1.3	16
9494	Molecular pathways of varicocele and its repair – A paired labelled shotgun proteomics approach. <i>Journal of Proteomics</i> , 2019, 196, 22-32.	1.2	20
9495	Remote Induction of Cell Autophagy by 2D MoS <sub>2</sub> Nanosheets via Perturbing Cell Surface Receptors and mTOR Pathway from Outside of Cells. <i>ACS Applied Materials &amp; Interfaces</i> , 2019, 11, 6829-6839.	4.0	30
9496	Haplotype analysis of key genes governing grain yield and quality traits across 3K <i>RG</i> panel reveals scope for the development of tailor-made rice with enhanced genetic gains. <i>Plant Biotechnology Journal</i> , 2019, 17, 1612-1622.	4.1	87
9497	The Purple Sea Urchin <i>Strongylocentrotus purpuratus</i> Demonstrates a Compartmentalization of Gut Bacterial Microbiota, Predictive Functional Attributes, and Taxonomic Co-Occurrence. <i>Microorganisms</i> , 2019, 7, 35.	1.6	24
9498	Identification of prognostic biomarkers for patients with hepatocellular carcinoma after hepatectomy. <i>Oncology Reports</i> , 2019, 41, 1586-1602.	1.2	26
9499	<i>VCAN</i> Canonical Splice Site Mutation is Associated With Vitreoretinal Degeneration and Disrupts an MMP Proteolytic Site. , 2019, 60, 282.		19
9500	Re-analysis of the coral <i>Acropora digitifera</i> transcriptome reveals a complex lncRNAs-mRNAs interaction network implicated in Symbiodinium infection. <i>BMC Genomics</i> , 2019, 20, 48.	1.2	13
9501	The Plant-Transpiration Response to Vapor Pressure Deficit (VPD) in Durum Wheat Is Associated With Differential Yield Performance and Specific Expression of Genes Involved in Primary Metabolism and Water Transport. <i>Frontiers in Plant Science</i> , 2018, 9, 1994.	1.7	45
9502	Mutations in gliclazide-associated genes may predict poor bladder cancer prognosis. <i>FEBS Open Bio</i> , 2019, 9, 457-467.	1.0	6
9503	Coexpression network analysis of platelet genes in sickle cell disease. <i>Platelets</i> , 2019, 30, 1022-1029.	1.1	5
9504	Ketamine Reduces Inflammation Pathways in the Hypothalamus and Hippocampus Following Transient Hypoxia in the Late-Gestation Fetal Sheep. <i>Frontiers in Physiology</i> , 2019, 9, 1858.	1.3	12

#	ARTICLE	IF	CITATIONS
9505	Exploring the cause of the inhibitor 4AX attaching to binding site disrupting protein tyrosine phosphatase 4A1 trimerization by molecular dynamic simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 4840-4851.	2.0	19
9506	Pregnancy Epigenetic Signature in T Helper 17 and T Regulatory Cells in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2018, 9, 3075.	2.2	26
9507	Bioinformatics Analysis of Key Differentially Expressed Genes in Nonalcoholic Fatty Liver Disease Mice Models. <i>Gene Expression</i> , 2019, 19, 25-35.	0.5	13
9508	Potential Biomarkers for Primary Open-Angle Glaucoma Identified by Long Noncoding RNA Profiling in the Aqueous Humor. <i>American Journal of Pathology</i> , 2019, 189, 739-752.	1.9	26
9509	Brain-enriched MicroRNA-184 is downregulated in older adults with major depressive disorder: A translational study. <i>Journal of Psychiatric Research</i> , 2019, 111, 110-120.	1.5	19
9510	Systems biology reveals how altered TGF $\beta$ 2 signalling with age reduces protection against pro-inflammatory stimuli. <i>PLoS Computational Biology</i> , 2019, 15, e1006685.	1.5	12
9511	Integrated Transcriptome Analysis Reveals Plant Hormones Jasmonic Acid and Salicylic Acid Coordinate Growth and Defense Responses upon Fungal Infection in Poplar. <i>Biomolecules</i> , 2019, 9, 12.	1.8	72
9512	Revealing the Presence of a Symbolic Sequence Representing Multiple Nucleotides Based on K-Means Clustering of Oligonucleotides. <i>Molecules</i> , 2019, 24, 348.	1.7	1
9513	Identification of key genes and pathways involved in microsatellite instability in colorectal cancer. <i>Molecular Medicine Reports</i> , 2019, 19, 2065-2076.	1.1	25
9514	Identification and characterization of circular RNAs during the sea buckthorn fruit development. <i>RNA Biology</i> , 2019, 16, 354-361.	1.5	30
9515	Graph-Based Hub Gene Selection Technique Using Protein Interaction Information: Application to Sample Classification. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 2670-2676.	3.9	15
9516	World influence and interactions of universities from Wikipedia networks. <i>European Physical Journal B</i> , 2019, 92, 1.	0.6	22
9517	Vasoactive intestinal peptide controls the suprachiasmatic circadian clock network via ERK1/2 and DUSP4 signalling. <i>Nature Communications</i> , 2019, 10, 542.	5.8	44
9518	Fungal Endophyte Communities of Three Agricultural Important Grass Species Differ in Their Response Towards Management Regimes. <i>Microorganisms</i> , 2019, 7, 37.	1.6	14
9519	Network Analysis Reveals TNF as a Major Hub of Reactive Inflammation Following Spinal Cord Injury. <i>Scientific Reports</i> , 2019, 9, 928.	1.6	12
9520	Integrative metabolomics reveals unique metabolic traits in Guillain-Barré Syndrome and its variants. <i>Scientific Reports</i> , 2019, 9, 1077.	1.6	16
9521	Mapping the Surface Microbiome and Metabolome of Brown Seaweed <i>Fucus vesiculosus</i> by Amplicon Sequencing, Integrated Metabolomics and Imaging Techniques. <i>Scientific Reports</i> , 2019, 9, 1061.	1.6	76
9522	High metabolic variation for seaweeds in response to environmental changes: a case study of the brown algae <i>Lobophora</i> in coral reefs. <i>Scientific Reports</i> , 2019, 9, 993.	1.6	26

#	ARTICLE	IF	CITATIONS
9523	Linking genetic, metabolic, and phenotypic diversity among <i>Saccharomyces cerevisiae</i> strains using multi-omics associations. <i>GigaScience</i> , 2019, 8, .	3.3	25
9524	Comparison of the metabolomic profiles of irritable bowel syndrome patients with ulcerative colitis patients and healthy controls: new insights into pathophysiology and potential biomarkers. <i>Alimentary Pharmacology and Therapeutics</i> , 2019, 49, 723-732.	1.9	37
9525	Comparison of splenocyte microRNA expression profiles of pigs during acute and chronic toxoplasmosis. <i>BMC Genomics</i> , 2019, 20, 97.	1.2	36
9526	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of <i>Eucalyptus grandis</i> Roots. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	17
9528	Transcriptome Analysis of Mesenchymal Stem Cells from Multiple Myeloma Patients Reveals Downregulation of Genes Involved in Cell Cycle Progression, Immune Response, and Bone Metabolism. <i>Scientific Reports</i> , 2019, 9, 1056.	1.6	28
9529	Construction of a high density genetic map of an interspecific cross of <i>Capsicum chinense</i> and <i>Capsicum annuum</i> and QTL analysis of floral traits. <i>Scientific Reports</i> , 2019, 9, 1054.	1.6	21
9530	Cafeteria Diet Consumption during Lactation in Rats, Rather than Obesity Per Se, alters miR-222, miR-200a, and miR-26a Levels in Milk. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1800928.	1.5	23
9531	Regulation of Growth and Flavonoid Formation of Tea Plants ( <i>Camellia sinensis</i> ) by Blue and Green Light. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2408-2419.	2.4	56
9532	Biochemical and structural investigation of sulfoacetaldehyde reductase from <i>Klebsiella oxytoca</i> . <i>Biochemical Journal</i> , 2019, 476, 733-746.	1.7	11
9533	Systemic oscillator-driven and nutrient-responsive hormonal regulation of daily expression rhythms for gluconeogenic enzyme genes in the mouse liver. <i>Chronobiology International</i> , 2019, 36, 591-615.	0.9	7
9534	Applying a multiscale systems biology approach to study the effect of chronic low-dose exposure to uranium in rat kidneys. <i>International Journal of Radiation Biology</i> , 2019, 95, 737-752.	1.0	11
9535	Spaceflight/microgravity inhibits the proliferation of hematopoietic stem cells by decreasing Kit-Ras/cAMP-CREB pathway networks as evidenced by RNA-seq assays. <i>FASEB Journal</i> , 2019, 33, 5903-5913.	0.2	25
9536	Hypoxic cancer-associated fibroblasts increase NCBP2-AS2/HIAR to promote endothelial sprouting through enhanced VEGF signaling. <i>Science Signaling</i> , 2019, 12, .	1.6	83
9537	Transcriptome sequencing in a 6-hydroxydopamine rat model of Parkinson's disease. <i>Genes and Genetic Systems</i> , 2019, 94, 61-69.	0.2	24
9538	Genome-Wide Identification and Transcriptional Expression of the PAL Gene Family in Common Walnut ( <i>Juglans Regia</i> L.). <i>Genes</i> , 2019, 10, 46.	1.0	31
9539	Identification of gene coexpression modules, hub genes, and pathways related to spinal cord injury using integrated bioinformatics methods. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6988-6997.	1.2	7
9540	<i>Streptomyces pactum</i> Act12 controls tomato yellow leaf curl virus disease and alters rhizosphere microbial communities. <i>Biology and Fertility of Soils</i> , 2019, 55, 149-169.	2.3	25
9541	The microbial network in naturally fertile paddy soil possibly facilitates functional recruitment in the rice mature stage. <i>Applied Soil Ecology</i> , 2019, 135, 174-181.	2.1	13



#	ARTICLE	IF	CITATIONS
9542	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. <i>Nature Communications</i> , 2019, 10, 296.	5.8	23
9543	LncRNA-mRNA competing endogenous RNA network depicts transcriptional regulation in ischaemia reperfusion injury. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 2272-2276.	1.6	25
9544	A Network Pharmacology Approach to Explore Mechanism of Action of Longzuan Tongbi Formula on Rheumatoid Arthritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-13.	0.5	8
9545	An interaction-based model for neuropsychiatric features of copy-number variants. <i>PLoS Genetics</i> , 2019, 15, e1007879.	1.5	39
9546	Metabolomic Analysis of Defense-Related Reprogramming in <i>Sorghum bicolor</i> in Response to <i>Colletotrichum sublineolum</i> Infection Reveals a Functional Metabolic Web of Phenylpropanoid and Flavonoid Pathways. <i>Frontiers in Plant Science</i> , 2018, 9, 1840.	1.7	83
9547	Differential damage and repair of DNA-adducts induced by anti-cancer drug cisplatin across mouse organs. <i>Nature Communications</i> , 2019, 10, 309.	5.8	131
9548	Transcriptome profiling of dorsal root ganglia in a rat model of complex regional pain syndrome type-I reveals potential mechanisms involved in pain. <i>Journal of Pain Research</i> , 2019, Volume 12, 1201-1216.	0.8	22
9549	Identification of key genes and pathways in seminoma by bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3683-3693.	1.0	10
9550	RNA sequencing uncovers the key long non-coding RNAs and potential molecular mechanism contributing to XAV939-mediated inhibition of non-small cell lung cancer. <i>Oncology Letters</i> , 2019, 17, 4994-5004.	0.8	28
9551	Association of lncL17RA1 with increased radiation sensitivity and improved prognosis of HPV-positive HNSCC. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 17438-17448.	1.2	15
9552	Quantitative proteomics analysis provides insight into the biological role of Hsp90 in BmNPV infection in <i>Bombyx mori</i> . <i>Journal of Proteomics</i> , 2019, 203, 103379.	1.2	23
9553	Omics Technologies to Understand Activation of a Biosynthetic Gene Cluster in <i>Micromonospora</i> sp. WMMB235: Deciphering Keyicin Biosynthesis. <i>ACS Chemical Biology</i> , 2019, 14, 1260-1270.	1.6	8
9554	A single-cell transcriptomic atlas of the developing chicken limb. <i>BMC Genomics</i> , 2019, 20, 401.	1.2	38
9555	Microbial community drivers of PK/NRP gene diversity in selected global soils. <i>Microbiome</i> , 2019, 7, 78.	4.9	30
9556	Evidence for fungi and gold redox interaction under Earth surface conditions. <i>Nature Communications</i> , 2019, 10, 2290.	5.8	25
9557	Exploratory Gene Ontology Analysis with Interactive Visualization. <i>Scientific Reports</i> , 2019, 9, 7793.	1.6	10
9558	ChEA3: transcription factor enrichment analysis by orthogonal omics integration. <i>Nucleic Acids Research</i> , 2019, 47, W212-W224.	6.5	512
9559	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, ChIP-Seq and ChIA-PET data. <i>BMC Genomics</i> , 2019, 20, 296.	1.2	12



#	ARTICLE	IF	CITATIONS
9560	Overlapping and unique roles played by ROCK1 and 2 in the modulation of coding and long noncoding RNA expression. <i>BMC Genomics</i> , 2019, 20, 409.	1.2	3
9561	Identification of genes underlying phenotypic plasticity of wing size via insulin signaling pathway by network-based analysis in <i>Sogatella furcifera</i> . <i>BMC Genomics</i> , 2019, 20, 396.	1.2	10
9562	Eleven genes associated with progression and prognosis of endometrial cancer (EC) identified by comprehensive bioinformatics analysis. <i>Cancer Cell International</i> , 2019, 19, 136.	1.8	61
9563	Stress hormone-mediated acceleration of breast cancer metastasis is halted by inhibition of nitric oxide synthase. <i>Cancer Letters</i> , 2019, 459, 59-71.	3.2	32
9564	Arabidopsis DGD1 SUPPRESSOR1 Is a Subunit of the Mitochondrial Contact Site and Cristae Organizing System and Affects Mitochondrial Biogenesis. <i>Plant Cell</i> , 2019, 31, 1856-1878.	3.1	19
9565	Identification and validation of key genes associated with non-small cell lung cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 22742-22752.	2.0	68
9566	Proteomics Profiling of Host Cell Response via Protein Expression and Phosphorylation upon Dengue Virus Infection. <i>Virologica Sinica</i> , 2019, 34, 549-562.	1.2	23
9567	Genome-wide analysis of bHLH transcription factor family reveals their involvement in biotic and abiotic stress responses in wheat ( <i>Triticum aestivum</i> L.). <i>3 Biotech</i> , 2019, 9, 236.	1.1	41
9568	Microcystin-LR-regulated transcriptome dynamics in ZFL cells. <i>Aquatic Toxicology</i> , 2019, 212, 222-232.	1.9	11
9569	Mitochondrial metabolism promotes adaptation to proteotoxic stress. <i>Nature Chemical Biology</i> , 2019, 15, 681-689.	3.9	275
9570	Network analysis of hyphae forming proteins in <i>Candida albicans</i> identifies important proteins responsible for pathovirulence in the organism. <i>Heliyon</i> , 2019, 5, e01916.	1.4	11
9571	Advancing integration of data on food microbiome studies: FoodMicrobionet 3.1, a major upgrade of the FoodMicrobionet database. <i>International Journal of Food Microbiology</i> , 2019, 305, 108249.	2.1	32
9572	ABC Transporter Genes Show Upregulated Expression in Drug-Resistant Clinical Isolates of <i>Candida auris</i> : A Genome-Wide Characterization of ATP-Binding Cassette (ABC) Transporter Genes. <i>Frontiers in Microbiology</i> , 2019, 10, 1445.	1.5	55
9573	The Ubiquitin Proteasome System Is a Key Regulator of Pluripotent Stem Cell Survival and Motor Neuron Differentiation. <i>Cells</i> , 2019, 8, 581.	1.8	31
9574	Uncovering the pharmacological mechanism of <i>Carthamus tinctorius</i> L. on cardiovascular disease by a systems pharmacology approach. <i>Biomedicine and Pharmacotherapy</i> , 2019, 117, 109094.	2.5	56
9575	Combined Inhibitory Effects of Citrinin, Ochratoxin-A, and T-2 Toxin on Aquaporin-2. <i>Journal of Physical Chemistry B</i> , 2019, 123, 5755-5768.	1.2	8
9576	Mediator complex interaction partners organize the transcriptional network that defines neural stem cells. <i>Nature Communications</i> , 2019, 10, 2669.	5.8	53
9577	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	2.5	14

#	ARTICLE	IF	CITATIONS
9578	CircRNA_28313/miR-195a/CSF1 axis modulates osteoclast differentiation to affect OVX-induced bone absorption in mice. <i>RNA Biology</i> , 2019, 16, 1249-1262.	1.5	104
9579	Diagnostic and prognostic significance of mRNA expressions of apolipoprotein A and C family genes in hepatitis B virus-related hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 18246-18265.	1.2	25
9580	Integrated analysis of clinical significance and functional involvement of microRNAs in hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 23581-23595.	2.0	23
9581	The Phosphatase PRL-3 Is Involved in Key Steps of Cancer Metastasis. <i>Journal of Molecular Biology</i> , 2019, 431, 3056-3067.	2.0	21
9582	Overexpression of Osmosensitive Ca <sup>2+</sup> -Permeable Channel TMEM63B Promotes Migration in HEK293T Cells. <i>Biochemistry</i> , 2019, 58, 2861-2866.	1.2	13
9583	Neocarzinil A Is a Potent Inhibitor of Cancer Cell Motility Targeting VAT-1 Controlled Pathways. <i>ACS Central Science</i> , 2019, 5, 1170-1178.	5.3	12
9584	Extracting Pathway-level Signatures from Proteogenomic Data in Breast Cancer Using Independent Component Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S169-S182.	2.5	15
9585	Survival analysis and functional annotation of long non-coding RNAs in lung adenocarcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5600-5617.	1.6	25
9586	Differentially expressed mRNAs, proteins and miRNAs associated to energy metabolism in skeletal muscle of beef cattle identified for low and high residual feed intake. <i>BMC Genomics</i> , 2019, 20, 501.	1.2	22
9587	Platelet count, aspirin use, and characteristics of host inflammatory responses in colorectal cancer. <i>Journal of Translational Medicine</i> , 2019, 17, 199.	1.8	16
9588	Nutrient Acquisition, Rather Than Stress Response Over Diel Cycles, Drives Microbial Transcription in a Hyper-Arid Namib Desert Soil. <i>Frontiers in Microbiology</i> , 2019, 10, 1054.	1.5	37
9589	Tree Species Shape Soil Bacterial Community Structure and Function in Temperate Deciduous Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 1519.	1.5	71
9590	MicroRNA-329 upregulation impairs the HMGB2/Î²-catenin pathway and regulates cell biological behaviors in melanoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 23518-23527.	2.0	24
9591	Enumerating Dominant Pathways in Biological Networks by Information Flow Analysis. <i>Lecture Notes in Computer Science</i> , 2019, , 39-51.	1.0	0
9592	Characterization of Protein Profiling and mRNA Expression of LLC Exosomes. <i>Protein Journal</i> , 2019, 38, 586-597.	0.7	5
9593	Identification of a module of HAP transcription factors for seed development in rice. <i>Plant Biotechnology Reports</i> , 2019, 13, 389-397.	0.9	0
9594	Genome-wide Integrative Analysis of Zika-Virus-Infected Neuronal Stem Cells Reveals Roles for MicroRNAs in Cell Cycle and Stemness. <i>Cell Reports</i> , 2019, 27, 3618-3628.e5.	2.9	50
9595	Comparative analysis of the transcriptomes of the calyx abscission zone of sweet orange insights into the huanglongbing-associated fruit abscission. <i>Horticulture Research</i> , 2019, 6, 71.	2.9	39

#	ARTICLE	IF	CITATIONS
9596	Leaf Energy Balance Requires Mitochondrial Respiration and Export of Chloroplast NADPH in the Light. <i>Plant Physiology</i> , 2019, 180, 1947-1961.	2.3	80
9597	Comprehensive epigenetic analyses reveal master regulators driving lung metastasis of breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5415-5431.	1.6	17
9598	Shank3 regulates striatal synaptic abundance of Cyld, a deubiquitinase specific for Lys63-linked polyubiquitin chains. <i>Journal of Neurochemistry</i> , 2019, 150, 776-786.	2.1	22
9599	Varieties of regional integration, international trade networks and risk. <i>World Economy</i> , 2019, 42, 2790-2815.	1.4	2
9600	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	1.1	11
9601	Correlations Between LC-MS/MS-Detected Glycomics and NMR-Detected Metabolomics in <i>Caenorhabditis elegans</i> Development. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 49.	1.6	8
9602	Prediction of VEGF-C as a Key Target of Pure Total Flavonoids From Citrus Against NAFLD in Mice via Network Pharmacology. <i>Frontiers in Pharmacology</i> , 2019, 10, 582.	1.6	22
9603	Mechanism Investigation of <i>Tagetes patula</i> L. against Chronic Nonbacterial Prostatitis by Metabolomics and Network Pharmacology. <i>Molecules</i> , 2019, 24, 2266.	1.7	8
9604	Multi-omics insights into functional alterations of the liver in insulin-deficient diabetes mellitus. <i>Molecular Metabolism</i> , 2019, 26, 30-44.	3.0	26
9605	Analysis of Peripheral Blood Cells' Transcriptome in Patients With Subarachnoid Hemorrhage From Ruptured Aneurysm Reveals Potential Biomarkers. <i>World Neurosurgery</i> , 2019, 129, e16-e22.	0.7	20
9606	Eukaryotic and cyanobacterial communities associated with marine snow particles in the oligotrophic Sargasso Sea. <i>Scientific Reports</i> , 2019, 9, 8891.	1.6	20
9607	Ancient duplications and grass-specific transposition influenced the evolution of LEAFY transcription factor genes. <i>Communications Biology</i> , 2019, 2, 237.	2.0	16
9608	Systems-level Analysis Reveals Multiple Modulators of Epithelial-mesenchymal Transition and Identifies DNAJB4 and CD81 as Novel Metastasis Inducers in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1756-1771.	2.5	29
9609	De novo transcriptome analysis of <i>Fraxinus velutina</i> Torr in response to NaCl stress. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	3
9610	Vegetation type impacts microbial interaction with antimony contaminants in a mining-contaminated soil environment. <i>Environmental Pollution</i> , 2019, 252, 1872-1881.	3.7	27
9611	Methylation and transcription patterns are distinct in IDH mutant gliomas compared to other IDH mutant cancers. <i>Scientific Reports</i> , 2019, 9, 8946.	1.6	44
9612	An Integrative Analysis of Tumor Proteomic and Phosphoproteomic Profiles to Examine the Relationships Between Kinase Activity and Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S26-S36.	2.5	25
9613	STAT4 silencing underlies a novel inhibitory role of microRNA-141-3p in inflammation response of mice with experimental autoimmune myocarditis. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2019, 317, H531-H540.	1.5	23

#	ARTICLE	IF	CITATIONS
9614	<i>De Novo</i> Assembly and Annotation of the Larval Transcriptome of Two Spadefoot Toads Widely Divergent in Developmental Rate. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2647-2655.	0.8	5
9615	Drinking Warm Water Improves Growth Performance and Optimizes the Gut Microbiota in Early Postweaning Rabbits during Winter. <i>Animals</i> , 2019, 9, 346.	1.0	25
9616	Protein-Protein Interaction Network Analysis Reveals Several Diseases Highly Associated with Polycystic Ovarian Syndrome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2959.	1.8	31
9617	Copy number variations in individuals with conotruncal heart defects reveal some shared developmental pathways irrespective of 22q11.2 deletion status. <i>Birth Defects Research</i> , 2019, 111, 888-905.	0.8	3
9618	Genome-wide alternative splicing landscapes modulated by biotrophic sugarcane smut pathogen. <i>Scientific Reports</i> , 2019, 9, 8876.	1.6	24
9619	Integrated analysis of long non-coding RNA and mRNA expression in different colored skin of koi carp. <i>BMC Genomics</i> , 2019, 20, 515.	1.2	44
9620	Integrating microRNA and mRNA expression in rapamycin-treated T-cell acute lymphoblastic leukemia. <i>Pathology Research and Practice</i> , 2019, 215, 152494.	1.0	3
9621	Active repurposing of drug candidates for melanoma based on GWAS, PheWAS and a wide range of omics data. <i>Molecular Medicine</i> , 2019, 25, 30.	1.9	21
9622	Effects of Qi Teng Xiao Zhuo granules on circRNA expression profiles in rats with chronic glomerulonephritis. <i>Drug Design, Development and Therapy</i> , 2019, Volume 13, 1901-1913.	2.0	11
9623	Identification of microRNAs associated with the aggressiveness of prolactin pituitary tumors using bioinformatic analysis. <i>Oncology Reports</i> , 2019, 42, 533-548.	1.2	12
9624	Identification of a Hotspot Residue for Improving the Thermostability of a Flavin-Dependent Monooxygenase. <i>ChemBioChem</i> , 2019, 20, 3020-3031.	1.3	27
9625	A comprehensive analysis of core polyadenylation sequences and regulation by microRNAs in a set of cancer predisposition genes. <i>Gene</i> , 2019, 712, 143943.	1.0	2
9626	Diversity of tetracycline- and erythromycin-resistant bacteria in aerosols and manures from four types of animal farms in China. <i>Environmental Science and Pollution Research</i> , 2019, 26, 24213-24222.	2.7	20
9627	Identification of differentially expressed genes in small and non-small cell lung cancer based on meta-analysis of mRNA. <i>Heliyon</i> , 2019, 5, e01707.	1.4	20
9628	Mosaic origin of the eukaryotic kinetochore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12873-12882.	3.3	76
9629	Substrate selectivity in starch polysaccharide monooxygenases. <i>Journal of Biological Chemistry</i> , 2019, 294, 12157-12166.	1.6	31
9630	Genomic identification of AP2/ERF transcription factors and functional characterization of two cold resistance-related AP2/ERF genes in celery ( <i>Apium graveolens</i> L.). <i>Planta</i> , 2019, 250, 1265-1280.	1.6	23
9631	Bacterial diversity and metabolite profiles of curd prepared by natural fermentation of raw milk and back sloping of boiled milk. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 102.	1.7	29

#	ARTICLE	IF	CITATIONS
9632	From parts to mechanisms: research heuristics for addressing heterogeneity in cancer genetics. <i>History and Philosophy of the Life Sciences</i> , 2019, 41, 27.	0.6	3
9633	Identification of two abundant <i>Aerococcus urinae</i> cell wall-anchored proteins. <i>International Journal of Medical Microbiology</i> , 2019, 309, 151325.	1.5	3
9634	Targeted and Interactome Proteomics Revealed the Role of PHD2 in Regulating BRD4 Proline Hydroxylation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1772-1781.	2.5	18
9635	Human exposure to trichloroethylene is associated with increased variability of blood DNA methylation that is enriched in genes and pathways related to autoimmune disease and cancer. <i>Epigenetics</i> , 2019, 14, 1112-1124.	1.3	24
9636	Mining traits for the enrichment and isolation of not-yet-cultured populations. <i>Microbiome</i> , 2019, 7, 96.	4.9	8
9637	Integrated analysis of microRNA regulation and its interaction with mechanisms of epigenetic regulation in the etiology of systemic lupus erythematosus. <i>PLoS ONE</i> , 2019, 14, e0218116.	1.1	11
9638	Expression Patterns of MYB (V-myb Myeloblastosis Viral Oncogene Homolog) Gene Family in Resistant and Susceptible Tung Trees Responding to Fusarium Wilt Disease. <i>Forests</i> , 2019, 10, 193.	0.9	3
9639	Survey of Biosynthetic Gene Clusters from Sequenced Myxobacteria Reveals Unexplored Biosynthetic Potential. <i>Microorganisms</i> , 2019, 7, 181.	1.6	31
9640	MicroRNAs associated with lung squamous cell carcinoma: New prognostic biomarkers and therapeutic targets. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 18956-18966.	1.2	33
9641	Systems pharmacology uncovers serotonergic pathway mediated psychotherapeutic effects of <i>Lonicerae Japonicae Flos</i> . <i>Journal of Functional Foods</i> , 2019, 60, 103407.	1.6	2
9642	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. <i>Cell Death Discovery</i> , 2019, 5, 105.	2.0	14
9643	Discovery and characterization of functional modules associated with body weight in broilers. <i>Scientific Reports</i> , 2019, 9, 9125.	1.6	18
9644	Genome wide identification and comparative analysis of glutathione transferases (GST) family genes in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2019, 9, 9196.	1.6	34
9645	Is it time for artificial intelligence to predict the function of natural products based on 2D-structure. <i>MedChemComm</i> , 2019, 10, 1667-1677.	3.5	9
9646	ProSNEx: a web-based application for exploration and analysis of protein structures using network formalism. <i>Nucleic Acids Research</i> , 2019, 47, W471-W476.	6.5	15
9647	Therapeutic effects of soluble guanylate cyclase stimulation on pulmonary hemodynamics and emphysema development in guinea pigs chronically exposed to cigarette smoke. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 317, L222-L234.	1.3	7
9648	Identification of Endogenous Adenomatous Polyposis Coli Interaction Partners and $\beta$ -Catenin-Independent Targets by Proteomics. <i>Molecular Cancer Research</i> , 2019, 17, 1828-1841.	1.5	5
9649	Temporal proteome dynamics of <i>Clostridium cellulovorans</i> cultured with major plant cell wall polysaccharides. <i>BMC Microbiology</i> , 2019, 19, 118.	1.3	9

#	ARTICLE	IF	CITATIONS
9650	Identification of key genes and pathways of thyroid cancer by integrated bioinformatics analysis. <i>Journal of Cellular Physiology</i> , 2019, 234, 23647-23657.	2.0	41
9651	Transcriptome and Gene Coexpression Network Analyses of Two Wild Populations Provides Insight into the High-Salinity Adaptation Mechanisms of <i>Crassostrea ariakensis</i> . <i>Marine Biotechnology</i> , 2019, 21, 596-612.	1.1	24
9652	Highly diverse fungal communities in carbon-rich aquifers of two contrasting lakes in Northeast Germany. <i>Fungal Ecology</i> , 2019, 41, 116-125.	0.7	9
9653	Noursamycins, Chlorinated Cyclohexapeptides Identified from Molecular Networking of <i>Streptomyces noursei</i> NTR-SR4. <i>Journal of Natural Products</i> , 2019, 82, 1478-1486.	1.5	25
9654	Identification of core genes and clinical roles in pregnancy-associated breast cancer based on integrated analysis of different microarray profile datasets. <i>Bioscience Reports</i> , 2019, 39, .	1.1	16
9655	Endometriosis Knowledgebase: a gene-based resource on endometriosis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	16
9656	Convergent evolution in <i>Arabidopsis halleri</i> and <i>Arabidopsis arenosa</i> on calamine metalliferous soils. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180243.	1.8	43
9657	Combined genetic and transcriptome analysis of patients with SLE: distinct, targetable signatures for susceptibility and severity. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1079-1089.	0.5	109
9658	miR-10b-3p, miR-8112 and let-7j as potential biomarkers for autoimmune inner ear diseases. <i>Molecular Medicine Reports</i> , 2019, 20, 171-181.	1.1	3
9659	Induction of Tyrosine Hydroxylase Gene Expression in Embryonal Carcinoma Stem Cells Using a Natural Tissue-Specific Inducer. <i>Developmental Neurobiology</i> , 2019, 79, 559-577.	1.5	4
9660	Characterizing the metabolites and the microbial communities of the soy sauce mash affected by temperature and hydrostatic pressure. <i>Food Research International</i> , 2019, 123, 801-808.	2.9	27
9661	Legacy of a Pleistocene bacterial community: Patterns in community dynamics through changing ecosystems. <i>Microbiological Research</i> , 2019, 226, 65-73.	2.5	2
9662	How children develop their ability to combine words: a network-based approach. <i>Adaptive Behavior</i> , 2019, 27, 307-330.	1.1	1
9664	Novel Strategies for Soil-Borne Diseases: Exploiting the Microbiome and Volatile-Based Mechanisms Toward Controlling Meloidogyne-Based Disease Complexes. <i>Frontiers in Microbiology</i> , 2019, 10, 1296.	1.5	60
9665	Transcriptome dynamics of cork oak ( <i>Quercus suber</i> ) somatic embryogenesis reveals active gene players in transcription regulation and phytohormone homeostasis of embryo development. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	11
9666	Tumor Heterogeneity Underlies Differential Cisplatin Sensitivity in Mouse Models of Small-Cell Lung Cancer. <i>Cell Reports</i> , 2019, 27, 3345-3358.e4.	2.9	42
9667	Differential Expression Profile of NLRs and AIM2 in Glioma and Implications for NLRP12 in Glioblastoma. <i>Scientific Reports</i> , 2019, 9, 8480.	1.6	27
9668	Detection of novel biomarkers for early detection of Non-Muscle-Invasive Bladder Cancer using Competing Endogenous RNA network analysis. <i>Scientific Reports</i> , 2019, 9, 8434.	1.6	34



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9669	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. Challenges and Advances in Computational Chemistry and Physics, 2019, , 75-97.	0.6	1
9670	System Network Biology Approaches in Exploring of Mechanism Behind Mutagenesis. Environmental Science and Engineering, 2019, , 117-136.	0.1	0
9671	Opioid-Induced Hyperalgesia Is Associated with Dysregulation of Circadian Rhythm and Adaptive Immune Pathways in the Mouse Trigeminal Ganglia and Nucleus Accumbens. Molecular Neurobiology, 2019, 56, 7929-7949.	1.9	34
9672	Extracellular DNA release, quorum sensing, and PrrF1/F2 small RNAs are key players in Pseudomonas aeruginosa tobramycin-enhanced biofilm formation. Npj Biofilms and Microbiomes, 2019, 5, 15.	2.9	61
9673	Identification of lncRNAs Responsive to Infection by <i>Plasmodiophora brassicae</i> in Clubroot-Susceptible and -Resistant <i>Brassica napus</i> Lines Carrying Resistance Introgressed from Rutabaga. Molecular Plant-Microbe Interactions, 2019, 32, 1360-1377.	1.4	24
9674	Transcriptome Analysis of the Breast Muscle of Xichuan Black-Bone Chickens Under Tyrosine Supplementation Revealed the Mechanism of Tyrosine-Induced Melanin Deposition. Frontiers in Genetics, 2019, 10, 457.	1.1	19
9675	Identifying the Growth Modulon of <i>Corynebacterium glutamicum</i> . Frontiers in Microbiology, 2019, 10, 974.	1.5	12
9676	2-Pyrrolidinone and Succinimide as Clinical Screening Biomarkers for GABA-Transaminase Deficiency: Anti-seizure Medications Impact Accurate Diagnosis. Frontiers in Neuroscience, 2019, 13, 394.	1.4	23
9677	Overexpression of NCAPH is upregulated and predicts a poor prognosis in prostate cancer. Oncology Letters, 2019, 17, 5768-5776.	0.8	23
9678	ceRNA network analysis reveals prognostic markers for glioblastoma. Oncology Letters, 2019, 17, 5545-5557.	0.8	16
9679	Transcriptome analysis reveals lncRNA-mediated complex regulatory network response to DNA damage in the liver tissue of <i>Rattus norvegicus</i> . Journal of Cellular Physiology, 2019, 234, 23216-23231.	2.0	6
9680	Genome-wide integrated analysis of miRNA and mRNA expression profiles to identify differentially expressed miR-22-5p and miR-27b-5p in response to classical swine fever vaccine virus. Functional and Integrative Genomics, 2019, 19, 901-918.	1.4	6
9681	Aqueous extract from <i>Madhuca indica</i> bark protects cells from oxidative stress caused by electron beam radiation: in vitro, in vivo and in silico approach. Heliyon, 2019, 5, e01749.	1.4	5
9682	Integrated pathological cell fishing and network pharmacology approach to investigate main active components of Er-Xian decoction for treating osteoporosis. Journal of Ethnopharmacology, 2019, 241, 111977.	2.0	25
9683	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
9684	Global Proteome and Ubiquitinome Changes in the Soluble and Insoluble Fractions of Q175 Huntington Mice Brains. Molecular and Cellular Proteomics, 2019, 18, 1705-1720.	2.5	26
9685	Identification and development of long non-coding RNA-associated regulatory network in colorectal cancer. Journal of Cellular and Molecular Medicine, 2019, 23, 5200-5210.	1.6	19
9686	Comprehensive characterization of immune- and inflammation-associated biomarkers based on multi-omics integration in kidney renal clear cell carcinoma. Journal of Translational Medicine, 2019, 17, 177.	1.8	18



#	ARTICLE	IF	CITATIONS
9687	Yap1b, a divergent Yap/Taz family member, cooperates with yap1 in survival and morphogenesis via common transcriptional targets. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	10
9688	Molecular mechanisms involved in drug-induced liver injury caused by urate-lowering Chinese herbs: A network pharmacology study and biology experiments. <i>PLoS ONE</i> , 2019, 14, e0216948.	1.1	20
9689	Delineating the Plausible Molecular Vaccine Candidates and Drug Targets of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 203.	1.8	19
9690	LC-MS/MS analysis and network pharmacology of <i>Trigonella foenum-graecum</i> – A plant from Ayurveda against hyperlipidemia and hyperglycemia with combination synergy. <i>Phytomedicine</i> , 2019, 60, 152944.	2.3	47
9691	Gegen Qinlian decoction enhances the effect of PD-1 blockade in colorectal cancer with microsatellite stability by remodelling the gut microbiota and the tumour microenvironment. <i>Cell Death and Disease</i> , 2019, 10, 415.	2.7	121
9692	Inhibition of nucleotide synthesis promotes replicative senescence of human mammary epithelial cells. <i>Journal of Biological Chemistry</i> , 2019, 294, 10564-10578.	1.6	33
9693	Controlling distinct signaling states in cultured cancer cells provides a new platform for drug discovery. <i>FASEB Journal</i> , 2019, 33, 9235-9249.	0.2	7
9694	Reconstruction and inference of the <i>Lactococcus lactis</i> MG1363 gene co-expression network. <i>PLoS ONE</i> , 2019, 14, e0214868.	1.1	5
9695	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27
9696	Genome-wide identification of silique-related traits based on high-density genetic linkage map in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	16
9697	Network pharmacology-based identification of potential targets of the flower of <i>Trollius chinensis</i> Bunge acting on anti-inflammatory effects. <i>Scientific Reports</i> , 2019, 9, 8109.	1.6	21
9698	Resolution of quantitative resistance to clubroot into QTL-specific metabolic modules. <i>Journal of Experimental Botany</i> , 2019, 70, 5375-5390.	2.4	22
9699	Response of Beef Cattle Fecal Microbiota to Grazing on Toxic Tall Fescue. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	19
9700	Circuit diversification in a biofilm regulatory network. <i>PLoS Pathogens</i> , 2019, 15, e1007787.	2.1	79
9701	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	1.5	27
9702	Business Network Analytics: From Graphs to Supernetworks. , 2019, , 307-400.		2
9703	Physiological and Biochemical Effects of Heat Shock Stress and Determination of Molecular Markers Related to Heat Tolerance in Maize Hybrids. <i>Gesunde Pflanzen</i> , 2019, 71, 213-222.	1.7	14
9704	Autotetraploidization in <i>Ziziphus jujuba</i> Mill. var. <i>spinosa</i> enhances salt tolerance conferred by active, diverse stress responses. <i>Environmental and Experimental Botany</i> , 2019, 165, 92-107.	2.0	20

#	ARTICLE	IF	CITATIONS
9705	Analysis of the epigenetic regulation of TNF receptor superfamily 25 (TNFRSF25) in rheumatoid arthritis. <i>Gene Reports</i> , 2019, 16, 100424.	0.4	1
9706	Interactome Analyses implicated CAMK2A in the genetic predisposition and pharmacological mechanism of Bipolar Disorder. <i>Journal of Psychiatric Research</i> , 2019, 115, 165-175.	1.5	12
9707	Whole transcriptome analysis of the Atlantic cod vaccine response reveals subtle changes in adaptive immunity. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100597.	0.4	30
9708	Computational de-orphanization of the olive oil biophenol oleacein: Discovery of new metabolic and epigenetic targets. <i>Food and Chemical Toxicology</i> , 2019, 131, 110529.	1.8	15
9709	Gene expression profiling of the canine placenta during normal and antigestagen-induced luteolysis. <i>General and Comparative Endocrinology</i> , 2019, 282, 113194.	0.8	16
9710	Mechanistic Insights from Replica Exchange Molecular Dynamics Simulations into Mutation Induced Disordered-to-Ordered Transition in Hahellin, a $^{12}I^{13}$ -Crystallin. <i>Journal of Physical Chemistry B</i> , 2019, 123, 5086-5098.	1.2	7
9711	Proteome-wide analysis of chaperone-mediated autophagy targeting motifs. <i>PLoS Biology</i> , 2019, 17, e3000301.	2.6	136
9712	Effect of raw material and starters on the metabolite constituents and microbial community diversity of fermented soy sauce. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 5687-5695.	1.7	31
9713	Centrality in Networks: Finding the Most Important Nodes. , 2019, , 401-433.		17
9714	m6A Regulates Neurogenesis and Neuronal Development by Modulating Histone Methyltransferase Ezh2. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 154-168.	3.0	135
9715	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	3.8	518
9716	Secondary Metabolites of Onygenales Fungi Exemplified by <i>Aiolomyces pyridodomos</i> . <i>Journal of Natural Products</i> , 2019, 82, 1616-1626.	1.5	8
9717	Dysregulation of a specific immune-related network of genes biologically defines a subset of schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 156.	2.4	24
9718	BioUML: an integrated environment for systems biology and collaborative analysis of biomedical data. <i>Nucleic Acids Research</i> , 2019, 47, W225-W233.	6.5	32
9719	Ruminal microbiome-host crosstalk stimulates the development of the ruminal epithelium in a lamb model. <i>Microbiome</i> , 2019, 7, 83.	4.9	116
9720	GLI2 Modulated by SUFU and SPOP Induces Intestinal Stem Cell Niche Signals in Development and Tumorigenesis. <i>Cell Reports</i> , 2019, 27, 3006-3018.e4.	2.9	29
9721	Lower connectivity of tumor coexpression networks is not specific to cancer. <i>In Silico Biology</i> , 2019, 13, 41-53.	0.4	6
9722	Competing Endogenous RNA Network Analysis Reveals Pivotal ceRNAs in Adrenocortical Carcinoma. <i>Frontiers in Endocrinology</i> , 2019, 10, 301.	1.5	5

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9723	Dysregulation of Mesenchymal Cell Survival Pathways in Severe Fibrotic Lung Disease: The Effect of Nintedanib Therapy. <i>Frontiers in Pharmacology</i> , 2019, 10, 532.	1.6	18
9724	Identification and integrative analysis of microRNAs and mRNAs involved in proliferation and invasion of pressure-treated human liver cancer cell lines. <i>Molecular Medicine Reports</i> , 2019, 20, 375-387.	1.1	8
9725	Data set of in silico simulation for the production of clavulanic acid and cephamycin C by <i>Streptomyces clavuligerus</i> using a genome scale metabolic model. <i>Data in Brief</i> , 2019, 24, 103992.	0.5	4
9726	Importance of Species Sorting and Immigration on the Bacterial Assembly of Different-Sized Aggregates in a Full-Scale Aerobic Granular Sludge Plant. <i>Environmental Science &amp; Technology</i> , 2019, 53, 8291-8301.	4.6	93
9727	microRNA-328 in exosomes derived from M2 macrophages exerts a promotive effect on the progression of pulmonary fibrosis via FAM13A in a rat model. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-16.	3.2	58
9728	T-Cell Deletion of MyD88 Connects IL17 and $\text{Î}^{\text{B}}\text{Î}^{\text{T}}$ to RAS Oncogenesis. <i>Molecular Cancer Research</i> , 2019, 17, 1759-1773.	1.5	9
9729	Assessment of risk based on variant pathways and establishment of an artificial neural network model of thyroid cancer. <i>BMC Medical Genetics</i> , 2019, 20, 92.	2.1	7
9730	Phenotypic heterogeneity and evolution of melanoma cells associated with targeted therapy resistance. <i>PLoS Computational Biology</i> , 2019, 15, e1007034.	1.5	41
9731	NetR and AttR, Two New Bioinformatic Tools to Integrate Diverse Datasets into Cytoscape Network and Attribute Files. <i>Genes</i> , 2019, 10, 423.	1.0	1
9732	Gene regulation and prognostic indicators of lung squamous cell carcinoma: TCGA-derived miRNA/mRNA sequencing and DNA methylation data. <i>Journal of Cellular Physiology</i> , 2019, 234, 22896-22910.	2.0	6
9733	Individual Oligodendrocytes Show Bias for Inhibitory Axons in the Neocortex. <i>Cell Reports</i> , 2019, 27, 2799-2808.e3.	2.9	83
9734	Upregulation of the APE1 and H2AX genes and miRNAs involved in DNA damage response and repair in gastric cancer. <i>Genes and Diseases</i> , 2019, 6, 176-184.	1.5	21
9735	Bioinformatics Analysis of Stromal Molecular Signatures Associated with Breast and Prostate Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 1130-1139.	0.8	12
9736	A novel lncRNA-miRNA-mRNA triple network identifies lncRNA TWF1 as an important regulator of miRNA and gene expression in coronary artery disease. <i>Nutrition and Metabolism</i> , 2019, 16, 39.	1.3	16
9737	Deciphering molecular mechanism of silver by integrated omic approaches enables enhancing its antimicrobial efficacy in <i>E. coli</i> . <i>PLoS Biology</i> , 2019, 17, e3000292.	2.6	66
9738	Genetic Predisposition for Immune System, Hormone, and Metabolic Dysfunction in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome: A Pilot Study. <i>Frontiers in Pediatrics</i> , 2019, 7, 206.	0.9	24
9739	RNA-seq analyses of antibiotic resistance mechanisms in <i>Serratia</i> $\frac{1}{2}$ <i>marcescens</i> . <i>Molecular Medicine Reports</i> , 2019, 20, 745-754.	1.1	6
9740	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. <i>Cell Host and Microbe</i> , 2019, 25, 789-802.e5.	5.1	441

#	ARTICLE	IF	CITATIONS
9741	The initiation of puberty in Atlantic salmon brings about large changes in testicular gene expression that are modulated by the energy status. <i>BMC Genomics</i> , 2019, 20, 475.	1.2	15
9742	<i>PDXK</i> mutations cause polyneuropathy responsive to pyridoxal 5-phosphate supplementation. <i>Annals of Neurology</i> , 2019, 86, 225-240.	2.8	54
9743	Identification of genes and pathways in human antigen-presenting cell subsets in response to polio vaccine by bioinformatical analysis. <i>Journal of Medical Virology</i> , 2019, 91, 1729-1736.	2.5	5
9744	Gene and microRNA Signatures Are Associated with the Development and Survival of Glioblastoma Patients. <i>DNA and Cell Biology</i> , 2019, 38, 688-699.	0.9	6
9745	Archaeal Communities in Deep Terrestrial Subsurface Underneath the Deccan Traps, India. <i>Frontiers in Microbiology</i> , 2019, 10, 1362.	1.5	15
9746	The gut microbiome and metabolome of saddleback tamarins ( <i>Leontocebus weddelli</i> ): Insights into the foraging ecology of a small-bodied primate. <i>American Journal of Primatology</i> , 2019, 81, e23003.	0.8	10
9747	Phospho-peptide binding domains in <i>S. cerevisiae</i> model organism. <i>Biochimie</i> , 2019, 163, 117-127.	1.3	10
9748	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632.	5.8	93
9749	Bioinformatics Analysis of Gene Expression Profiles of Sex Differences in Ischemic Stroke. <i>BioMed Research International</i> , 2019, 2019, 1-7.	0.9	9
9750	Geochemical-Compositional-Functional Changes in Arctic Soil Microbiomes Post Land Submergence Revealed by Metagenomics. <i>Microbes and Environments</i> , 2019, 34, 180-190.	0.7	6
9751	<i>Aspergillus fumigatus</i> Challenged by Human Dendritic Cells: Metabolic and Regulatory Pathway Responses Testify a Tight Battle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 168.	1.8	19
9752	Oncoproteomics: Current status and future opportunities. <i>Clinica Chimica Acta</i> , 2019, 495, 611-624.	0.5	20
9753	Long-range interactions between proximal and distal regulatory regions in maize. <i>Nature Communications</i> , 2019, 10, 2633.	5.8	79
9754	Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. <i>Microbiome</i> , 2019, 7, 92.	4.9	230
9755	Transcriptome analysis reveals immune-related gene expression changes with age in giant panda ( <i>Ailuropoda melanoleuca</i> ) blood. <i>Aging</i> , 2019, 11, 249-262.	1.4	17
9756	PopNetD3—A Network-Based Web Resource for Exploring Population Structure. <i>Genome Biology and Evolution</i> , 2019, 11, 1730-1735.	1.1	1
9757	Multi-year dynamics of fine-scale marine cyanobacterial populations are more strongly explained by phage interactions than abiotic, bottom-up factors. <i>Environmental Microbiology</i> , 2019, 21, 2948-2963.	1.8	45
9758	Opposite T3 Response of ACTG1—FOS Subnetwork Differentiate Tailfin Fate in <i>Xenopus</i> Tadpole and Post-hatching Axolotl. <i>Frontiers in Endocrinology</i> , 2019, 10, 194.	1.5	7

#	ARTICLE	IF	CITATIONS
9759	Co-expression network analysis of the lncRNAs and mRNAs associated with cervical cancer progression. <i>Archives of Medical Science</i> , 2019, 15, 754-764.	0.4	18
9760	An Atlas of Vagal Sensory Neurons and Their Molecular Specialization. <i>Cell Reports</i> , 2019, 27, 2508-2523.e4.	2.9	259
9761	Novel susceptibility genes were found in a targeted sequencing of stroke patients with or without depression in the Chinese Han population. <i>Journal of Affective Disorders</i> , 2019, 255, 1-9.	2.0	11
9762	Evolving neural networks to follow trajectories of arbitrary complexity. <i>Neural Networks</i> , 2019, 116, 224-236.	3.3	1
9763	Sexually differential gene expressions in poplar roots in response to nitrogen deficiency. <i>Tree Physiology</i> , 2019, 39, 1614-1629.	1.4	33
9764	Poplar carbohydrate-active enzymes: whole-genome annotation and functional analyses based on <i>scp</i> RNA expression data. <i>Plant Journal</i> , 2019, 99, 589-609.	2.8	39
9765	Identification of key genes and molecular mechanisms associated with low egg production of broiler breeder hens in ad libitum. <i>BMC Genomics</i> , 2019, 20, 408.	1.2	14
9766	An integrated insight into the response of bacterial communities to anthropogenic contaminants in a river: A case study of the Wonderfonteinspruit catchment area, South Africa. <i>PLoS ONE</i> , 2019, 14, e0216758.	1.1	23
9767	Identification of the iduronate-2-sulfatase proteome in wild-type mouse brain. <i>Heliyon</i> , 2019, 5, e01667.	1.4	8
9769	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	3.2	39
9770	Meta-analysis of drought-tolerant genotypes in <i>Oryza sativa</i> : A network-based approach. <i>PLoS ONE</i> , 2019, 14, e0216068.	1.1	40
9771	Identification of Hub Genes Associated With Progression and Prognosis in Patients With Bladder Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 408.	1.1	23
9772	Expression Profile Analysis Identifies a Novel Five-Gene Signature to Improve Prognosis Prediction of Glioblastoma. <i>Frontiers in Genetics</i> , 2019, 10, 419.	1.1	52
9773	Microbial Co-Occurrence Patterns and Keystone Species in the Gut Microbial Community of Mice in Response to Stress and Chondroitin Sulfate Disaccharide. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2130.	1.8	15
9774	Chromatin Decondensation by FOXP2 Promotes Human Neuron Maturation and Expression of Neurodevelopmental Disease Genes. <i>Cell Reports</i> , 2019, 27, 1699-1711.e9.	2.9	40
9775	Defining Reprogramming Checkpoints from Single-Cell Analyses of Induced Pluripotency. <i>Cell Reports</i> , 2019, 27, 1726-1741.e5.	2.9	44
9776	Taxonomic diversity of antimicrobial-resistant bacteria and genes in the Red Sea coast. <i>Science of the Total Environment</i> , 2019, 677, 474-483.	3.9	23
9777	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804.	15.2	329

#	ARTICLE	IF	CITATIONS
9778	Induction of mTOR-dependent autophagy by WS <sub>2</sub> nanosheets from both inside and outside of human cells. <i>Nanoscale</i> , 2019, 11, 10684-10694.	2.8	14
9779	Heme catabolism in the causative agent of anthrax. <i>Molecular Microbiology</i> , 2019, 112, 515-531.	1.2	4
9780	The ethylene response factor Va<sc>ERF</sc>092 from Amur grape regulates the transcription factor Va<sc>WRKY</sc>33, improving cold tolerance. <i>Plant Journal</i> , 2019, 99, 988-1002.	2.8	77
9781	Silencing of SAA1 inhibits palmitate- or high-fat diet induced insulin resistance through suppression of the NF- $\kappa$ B pathway. <i>Molecular Medicine</i> , 2019, 25, 17.	1.9	20
9782	Human COQ10A and COQ10B are distinct lipid-binding START domain proteins required for coenzyme Q function. <i>Journal of Lipid Research</i> , 2019, 60, 1293-1310.	2.0	38
9783	TASmania: A bacterial Toxin-Antitoxin Systems database. <i>PLoS Computational Biology</i> , 2019, 15, e1006946.	1.5	95
9784	Estudio proteómico 2DE-DIGE en plasma sanguíneo de pacientes en etapa infantil con leucemia linfoblástica aguda. <i>Revista Colombiana De Química</i> , 2019, 48, 5-15.	0.2	1
9785	Leaf and Root Endospheres Harbor Lower Fungal Diversity and Less Complex Fungal Co-occurrence Patterns Than Rhizosphere. <i>Frontiers in Microbiology</i> , 2019, 10, 1015.	1.5	60
9786	Transcriptome Changes in the Mink Uterus during Blastocyst Dormancy and Reactivation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2099.	1.8	8
9787	Clinical significance of miRNA-1 and its potential target gene network in lung squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2019, 19, 5063-5078.	1.1	2
9788	Identification of time-series differentially expressed genes and pathways associated with heart failure post-myocardial infarction using integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 5281-5290.	1.1	6
9789	LncRNAs associated with multiple sclerosis expressed in the Th1 cell lineage. <i>Journal of Cellular Physiology</i> , 2019, 234, 22153-22162.	2.0	16
9790	Deciphering the Role of PKC in Calpain-CAST System Through Formal Modeling Approach. <i>Lecture Notes in Computer Science</i> , 2019, , 60-71.	1.0	1
9791	Standardized human bone marrow-derived stem cells infusion improves survival and recovery in a rat model of spinal cord injury. <i>Journal of the Neurological Sciences</i> , 2019, 402, 16-29.	0.3	12
9792	Identification of core genes and potential molecular mechanisms in breast cancer using bioinformatics analysis. <i>Pathology Research and Practice</i> , 2019, 215, 152436.	1.0	14
9793	Identification of Transcription Factors Regulating Senescence in Wheat through Gene Regulatory Network Modelling. <i>Plant Physiology</i> , 2019, 180, 1740-1755.	2.3	73
9794	Lineage specific histories of <i>Mycobacterium tuberculosis</i> dispersal in Africa and Eurasia. <i>Molecular Ecology</i> , 2019, 28, 3241-3256.	2.0	86
9795	Temporal patterning of apical progenitors and their daughter neurons in the developing neocortex. <i>Science</i> , 2019, 364, .	6.0	275



#	ARTICLE	IF	CITATIONS
9796	Elevated CCL19/CCR7 Expression During the Disease Process of Primary Sjögren's Syndrome. <i>Frontiers in Immunology</i> , 2019, 10, 795.	2.2	28
9797	Comprehensive analysis of the aberrantly expressed lncRNA-associated ceRNA network in breast cancer. <i>Molecular Medicine Reports</i> , 2019, 19, 4697-4710.	1.1	21
9798	miR-148 family members are putative biomarkers for sepsis. <i>Molecular Medicine Reports</i> , 2019, 19, 5133-5141.	1.1	11
9799	Identification of circular RNA-associated competing endogenous RNA network in the development of cleft palate. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16062-16074.	1.2	9
9800	Investigation of systemic lupus erythematosus (SLE) with integrating transcriptomics and genome wide association information. <i>Gene</i> , 2019, 706, 181-187.	1.0	19
9801	Initial Development toward Non-Invasive Drug Monitoring via Untargeted Mass Spectrometric Analysis of Human Skin. <i>Analytical Chemistry</i> , 2019, 91, 8062-8069.	3.2	17
9802	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. <i>Communications Biology</i> , 2019, 2, 165.	2.0	29
9803	Fungal acetylome comparative analysis identifies an essential role of acetylation in human fungal pathogen virulence. <i>Communications Biology</i> , 2019, 2, 154.	2.0	38
9804	4q-D4Z4 chromatin architecture regulates the transcription of muscle atrophic genes in facioscapulohumeral muscular dystrophy. <i>Genome Research</i> , 2019, 29, 883-895.	2.4	18
9805	The sucrose-to-malate ratio correlates with the faster $\text{CO}_2$ and light stomatal responses of angiosperms compared to ferns. <i>New Phytologist</i> , 2019, 223, 1873-1887.	3.5	22
9806	Towards the new normal: Transcriptomic convergence and genomic legacy of the two subgenomes of an allopolyploid weed ( <i>Capsella bursa-pastoris</i> ). <i>PLoS Genetics</i> , 2019, 15, e1008131.	1.5	27
9807	6mA-DNA-binding factor Jumu controls maternal-to-zygotic transition upstream of Zelda. <i>Nature Communications</i> , 2019, 10, 2219.	5.8	37
9808	SETD1A Methyltransferase Is Physically and Functionally Linked to the DNA Damage Repair Protein RAD18. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1428-1436.	2.5	17
9809	Bioinformatics Resource Manager: a systems biology web tool for microRNA and omics data integration. <i>BMC Bioinformatics</i> , 2019, 20, 255.	1.2	5
9810	Alternative polyadenylation of single cells delineates cell types and serves as a prognostic marker in early stage breast cancer. <i>PLoS ONE</i> , 2019, 14, e0217196.	1.1	23
9811	Intraductal Adaptation of the 4T1 Mouse Model of Breast Cancer Reveals Effects of the Epithelial Microenvironment on Tumor Progression and Metastasis. <i>Anticancer Research</i> , 2019, 39, 2277-2287.	0.5	19
9812	The Variation of Nasal Microbiota Caused by Low Levels of Gaseous Ammonia Exposure in Growing Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 1083.	1.5	19
9813	iTRAQ comparison of proteomic profiles of endometrial receptivity. <i>Journal of Proteomics</i> , 2019, 203, 103381.	1.2	16



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9814	A systems biology approach uncovers cell-specific gene regulatory effects of genetic associations in multiple sclerosis. <i>Nature Communications</i> , 2019, 10, 2236.	5.8	65
9815	Cyclo(tetrahydroxybutyrate) production is sufficient to distinguish between <i>Xenorhabdus</i> and <i>Photorhabdus</i> isolates in Thailand. <i>Environmental Microbiology</i> , 2019, 21, 2921-2932.	1.8	1
9816	Genetic dissection of harvest index and related traits through genome-wide quantitative trait locus mapping in <i>Brassica napus</i> L. <i>Breeding Science</i> , 2019, 69, 104-116.	0.9	10
9817	Bacterial Community Dynamics in an Oyster Hatchery in Response to Probiotic Treatment. <i>Frontiers in Microbiology</i> , 2019, 10, 1060.	1.5	35
9818	Elucidation of <i>Akkermansia muciniphila</i> Probiotic Traits Driven by Mucin Depletion. <i>Frontiers in Microbiology</i> , 2019, 10, 1137.	1.5	85
9819	A network pharmacology approach to investigate the pharmacological effect of curcumin and capsaicin targets in cancer angiogenesis by module-based PPI network analysis. <i>Journal of Proteins and Proteomics</i> , 2019, 10, 109-120.	1.0	5
9820	Influence of Environmental Drivers and Potential Interactions on the Distribution of Microbial Communities From Three Permanently Stratified Antarctic Lakes. <i>Frontiers in Microbiology</i> , 2019, 10, 1067.	1.5	20
9821	Functional Proteomics of Nuclear Proteins in <i>Tetrahymena thermophila</i> : A Review. <i>Genes</i> , 2019, 10, 333.	1.0	11
9822	Transcriptome analysis of body wall reveals growth difference between the largest and smallest individuals in the pure and hybrid populations of <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100591.	0.4	10
9823	Short-term exposure to traffic-related air pollution reveals a compound-specific circulating miRNA profile indicating multiple disease risks. <i>Environment International</i> , 2019, 128, 193-200.	4.8	33
9824	Identification of possible new salivary biomarkers of stress in sheep using a high-resolution quantitative proteomic technique. <i>Research in Veterinary Science</i> , 2019, 124, 338-345.	0.9	7
9825	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10705-10710.	3.3	119
9826	Identification of differentially expressed gene sets using the Generalized Berkâ€“Jones statistic. <i>Bioinformatics</i> , 2019, 35, 4568-4576.	1.8	8
9827	Microbiota Associated with Sclerotia of Soilborne Fungal Pathogens â€“ A Novel Source of Biocontrol Agents Producing Bioactive Volatiles. <i>Phytobiomes Journal</i> , 2019, 3, 125-136.	1.4	41
9828	Single-cell expression profiling reveals dynamic flux of cardiac stromal, vascular and immune cells in health and injury. <i>ELife</i> , 2019, 8, .	2.8	379
9829	Knockdown of RAD18 inhibits glioblastoma development. <i>Journal of Cellular Physiology</i> , 2019, 234, 21100-21112.	2.0	8
9830	LOC103691336/miRâ€“138â€“5p/BMP2 axis modulates Mgâ€“mediated osteogenic differentiation in rat femoral fracture model and rat primary bone marrow stromal cells. <i>Journal of Cellular Physiology</i> , 2019, 234, 21316-21330.	2.0	36
9832	Heat-shock treatment applied to inocula for H2 production decreases microbial diversities, interspecific interactions and performance using cellulose as substrate. <i>International Journal of Hydrogen Energy</i> , 2019, 44, 13126-13134.	3.8	22

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9833	Systematic profiling of SH3-mediated Tauâ€œPartner interaction network in Alzheimer's disease by integrating in silico analysis and in vitro assay. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 90, 265-272.	1.3	6
9834	Optimized Cross-Linking Mass Spectrometry for in Situ Interaction Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 2545-2558.	1.8	32
9835	Identification of Resistance Genes and Response to Arsenic in <i>Rhodococcus aetherivorans</i> BCP1. <i>Frontiers in Microbiology</i> , 2019, 10, 888.	1.5	38
9836	Dynamic Transcriptome Changes Related to Oil Accumulation in Developing Soybean Seeds. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2202.	1.8	26
9837	Oxidative opening of the aromatic ring: Tracing the natural history of a large superfamily of dioxygenase domains and their relatives. <i>Journal of Biological Chemistry</i> , 2019, 294, 10211-10235.	1.6	24
9838	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784314 rgBT /Overlock 10 6.58 3,302	6.58	3,302
9839	Exploring integument transcriptomes, cuticle ultrastructure, and cuticular hydrocarbons profiles in eusocial and solitary bee species displaying heterochronic adult cuticle maturation. <i>PLoS ONE</i> , 2019, 14, e0213796.	1.1	19
9840	Screening candidate microRNAâ€œmRNA network for predicting the response to chemoresistance in osteosarcoma by bioinformatics analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16798-16810.	1.2	12
9841	In silico analysis revealed Zika virus miRNAs associated with viral pathogenesis through alteration of host genes involved in immune response and neurological functions. <i>Journal of Medical Virology</i> , 2019, 91, 1584-1594.	2.5	28
9842	Identification and the potential roles of long non-coding RNAs in cotton leaves damaged by <i>Aphis gossypii</i> . <i>Plant Growth Regulation</i> , 2019, 88, 215-225.	1.8	17
9843	Computationally-assisted discovery and structure elucidation of natural products. <i>Journal of Natural Medicines</i> , 2019, 73, 687-695.	1.1	18
9844	Quantitative proteomics analysis reveals resistance differences of banana cultivar â€œBrazilianâ€™ to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> races 1 and 4. <i>Journal of Proteomics</i> , 2019, 203, 103376.	1.2	20
9845	In silico prediction of housekeeping long intergenic non-coding RNAs reveals HKlincR1 as an essential player in lung cancer cell survival. <i>Scientific Reports</i> , 2019, 9, 7372.	1.6	2
9846	Identification of novel blood-based HCC-specific diagnostic biomarkers for human hepatocellular carcinoma. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2019, 47, 1908-1916.	1.9	34
9847	mirTime: Identifying Condition-Specific Targets of MicroRNA in Time-series Transcript Data using Gaussian Process Model and Spherical Vector Clustering. <i>Bioinformatics</i> , 2019, , .	1.8	8
9848	Bioinformatics analysis suggests that COL4A1 may play an important role in gastric carcinoma recurrence. <i>Journal of Digestive Diseases</i> , 2019, 20, 391-400.	0.7	16
9849	Tracing the phylogenetic history of the Crl regulon through the Bacteria and Archaea genomes. <i>BMC Genomics</i> , 2019, 20, 299.	1.2	8
9850	How an essential Zn2Cys6 transcription factor PoxCxA regulates cellulase gene expression in ascomycete fungi?. <i>Biotechnology for Biofuels</i> , 2019, 12, 105.	6.2	15

#	ARTICLE	IF	CITATIONS
9851	Data-Driven Analysis of Age, Sex, and Tissue Effects on Gene Expression Variability in Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2019, 13, 392.	1.4	22
9852	Rhizocompartments and environmental factors affect microbial composition and variation in native plants. <i>Journal of Microbiology</i> , 2019, 57, 550-561.	1.3	8
9853	Coronary artery disease associated specific modules and feature genes revealed by integrative methods of WGCNA, MetaDE and machine learning. <i>Gene</i> , 2019, 710, 122-130.	1.0	14
9854	Disease networks and their contribution to disease understanding: A review of their evolution, techniques and data sources. <i>Journal of Biomedical Informatics</i> , 2019, 94, 103206.	2.5	26
9855	Associating expression and genomic data using co-occurrence measures. <i>Biology Direct</i> , 2019, 14, 10.	1.9	7
9856	The GMC superfamily of oxidoreductases revisited: analysis and evolution of fungal GMC oxidoreductases. <i>Biotechnology for Biofuels</i> , 2019, 12, 118.	6.2	84
9857	Integrated analysis of the critical region 5p15.3â€”p15.2 associated with cri-du-chat syndrome. <i>Genetics and Molecular Biology</i> , 2019, 42, 186-196.	0.6	16
9858	Implementing a concept network model. <i>Behavior Research Methods</i> , 2019, 51, 1717-1736.	2.3	11
9859	Integrative analyses of triple negative dysregulated transcripts compared with nonâ€”triple negative tumors and their functional and molecular interactions. <i>Journal of Cellular Physiology</i> , 2019, 234, 22386-22399.	2.0	15
9860	Strand-specific RNA-seq based identification and functional prediction of lncRNAs in response to melatonin and simulated drought stresses in cassava. <i>Plant Physiology and Biochemistry</i> , 2019, 140, 96-104.	2.8	30
9861	Coordination of ABA and Chaperone Signaling in Plant Stress Responses. <i>Trends in Plant Science</i> , 2019, 24, 636-651.	4.3	43
9862	Kinetic Investigation of a Presumed Nitronate Monooxygenase from <i>Pseudomonas aeruginosa</i> PAO1 Establishes a New Class of NAD(P)H:Quinone Reductases. <i>Biochemistry</i> , 2019, 58, 2594-2607.	1.2	2
9863	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2019, 58, 2617-2627.	1.2	6
9864	Complex Microbial Communities Drive Iron and Sulfur Cycling in Arctic Fjord Sediments. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	58
9865	Transcriptome profiling of anthocyanin biosynthesis in the peel of â€”Granny Smithâ€” apples ( <i>Malus</i> ) Tj ETQq0 0 0,rgBT /Overlock 10	1.2	28
9866	Evolutionary framework of the human interactome: Unicellular and multicellular giant clusters. <i>BioSystems</i> , 2019, 181, 82-87.	0.9	15
9867	Does nano silver promote the selection of antibiotic resistance genes in soil and plant?. <i>Environment International</i> , 2019, 128, 399-406.	4.8	59
9868	VitiVar: A locus specific database of vitiligo associated genes and variations. <i>Gene: X</i> , 2019, 721, 100018.	2.3	6

#	ARTICLE	IF	CITATIONS
9869	VPAC: Variational projection for accurate clustering of single-cell transcriptomic data. <i>BMC Bioinformatics</i> , 2019, 20, 0.	1.2	8
9870	Reproducibility of biomarker identifications from mass spectrometry proteomic data in cancer studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.2	3
9871	NMR-Based Tissue and Developmental Metabolomics of Tomato Fruit. <i>Metabolites</i> , 2019, 9, 93.	1.3	18
9872	Prokaryotic and viral community of the sulfate-rich crust from Peñahueca ephemeral lake, an astrobiology analogue. <i>Environmental Microbiology</i> , 2019, 21, 3577-3600.	1.8	9
9873	Prediction and Characterization of miRNA/Target Pairs in Non-Model Plants Using RNA-seq. <i>Current Protocols in Plant Biology</i> , 2019, 4, e20090.	2.8	1
9874	Laryngotracheal Microbiota in Adult Laryngotracheal Stenosis. <i>MSphere</i> , 2019, 4, .	1.3	30
9875	Extracting predictors for lung adenocarcinoma based on Granger causality test and stepwise character selection. <i>BMC Bioinformatics</i> , 2019, 20, 197.	1.2	4
9876	Combining loss of function of FOLYLPOLYGLUTAMATE SYNTHETASE1 and CAFFEOYL-COA 3-O-METHYLTRANSFERASE1 for lignin reduction and improved saccharification efficiency in <i>Arabidopsis thaliana</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 108.	6.2	18
9877	Identification of LIFR, PIK3R1, and MMP12 as Novel Prognostic Signatures in Gallbladder Cancer Using Network-Based Module Analysis. <i>Frontiers in Oncology</i> , 2019, 9, 325.	1.3	15
9878	Revisiting the Role of Transcription Factors in Coordinating the Defense Response Against Citrus Bark Cracking Viroid Infection in Commercial Hop ( <i>Humulus Lupulus</i> L.). <i>Viruses</i> , 2019, 11, 419.	1.5	22
9879	microRNA-165p-containing exosomes derived from bone marrow-derived mesenchymal stem cells inhibit proliferation, migration, and invasion, while promoting apoptosis of colorectal cancer cells by downregulating ITGA2. <i>Journal of Cellular Physiology</i> , 2019, 234, 21380-21394.	2.0	114
9880	A systems biology approach to propose a new mechanism of regulation of repetitive prophylaxis of stable iodide on sodium/iodide symporter (NIS). <i>Biochimie</i> , 2019, 162, 208-215.	1.3	4
9881	Low-dose aspirin protective effects are correlated with deregulation of HNF factor expression in the preclamptic placentas from mice and humans. <i>Cell Death Discovery</i> , 2019, 5, 94.	2.0	12
9882	Genome-wide association studies for 30 haematological and blood clinical-biochemical traits in Large White pigs reveal genomic regions affecting intermediate phenotypes. <i>Scientific Reports</i> , 2019, 9, 7003.	1.6	55
9883	Characterizing Relationship of Microbial Diversity and Metabolite in Sichuan Xiaoku. <i>Frontiers in Microbiology</i> , 2019, 10, 696.	1.5	57
9884	RGS1 silencing inhibits the inflammatory response and angiogenesis in rheumatoid arthritis rats through the inactivation of Toll-like receptor signaling pathway. <i>Journal of Cellular Physiology</i> , 2019, 234, 20432-20442.	2.0	32
9885	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	0.4	13
9886	Transcriptomic Hallmarks of Tumor Plasticity and Stromal Interactions in Brain Metastasis. <i>Cell Reports</i> , 2019, 27, 1277-1292.e7.	2.9	49

#	ARTICLE	IF	CITATIONS
9887	Implications of the mitochondrial interactome of mammalian thioredoxin 2 for normal cellular function and disease. <i>Free Radical Biology and Medicine</i> , 2019, 137, 59-73.	1.3	10
9888	Fate of antibiotics and antibiotic resistance genes in a full-scale restaurant food waste treatment plant: Implications of the roles beyond heavy metals and mobile genetic elements. <i>Journal of Environmental Sciences</i> , 2019, 85, 17-34.	3.2	62
9889	Leveraging Human Microbiome Features to Diagnose and Stratify Children with Irritable Bowel Syndrome. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 449-461.	1.2	59
9890	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. <i>Water Research</i> , 2019, 159, 464-479.	5.3	51
9891	Exploration of Target Synergy in Cancer Treatment by Cell-Based Screening Assay and Network Propagation Analysis. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3072-3079.	2.5	1
9892	A small molecule promotes cartilage extracellular matrix generation and inhibits osteoarthritis development. <i>Nature Communications</i> , 2019, 10, 1914.	5.8	134
9893	The extracellular matrix protects <i>Bacillus subtilis</i> colonies from <i>Pseudomonas</i> invasion and modulates plant co-colonization. <i>Nature Communications</i> , 2019, 10, 1919.	5.8	102
9894	Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects. <i>Epigenetics</i> , 2019, 14, 589-601.	1.3	35
9895	<i>Ureaplasma diversum</i> protein interaction networks: evidence of horizontal gene transfer and evolution of reduced genomes among <i>Mollicutes</i> . <i>Canadian Journal of Microbiology</i> , 2019, 65, 596-612.	0.8	3
9896	Identification of significant genes with poor prognosis in ovarian cancer via bioinformatical analysis. <i>Journal of Ovarian Research</i> , 2019, 12, 35.	1.3	111
9897	Identification of key regulatory genes connected to NF- $\kappa$ B family of proteins in visceral adipose tissues using gene expression and weighted protein interaction network. <i>PLoS ONE</i> , 2019, 14, e0214337.	1.1	23
9898	Identification of key candidate genes and pathways in oral squamous cell carcinoma by integrated Bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 4089-4099.	0.8	15
9899	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. <i>Cell Reports</i> , 2019, 27, 1090-1102.e10.	2.9	59
9900	Effects of C-Terminal Carboxylation on $\hat{1}\pm$ -Conotoxin LsIA Interactions with Human $\hat{1}\pm$ 7 Nicotinic Acetylcholine Receptor: Molecular Simulation Studies. <i>Marine Drugs</i> , 2019, 17, 206.	2.2	8
9901	In Silico Investigation of the Anti-Tumor Mechanisms of Epigallocatechin-3-Gallate. <i>Molecules</i> , 2019, 24, 1445.	1.7	17
9902	Disordered APC/C-mediated cell cycle progression and IGF1/PI3K/AKT signalling are the potential basis of Sertoli cell-only syndrome. <i>Andrologia</i> , 2019, 51, e13288.	1.0	12
9903	Quantifying local malignant adaptation in tissue-specific evolutionary trajectories by harnessing cancer's repeatability at the genetic level. <i>Evolutionary Applications</i> , 2019, 12, 1062-1075.	1.5	2
9904	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. <i>MBio</i> , 2019, 10, .	1.8	20

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9905	Metabopolis: scalable network layout for biological pathway diagrams in urban map style. <i>BMC Bioinformatics</i> , 2019, 20, 187.	1.2	8
9906	The impact of JAK/STAT inhibitor ruxolitinib on the genesis of lymphoproliferative diseases. <i>Turkish Journal of Medical Sciences</i> , 2019, 49, 661-674.	0.4	6
9907	Considerations for Identifying Endogenous Protein Complexes from Tissue via Immunoaffinity Purification and Quantitative Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1977, 115-143.	0.4	5
9908	HCV-Induced Epigenetic Changes Associated With Liver Cancer Risk Persist After Sustained Virologic Response. <i>Gastroenterology</i> , 2019, 156, 2313-2329.e7.	0.6	184
9909	Integration of transcriptomic data in a genome-scale metabolic model to investigate the link between obesity and breast cancer. <i>BMC Bioinformatics</i> , 2019, 20, 162.	1.2	22
9910	Prediction of Recurrence in Cervical Cancer Using a Nine-lncRNA Signature. <i>Frontiers in Genetics</i> , 2019, 10, 284.	1.1	28
9911	Systems Pharmacological Approach to Investigate the Mechanism of <i>Ohwia caudata</i> for Application to Alzheimer's Disease. <i>Molecules</i> , 2019, 24, 1499.	1.7	11
9912	Functional Genomics of the Infant Human Thymus: AIRE and Minipuberty. , 2019, , 235-245.		0
9913	Structure and Function of an Inflammatory Cytokine, Interleukin-2, Analyzed Using the Bioinformatic Approach. <i>Protein Journal</i> , 2019, 38, 525-536.	0.7	4
9914	Conformational Dynamics and Allosteric Regulation Landscapes of Germline PTEN Mutations Associated with Autism Compared to Those Associated with Cancer. <i>American Journal of Human Genetics</i> , 2019, 104, 861-878.	2.6	45
9915	A proteomic and biochemical investigation on the effects of sulfadiazine in <i>Arabidopsis thaliana</i> . <i>Ecotoxicology and Environmental Safety</i> , 2019, 178, 146-158.	2.9	9
9916	The EntOptLayout Cytoscape plug-in for the efficient visualization of major protein complexes in protein-protein interaction and signalling networks. <i>Bioinformatics</i> , 2019, 35, 4490-4492.	1.8	25
9917	Effects of Xiaoyaosan on the Hippocampal Gene Expression Profile in Rats Subjected to Chronic Immobilization Stress. <i>Frontiers in Psychiatry</i> , 2019, 10, 178.	1.3	7
9918	Competing endogenous RNA network of endometrial carcinoma: A comprehensive analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15648-15660.	1.2	11
9919	Functional suppression of Epiregulin impairs angiogenesis and aggravates left ventricular remodeling by disrupting the extracellular-signal-regulated kinase1/2 signaling pathway in rats after acute myocardial infarction. <i>Journal of Cellular Physiology</i> , 2019, 234, 18653-18665.	2.0	11
9920	Disentangling the immune response and host-pathogen interactions in <i>Francisella noatunensis</i> infected Atlantic cod. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 333-346.	0.4	31
9921	Insights into mechanisms and severity of drug-induced liver injury via computational systems toxicology approach. <i>Toxicology Letters</i> , 2019, 312, 22-33.	0.4	13
9922	A single-cell atlas of mouse brain macrophages reveals unique transcriptional identities shaped by ontogeny and tissue environment. <i>Nature Neuroscience</i> , 2019, 22, 1021-1035.	7.1	603



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9923	Hdac4 Interactions in Huntington's Disease Viewed Through the Prism of Multiomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S92-S113.	2.5	28
9924	Specific chromatin changes mark lateral organ founder cells in the Arabidopsis inflorescence meristem. <i>Journal of Experimental Botany</i> , 2019, 70, 3867-3879.	2.4	17
9925	Rainbow Trout Red Blood Cells Exposed to Viral Hemorrhagic Septicemia Virus Up-Regulate Antigen-Processing Mechanisms and MHC I&II, CD86, and CD83 Antigen-presenting Cell Markers. <i>Cells</i> , 2019, 8, 386.	1.8	21
9926	Enhanced Awareness in Space Operations Using Web-Based Interactive Multipurpose Dynamic Network Analysis. , 2019, , 795-810.		1
9927	Integrative microRNA and gene expression analysis identifies new drug repurposing candidates for fetal hemoglobin induction in $\beta^2$ -hemoglobinopathies. <i>Gene</i> , 2019, 706, 77-83.	1.0	6
9928	Drug Resistance-Related Competing Interactions of lncRNA and mRNA across 19 Cancer Types. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 442-451.	2.3	25
9929	Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. <i>RNA Biology</i> , 2019, 16, 1010-1021.	1.5	7
9930	Marek's Disease Virus Regulates the Ubiquitylome of Chicken CD4+ T Cells to Promote Tumorigenesis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2089.	1.8	5
9931	MOSClip: multi-omic and survival pathway analysis for the identification of survival associated gene and modules. <i>Nucleic Acids Research</i> , 2019, 47, e80.	6.5	10
9932	Mouse genome-wide association and systems genetics identifies Lhfp as a regulator of bone mass. <i>PLoS Genetics</i> , 2019, 15, e1008123.	1.5	22
9933	A Comprehensive Functional Characterization of Escherichia coli Lipid Genes. <i>Cell Reports</i> , 2019, 27, 1597-1606.e2.	2.9	31
9934	A Convergent Study of Genetic Variants Associated With Crohn's Disease: Evidence From GWAS, Gene Expression, Methylation, eQTL and TWAS. <i>Frontiers in Genetics</i> , 2019, 10, 318.	1.1	19
9935	Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. <i>American Journal of Physical Anthropology</i> , 2019, 169, 575-585.	2.1	15
9936	Topological and functional comparison of community detection algorithms in biological networks. <i>BMC Bioinformatics</i> , 2019, 20, 212.	1.2	41
9937	Deciphering the phylogeny of violets based on multiplexed genetic and metabolomic approaches. <i>Phytochemistry</i> , 2019, 163, 99-110.	1.4	14
9938	Molecular dissection of box jellyfish venom cytotoxicity highlights an effective venom antidote. <i>Nature Communications</i> , 2019, 10, 1655.	5.8	35
9939	Microbiota of the Gut-Lymph Node Axis: Depletion of Mucosa-Associated Segmented Filamentous Bacteria and Enrichment of Methanobrevibacter by Colistin Sulfate and Linco-Spectin in Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 599.	1.5	11
9940	Immune microenvironments differ in immune characteristics and outcome of glioblastoma multiforme. <i>Cancer Medicine</i> , 2019, 8, 2897-2907.	1.3	25



#	ARTICLE	IF	CITATIONS
9941	Cryptochrome deletion in p53 mutant mice enhances apoptotic and anti-tumorigenic responses to UV damage at the transcriptome level. <i>Functional and Integrative Genomics</i> , 2019, 19, 729-742.	1.4	9
9942	Differential expression and bioinformatics analysis of circRNA in osteosarcoma. <i>Bioscience Reports</i> , 2019, 39, .	1.1	39
9943	In Silico Integration Approach Reveals Key MicroRNAs and Their Target Genes in Follicular Thyroid Carcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	11
9944	Novel insights into plant-associated archaea and their functioning in arugula ( <i>Eruca sativa</i> Mill.). <i>Journal of Advanced Research</i> , 2019, 19, 39-48.	4.4	49
9945	Virtual screening of active compounds from <i>Artemisia argyi</i> and potential targets against gastric ulcer based on Network pharmacology. <i>Bioorganic Chemistry</i> , 2019, 88, 102924.	2.0	32
9946	Pathway centrality in protein interaction networks identifies putative functional mediating pathways in pulmonary disease. <i>Scientific Reports</i> , 2019, 9, 5863.	1.6	7
9947	Quantitative Proteomic Analysis of Human Seminal Plasma from Normozoospermic and Asthenozoospermic Individuals. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	11
9948	A slow transcription rate causes embryonic lethality and perturbs kinetic coupling of neuronal genes. <i>EMBO Journal</i> , 2019, 38, .	3.5	46
9949	Elucidation of Novel Therapeutic Targets for Acute Myeloid Leukemias with RUNX1-RUNX1T1 Fusion. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1717.	1.8	8
9950	A prognostic signature based on three non-codingRNAs for prediction of the overall survival of glioma patients. <i>FEBS Open Bio</i> , 2019, 9, 682-692.	1.0	5
9951	MicroRNA regulation during <i>Nibeia albiflora</i> immuno-resistant against <i>Cryptocaryon irritans</i> challenge in fish skin. <i>Aquaculture</i> , 2019, 507, 211-221.	1.7	10
9952	Genome-Wide CRISPR-Cas9 Screens Expose Genetic Vulnerabilities and Mechanisms of Temozolomide Sensitivity in Glioblastoma Stem Cells. <i>Cell Reports</i> , 2019, 27, 971-986.e9.	2.9	139
9953	Metabolomics revealed decreased level of omega-3 PUFA-derived protective eicosanoids in pregnant women with pre-eclampsia. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2019, 46, 705-710.	0.9	18
9954	A Data Integration Multi-Omics Approach to Study Calorie Restriction-Induced Changes in Insulin Sensitivity. <i>Frontiers in Physiology</i> , 2018, 9, 1958.	1.3	39
9955	Toxicity of Cyanopeptides from Two <i>Microcystis</i> Strains on Larval Development of <i>Astyanax altiparanae</i> . <i>Toxins</i> , 2019, 11, 220.	1.5	22
9956	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. <i>JAMA Network Open</i> , 2019, 2, e191851.	2.8	10
9957	Silencing of microRNA-27a facilitates autophagy and apoptosis of melanoma cells through the activation of the SYK-dependent mTOR signaling pathway. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13262-13274.	1.2	13
9958	Synthesis of andrographolide analogues and their neuroprotection and neurite outgrowth-promoting activities. <i>Bioorganic and Medicinal Chemistry</i> , 2019, 27, 2209-2219.	1.4	18

#	ARTICLE	IF	CITATIONS
9959	A Comprehensive Drosophila melanogaster Transcription Factor Interactome. Cell Reports, 2019, 27, 955-970.e7.	2.9	66
9960	Growth performance, photosynthesis, and root characteristics are associated with nitrogen use efficiency in six poplar species. Environmental and Experimental Botany, 2019, 164, 40-51.	2.0	28
9961	Oxidative stress: One potential factor for arsenite-induced increase of N6-methyladenosine in human keratinocytes. Environmental Toxicology and Pharmacology, 2019, 69, 95-103.	2.0	51
9962	An extensively shared antibiotic resistome among four seasons suggests management prioritization in a subtropical riverine ecosystem. Science of the Total Environment, 2019, 673, 533-540.	3.9	14
9963	Comparison of multi-tissue aging between human and mouse. Scientific Reports, 2019, 9, 6220.	1.6	15
9964	<i>Klebsiella</i> and <i>Providencia</i> emerge as lone survivors following long-term starvation of oral microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8499-8504.	3.3	30
9965	High-throughput Exploration of the Network Dependent on AKT1 in Mouse Ovarian Granulosa Cells. Molecular and Cellular Proteomics, 2019, 18, 1307-1319.	2.5	10
9966	A Network-based Comparison between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	2
9967	Phosphoproteome Analysis of Cells Infected with Adapted and Nonadapted Influenza A Virus Reveals Novel Pro- and Antiviral Signaling Networks. Journal of Virology, 2019, 93, .	1.5	19
9968	Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis. BMC Genomics, 2019, 20, 185.	1.2	20
9969	Effect of paleopolyploidy and allopolyploidy on gene expression in banana. BMC Genomics, 2019, 20, 244.	1.2	22
9970	Stimulative role of ST6GALNAC1 in proliferation, migration and invasion of ovarian cancer stem cells via the Akt signaling pathway. Cancer Cell International, 2019, 19, 86.	1.8	22
9971	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. Microbiome, 2019, 7, 63.	4.9	51
9972	JAM3 functions as a novel tumor suppressor and is inactivated by DNA methylation in colorectal cancer. Cancer Management and Research, 2019, Volume 11, 2457-2470.	0.9	27
9973	Atomistic Modeling of the ABL Kinase Regulation by Allosteric Modulators Using Structural Perturbation Analysis and Community-Based Network Reconstruction of Allosteric Communications. Journal of Chemical Theory and Computation, 2019, 15, 3362-3380.	2.3	46
9974	Gene co-expression networks contributing to the expression of compensatory growth in metabolically active tissues in cattle. Scientific Reports, 2019, 9, 6093.	1.6	10
9975	A niche-dependent myeloid transcriptome signature defines dormant myeloma cells. Blood, 2019, 134, 30-43.	0.6	99
9976	Folding Status Is Determinant over Traffic-Competence in Defining CFTR Interactors in the Endoplasmic Reticulum. Cells, 2019, 8, 353.	1.8	21

#	ARTICLE	IF	CITATIONS
9977	Cryopreservation Differentially Alters the Proteome of Epididymal and Ejaculated Pig Spermatozoa. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1791.	1.8	29
9978	The Pathway to Cancer Cachexia: MicroRNA-Regulated Networks in Muscle Wasting Based on Integrative Meta-Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1962.	1.8	33
9979	Gene coexpression networks analysis of sickle stroke risk. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15182-15189.	1.2	1
9980	Insulin Induces Microtubule Stabilization and Regulates the Microtubule Plus-end Tracking Protein Network in Adipocytes. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1363-1381.	2.5	43
9981	ACE2 inhibits breast cancer angiogenesis via suppressing the VEGFa/VEGFR2/ERK pathway. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 173.	3.5	183
9982	Triggering MSR1 promotes JNK-mediated inflammation in IL-4-activated macrophages. <i>EMBO Journal</i> , 2019, 38, .	3.5	78
9983	Angiogenin mutations in Hungarian patients with amyotrophic lateral sclerosis: Clinical, genetic, computational, and functional analyses. <i>Brain and Behavior</i> , 2019, 9, e01293.	1.0	10
9984	Interaction network analysis of YBX1 for identification of therapeutic targets in adenocarcinomas. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	3
9985	How Microbes Shape Their Communities? A Microbial Community Model Based on Functional Genes. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 91-105.	3.0	18
9986	MiRNA profiling revealed enhanced susceptibility to oxidative stress of endothelial cells from bicuspid aortic valve. <i>Journal of Molecular and Cellular Cardiology</i> , 2019, 131, 146-154.	0.9	14
9987	Differentially expressed circulating miRNAs in postmenopausal osteoporosis: a meta-analysis. <i>Bioscience Reports</i> , 2019, 39, .	1.1	23
9988	Network reconstruction from infection cascades. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20180844.	1.5	22
9989	Current paradigms and new perspectives on fetal hypoxia: implications for fetal brain development in late gestation. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2019, 317, R1-R13.	0.9	17
9990	Identification of cucumber circular RNAs responsive to salt stress. <i>BMC Plant Biology</i> , 2019, 19, 164.	1.6	72
9991	Plasma Protein and MicroRNA Biomarkers of Insulin Resistance: A Network-Based Integrative -Omics Analysis. <i>Frontiers in Physiology</i> , 2019, 10, 379.	1.3	28
9992	Deciphering the complex interplay between microbiota, HPV, inflammation and cancer through cervicovaginal metabolic profiling. <i>EBioMedicine</i> , 2019, 44, 675-690.	2.7	142
9993	Overcoming the Challenges of Enzyme Evolution To Adapt Phosphotriesterase for V-Agent Decontamination. <i>Biochemistry</i> , 2019, 58, 2039-2053.	1.2	31
9994	Ocean Acidification Regulates the Activity, Community Structure, and Functional Potential of Heterotrophic Bacterioplankton in an Oligotrophic Gyre. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 1001-1017.	1.3	10

#	ARTICLE	IF	CITATIONS
9995	Contribution of time of day and the circadian clock to the heat stress responsive transcriptome in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2019, 9, 4814.	1.6	62
9996	Chronic ethanol consumption alters lamina propria leukocyte response to stimulation in a regionâ€dependent manner. <i>FASEB Journal</i> , 2019, 33, 7767-7777.	0.2	6
9997	Visual Analytics of Genomic and Cancer Data: A Systematic Review. <i>Cancer Informatics</i> , 2019, 18, 117693511983554.	0.9	18
9998	Dynamic transcriptome profiles within spermatogonial and spermatocyte populations during postnatal testis maturation revealed by single-cell sequencing. <i>PLoS Genetics</i> , 2019, 15, e1007810.	1.5	80
9999	Distributions of Extracellular Peptidases Across Prokaryotic Genomes Reflect Phylogeny and Habitat. <i>Frontiers in Microbiology</i> , 2019, 10, 413.	1.5	55
10000	A comprehensive in silico analysis of sortase superfamily. <i>Journal of Microbiology</i> , 2019, 57, 431-443.	1.3	18
10001	Systematic investigation of the mechanism of <i>Cichorium glandulosum</i> on type 2 diabetes mellitus accompanied with non-alcoholic fatty liver rats. <i>Food and Function</i> , 2019, 10, 2450-2460.	2.1	13
10002	Protein profiling of osteosarcoma tissue and soft callus unveils activation of the unfolded protein response pathway. <i>International Journal of Oncology</i> , 2019, 54, 1704-1718.	1.4	14
10003	Combining Rapid Data Independent Acquisition and CRISPR Gene Deletion for Studying Potential Protein Functions: A Case of HMGN1. <i>Proteomics</i> , 2019, 19, e1800438.	1.3	31
10004	Integrated analysis of gene expression and methylation profiles of novel pancreatic cancer cell lines with highly metastatic activity. <i>Science China Life Sciences</i> , 2019, 62, 791-806.	2.3	5
10005	New Insights of Salicylic Acid Into Stamen Abortion of Female Flowers in Tung Tree ( <i>Vernicia fordii</i> ). <i>Frontiers in Genetics</i> , 2019, 10, 316.	1.1	25
10006	micro-RNAs dependent regulation of DNMT and HIF1 $\beta$ gene expression in thrombotic disorders. <i>Scientific Reports</i> , 2019, 9, 4815.	1.6	6
10007	Relative effects of location relative to the corpus luteum and lactation on the transcriptome of the bovine oviduct epithelium. <i>BMC Genomics</i> , 2019, 20, 233.	1.2	19
10008	Spatiotemporal Developmental Trajectories in the <i>Arabidopsis</i> Root Revealed Using High-Throughput Single-Cell RNA Sequencing. <i>Developmental Cell</i> , 2019, 48, 840-852.e5.	3.1	367
10009	Early transcriptome profile of goat peripheral blood mononuclear cells (PBMCs) infected with peste des petits ruminant's vaccine virus (Sungri/96) revealed induction of antiviral response in an interferon independent manner. <i>Research in Veterinary Science</i> , 2019, 124, 166-177.	0.9	10
10010	Exploring the long-term effect of plastic on compost microbiome. <i>PLoS ONE</i> , 2019, 14, e0214376.	1.1	30
10011	Investigation into the underlying molecular mechanisms of non-small cell lung cancer using bioinformatics analysis. <i>Gene Reports</i> , 2019, 15, 100394.	0.4	4
10012	The expression of miR-375 in prostate cancer: A study based on GEO, TCGA data and bioinformatics analysis. <i>Pathology Research and Practice</i> , 2019, 215, 152375.	1.0	25

#	ARTICLE	IF	CITATIONS
10013	Glycolytic flux in <i>Saccharomyces cerevisiae</i> is dependent on RNA polymerase III and its negative regulator Maf1. <i>Biochemical Journal</i> , 2019, 476, 1053-1082.	1.7	9
10014	Regulation of proline-directed kinases and the trans-histone code H3K9me3/H4K20me3 during human myogenesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 8296-8308.	1.6	11
10015	Deletion of the KH1 Domain of <i>Fmr1</i> Leads to Transcriptional Alterations and Attentional Deficits in Rats. <i>Cerebral Cortex</i> , 2019, 29, 2228-2244.	1.6	22
10016	The Proteogenomic Landscape of Curable Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 414-427.e6.	7.7	168
10017	Multi-dimensional Transcriptional Remodeling by Physiological Insulin In Vivo. <i>Cell Reports</i> , 2019, 26, 3429-3443.e3.	2.9	62
10018	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019, 431, 1650-1670.	2.0	41
10019	Biomolecular Databases and Subnetwork Identification Approaches of Interest to Big Data Community: An Expert Review. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 138-151.	1.0	12
10020	New insight into the classification and evolution of glucose transporters in the Metazoa. <i>FASEB Journal</i> , 2019, 33, 7519-7528.	0.2	10
10021	Co-expression network analysis identified KIF2C in association with progression and prognosis in lung adenocarcinoma. <i>Cancer Biomarkers</i> , 2019, 24, 371-382.	0.8	41
10022	SIRT5 downregulation is associated with poor prognosis in glioblastoma. <i>Cancer Biomarkers</i> , 2019, 24, 449-459.	0.8	24
10023	Lateral Root Primordium Morphogenesis in Angiosperms. <i>Frontiers in Plant Science</i> , 2019, 10, 206.	1.7	61
10024	Metagenomic exploration of the interactions between N and P cycling and SOM turnover in an apple orchard with a cover crop fertilized for 9 years. <i>Biology and Fertility of Soils</i> , 2019, 55, 365-381.	2.3	37
10025	Genome-wide identification, phylogeny and expression profiling of class III peroxidases gene family in <i>Brachypodium distachyon</i> . <i>Gene</i> , 2019, 700, 149-162.	1.0	21
10026	Vertical profile of soil/sediment pollution and microbial community change by e-waste recycling operation. <i>Science of the Total Environment</i> , 2019, 669, 1001-1010.	3.9	37
10027	An integrative approach using systems biology, mutational analysis with molecular dynamics simulation to challenge the functionality of a target protein. <i>Chemical Biology and Drug Design</i> , 2019, 93, 1050-1060.	1.5	22
10028	Visualizing Protein Folding and Unfolding. <i>Journal of Molecular Biology</i> , 2019, 431, 1540-1564.	2.0	32
10029	Brain Imaging-Guided Analysis Reveals DNA Methylation Profiles Correlated with Insular Surface Area and Alcohol Use Disorder. <i>Alcoholism: Clinical and Experimental Research</i> , 2019, 43, 628-639.	1.4	3
10030	Low GAS5 Levels as a Predictor of Poor Survival in Patients with Lower-Grade Gliomas. <i>Journal of Oncology</i> , 2019, 2019, 1-15.	0.6	40

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10031	A Network Pharmacology Approach Used to Estimate the Active Ingredients of Moutan Cortex Charcoal and the Potential Targets in Hemorrhagic Diseases. <i>Biological and Pharmaceutical Bulletin</i> , 2019, 42, 432-441.	0.6	14
10032	Comparative Gene Expression Profiles in Parathyroid Adenoma and Normal Parathyroid Tissue. <i>Journal of Clinical Medicine</i> , 2019, 8, 297.	1.0	14
10033	Context-Adapted Urban Planning for Rapid Transitioning of Personal Mobility towards Sustainability: A Systematic Literature Review. <i>Sustainability</i> , 2019, 11, 1007.	1.6	23
10034	Changes in the soil microbial community are associated with the occurrence of <i>Panax quinquefolius</i> L. root rot diseases. <i>Plant and Soil</i> , 2019, 438, 143-156.	1.8	39
10035	Hepatocytes direct the formation of a pro-metastatic niche in the liver. <i>Nature</i> , 2019, 567, 249-252.	13.7	263
10036	Intensive tropical land use massively shifts soil fungal communities. <i>Scientific Reports</i> , 2019, 9, 3403.	1.6	86
10037	Early Stage Biomarkers Screening of Prostate Cancer Based on Weighted Gene Coexpression Network Analysis. <i>DNA and Cell Biology</i> , 2019, 38, 468-475.	0.9	2
10038	Disease Incidence in Sugar Beet Fields Is Correlated with Microbial Diversity and Distinct Biological Markers. <i>Phytobiomes Journal</i> , 2019, 3, 22-30.	1.4	47
10039	Chromatin capture links the metabolic enzyme AHCY to stem cell proliferation. <i>Science Advances</i> , 2019, 5, eaav2448.	4.7	38
10040	PAI-1 augments mucosal damage in colitis. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	44
10041	GeneLab Database Analyses Suggest Long-Term Impact of Space Radiation on the Cardiovascular System by the Activation of FYN Through Reactive Oxygen Species. <i>International Journal of Molecular Sciences</i> , 2019, 20, 661.	1.8	23
10042	Multiple Targets of 3-Dehydroxyceanothric Acid 2-Methyl Ester to Protect Against Cisplatin-Induced Cytotoxicity in Kidney Epithelial LLC-PK1 Cells. <i>Molecules</i> , 2019, 24, 878.	1.7	7
10043	Dominance network analysis provides a new framework for studying the diversity–stability relationship. <i>Ecological Monographs</i> , 2019, 89, e01358.	2.4	30
10044	Automated exploration of gene ontology term and pathway networks with ClueGO-REST. <i>Bioinformatics</i> , 2019, 35, 3864-3866.	1.8	48
10045	Multitrait genome-wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. <i>New Phytologist</i> , 2019, 223, 293-309.	3.5	85
10046	Construction of a Suite of Computable Biological Network Models Focused on Mucociliary Clearance in the Respiratory Tract. <i>Frontiers in Genetics</i> , 2019, 10, 87.	1.1	6
10047	MiRNAs from DLK1-DIO3 Imprinted Locus at 14q32 are Associated with Multiple Sclerosis: Gender-Specific Expression and Regulation of Receptor Tyrosine Kinases Signaling. <i>Cells</i> , 2019, 8, 133.	1.8	35
10048	Target discovery of chlorogenic acid derivatives from the flower buds of <i>Lonicera macranthoides</i> and their MAO B inhibitory mechanism. <i>FÄ-toterapÄ-Äç</i> , 2019, 134, 297-304.	1.1	19



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10049	Bone marrow mesenchymal stem cell-derived exosomes alleviate high phosphorus-induced vascular smooth muscle cells calcification by modifying microRNA profiles. <i>Functional and Integrative Genomics</i> , 2019, 19, 633-643.	1.4	33
10050	Refactoring the Cryptic Streptophenazine Biosynthetic Gene Cluster Unites Phenazine, Polyketide, and Nonribosomal Peptide Biochemistry. <i>Cell Chemical Biology</i> , 2019, 26, 724-736.e7.	2.5	48
10051	Identification of drought responsive proteins and related proteomic QTLs in barley. <i>Journal of Experimental Botany</i> , 2019, 70, 2823-2837.	2.4	28
10052	Mycobiome Profiles in Breast Milk from Healthy Women Depend on Mode of Delivery, Geographic Location, and Interaction with Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	76
10053	mtProtEvol: the resource presenting molecular evolution analysis of proteins involved in the function of Vertebrate mitochondria. <i>BMC Evolutionary Biology</i> , 2019, 19, 47.	3.2	2
10054	A modular analysis of microglia gene expression, insights into the aged phenotype. <i>BMC Genomics</i> , 2019, 20, 164.	1.2	24
10055	Gene expression meta-analysis of Parkinson's disease and its relationship with Alzheimer's disease. <i>Molecular Brain</i> , 2019, 12, 16.	1.3	52
10056	Protist communities are more sensitive to nitrogen fertilization than other microorganisms in diverse agricultural soils. <i>Microbiome</i> , 2019, 7, 33.	4.9	278
10057	Identification of novel candidate indicators for assessing zinc status during pregnancy in mice from microarray data. <i>BMC Pharmacology &amp; Toxicology</i> , 2019, 20, 12.	1.0	1
10058	The temporal profile of activity-dependent presynaptic phospho-signalling reveals long-lasting patterns of poststimulus regulation. <i>PLoS Biology</i> , 2019, 17, e3000170.	2.6	29
10059	Molecular Processes and Hub Genes of <i>Acropora Palmata</i> in Response to Thermal Stress And Bleaching. <i>Journal of Coastal Research</i> , 2019, 35, 26.	0.1	1
10060	Shared Gene Expression Between Multiple Sclerosis and Ischemic Stroke. <i>Frontiers in Genetics</i> , 2018, 9, 598.	1.1	9
10061	Network Pharmacology Databases for Traditional Chinese Medicine: Review and Assessment. <i>Frontiers in Pharmacology</i> , 2019, 10, 123.	1.6	731
10062	Gene-Specific Intron Retention Serves as Molecular Signature that Distinguishes Melanoma from Non-Melanoma Cancer Cells in Greek Patients. <i>International Journal of Molecular Sciences</i> , 2019, 20, 937.	1.8	8
10063	Identification of survival-associated key genes and long non-coding RNAs in glioblastoma multiforme by weighted gene co-expression network analysis. <i>International Journal of Molecular Medicine</i> , 2019, 43, 1709-1722.	1.8	13
10064	Identification of biomarkers associated with the recurrence of osteosarcoma using ceRNA regulatory network analysis. <i>International Journal of Molecular Medicine</i> , 2019, 43, 1723-1733.	1.8	23
10065	Prediction and analysis of weighted genes in hepatocellular carcinoma using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 2479-2488.	1.1	15
10066	Identification of key genes and pathways contributing to artery tertiary lymphoid organ development in advanced mouse atherosclerosis. <i>Molecular Medicine Reports</i> , 2019, 19, 3071-3086.	1.1	8



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10067	Reconstruction and analysis of circRNA-miRNA-mRNA network in the pathology of cervical cancer. <i>Oncology Reports</i> , 2019, 41, 2209-2225.	1.2	58
10068	Evolution of PEPC gene family in <i>Gossypium</i> reveals functional diversification and GhPEPC genes responding to abiotic stresses. <i>Gene</i> , 2019, 698, 61-71.	1.0	11
10069	Time-resolved decoding of metabolic signatures of in vitro growth of the hemibiotrophic pathogen <i>Colletotrichum sublineolum</i> . <i>Scientific Reports</i> , 2019, 9, 3290.	1.6	12
10070	Identification of key lncRNAs contributing to diabetic nephropathy by gene co-expression network analysis. <i>Scientific Reports</i> , 2019, 9, 3328.	1.6	19
10071	Analysis of the Functional Relevance of Epigenetic Chromatin Marks in the First Intron Associated with Specific Gene Expression Patterns. <i>Genome Biology and Evolution</i> , 2019, 11, 786-797.	1.1	13
10072	Isoform-specific GSK3A activity is negatively correlated with human sperm motility. <i>Molecular Human Reproduction</i> , 2019, 25, 171-183.	1.3	18
10073	Fungal-Bacterial Networks in the <i>Populus</i> Rhizobiome Are Impacted by Soil Properties and Host Genotype. <i>Frontiers in Microbiology</i> , 2019, 10, 481.	1.5	71
10074	The Eukaryotic Life on Microplastics in Brackish Ecosystems. <i>Frontiers in Microbiology</i> , 2019, 10, 538.	1.5	109
10075	Identifying the differentially expressed microRNAs in esophagus squamous cell carcinoma of Kazakh patients in Xinjiang. <i>Oncology Letters</i> , 2019, 17, 2657-2668.	0.8	4
10076	In silico analysis and gene expression of heat stress responses genes in <i>Hordeum vulgare</i> L.. <i>Biocatalysis and Agricultural Biotechnology</i> , 2019, 18, 101061.	1.5	1
10077	Systems biology approach identifies key regulators and the interplay between miRNAs and transcription factors for pathological cardiac hypertrophy. <i>Gene</i> , 2019, 698, 157-169.	1.0	9
10078	High Anti-Interfering Profiling of Endogenous Glycopeptides for Human Plasma by the Dual-Hydrophilic Metal-Organic Framework. <i>Analytical Chemistry</i> , 2019, 91, 4852-4859.	3.2	44
10079	Synergy from gene expression and network mining (SynGeNet) method predicts synergistic drug combinations for diverse melanoma genomic subtypes. <i>Npj Systems Biology and Applications</i> , 2019, 5, 6.	1.4	36
10080	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium <i>Burkholderia ambifaria</i> . <i>Nature Microbiology</i> , 2019, 4, 996-1005.	5.9	106
10081	Molecular characterization of <i>Histomonas meleagridis</i> exoproteome with emphasis on protease secretion and parasite-bacteria interaction. <i>PLoS ONE</i> , 2019, 14, e0212429.	1.1	6
10082	Exploring tRNA gene cluster in archaea. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180348.	0.8	5
10083	Stable and novel QTL identification and new insights into the genetic networks affecting seed fiber traits in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 1761-1775.	1.8	21
10084	Highly connected taxa located in the microbial network are prevalent in the rhizosphere soil of healthy plant. <i>Biology and Fertility of Soils</i> , 2019, 55, 299-312.	2.3	57

#	ARTICLE	IF	CITATIONS
10085	Identify the critical protein-coding genes and long noncoding RNAs in cardiac myxoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13441-13452.	1.2	3
10086	Comprehensive analysis of a ceRNA network reveals potential prognostic cytoplasmic lncRNAs involved in HCC progression. <i>Journal of Cellular Physiology</i> , 2019, 234, 18837-18848.	2.0	103
10087	Linking cropland ecosystem services to microbiome taxonomic composition and functional composition in a sandy loam soil with 28-year organic and inorganic fertilizer regimes. <i>Applied Soil Ecology</i> , 2019, 139, 1-9.	2.1	38
10088	Epigenetic effects of paternal cocaine on reward stimulus behavior and accumbens gene expression in mice. <i>Behavioural Brain Research</i> , 2019, 367, 68-81.	1.2	14
10089	Interaction of Discoidin Domain Receptor 1 with a 14-3-3-Beclin-1-Akt1 Complex Modulates Glioblastoma Therapy Sensitivity. <i>Cell Reports</i> , 2019, 26, 3672-3683.e7.	2.9	48
10090	Transcriptomic Analysis of Single Isolated Myofibers Identifies miR-27a-3p and miR-142-3p as Regulators of Metabolism in Skeletal Muscle. <i>Cell Reports</i> , 2019, 26, 3784-3797.e8.	2.9	55
10091	Identification and functional analysis of circular RNAs induced in rats by middle cerebral artery occlusion. <i>Gene</i> , 2019, 701, 139-145.	1.0	23
10092	Comparative analysis of proteomic and metabolomic profiles of different species of Paris. <i>Journal of Proteomics</i> , 2019, 200, 11-27.	1.2	16
10093	Seasonal dynamics of bacterial communities in the surface seawater around subtropical Xiamen Island, China, as determined by 16S rRNA gene profiling. <i>Marine Pollution Bulletin</i> , 2019, 142, 135-144.	2.3	39
10094	Metabolomic variability of four macroalgal species of the genus <i>Lobophora</i> using diverse approaches. <i>Phytochemistry</i> , 2019, 162, 165-172.	1.4	17
10095	ITGA6 and RPSA synergistically promote pancreatic cancer invasion and metastasis via PI3K and MAPK signaling pathways. <i>Experimental Cell Research</i> , 2019, 379, 30-47.	1.2	58
10096	Mapping a Systematic Ribozyme Fitness Landscape Reveals a Frustrated Evolutionary Network for Self-Aminoacylating RNA. <i>Journal of the American Chemical Society</i> , 2019, 141, 6213-6223.	6.6	67
10097	Foliar-feeding insects acquire microbiomes from the soil rather than the host plant. <i>Nature Communications</i> , 2019, 10, 1254.	5.8	135
10098	Integrative Bioinformatics Analysis Reveals Potential Gene Biomarkers and Analysis of Function in Human Degenerative Disc Annulus Fibrosus Cells. <i>BioMed Research International</i> , 2019, 2019, 1-8.	0.9	8
10099	Network structure underpinning (dys)homeostasis in chronic fatigue syndrome; Preliminary findings. <i>PLoS ONE</i> , 2019, 14, e0213724.	1.1	8
10100	Major Traditional Probiotics: Comparative Genomic Analyses and Roles in Gut Microbiome of Eight Cohorts. <i>Frontiers in Microbiology</i> , 2019, 10, 712.	1.5	13
10101	Identification of key genes involved in the metastasis of clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2019, 17, 4321-4328.	0.8	56
10102	Analysis of microRNA expression profiles reveals a microRNA prognostic signature for predicting overall survival time in patients with gastric adenocarcinoma. <i>Oncology Reports</i> , 2019, 41, 2775-2789.	1.2	3

#	ARTICLE	IF	CITATIONS
10103	A Common Embryonic Origin of Stem Cells Drives Developmental and Adult Neurogenesis. <i>Cell</i> , 2019, 177, 654-668.e15.	13.5	186
10104	Prdm12 Directs Nociceptive Sensory Neuron Development by Regulating the Expression of the NGF Receptor TrkA. <i>Cell Reports</i> , 2019, 26, 3522-3536.e5.	2.9	50
10105	Distinct communities of Cercozoa at different soil depths in a temperate agricultural field. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	21
10106	Uncovering the unexplored diversity of thioamidated ribosomal peptides in Actinobacteria using the RiPPER genome mining tool. <i>Nucleic Acids Research</i> , 2019, 47, 4624-4637.	6.5	98
10107	Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Maize Specialized Metabolites. <i>Plant Cell</i> , 2019, 31, 937-955.	3.1	75
10108	Deciphering the mechanism of Indirubin and its derivatives in the inhibition of Imatinib resistance using a "drug target prediction-gene microarray analysis-protein network construction" strategy. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 75.	3.7	4
10109	SUMOylation promotes protective responses to DNA-protein crosslinks. <i>EMBO Journal</i> , 2019, 38, .	3.5	73
10110	Detecting Diagnostic Biomarkers of Alzheimer's Disease by Integrating Gene Expression Data in Six Brain Regions. <i>Frontiers in Genetics</i> , 2019, 10, 157.	1.1	21
10111	Transcriptome Analysis Revealed a Highly Connected Gene Module Associated With Cirrhosis to Hepatocellular Carcinoma Development. <i>Frontiers in Genetics</i> , 2019, 10, 305.	1.1	26
10112	Comprehensive proteomic analysis and pathogenic role of membrane vesicles of <i>Listeria monocytogenes</i> serotype 4b reveals proteins associated with virulence and their possible interaction with host. <i>International Journal of Medical Microbiology</i> , 2019, 309, 199-212.	1.5	26
10113	Literature data based systems pharmacology uncovers the essence of "body fire" in traditional Chinese medicine: A case by Huang-Lian-Jie-Du-Tang. <i>Journal of Ethnopharmacology</i> , 2019, 237, 266-285.	2.0	12
10114	Urinary ionic analysis reveals new relationship between minerals and longevity in a Han Chinese population. <i>Journal of Trace Elements in Medicine and Biology</i> , 2019, 53, 69-75.	1.5	9
10115	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	5.8	32
10116	Network Pharmacology and Bioinformatics Approach Reveals the Therapeutic Mechanism of Action of Baicalein in Hepatocellular Carcinoma. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 1-15.	0.5	37
10117	Integrated transcriptome interactome study of oncogenes and tumor suppressor genes in breast cancer. <i>Genes and Diseases</i> , 2019, 6, 78-87.	1.5	19
10118	Agricultural intensification reduces microbial network complexity and the abundance of keystone taxa in roots. <i>ISME Journal</i> , 2019, 13, 1722-1736.	4.4	716
10119	Deciphering the complex role of thrombospondin-1 in glioblastoma development. <i>Nature Communications</i> , 2019, 10, 1146.	5.8	143
10120	Fitness and microbial networks of the common wasp, <i>Vespula vulgaris</i> (Hymenoptera: Vespidae), in its native and introduced ranges. <i>Ecological Entomology</i> , 2019, 44, 512-523.	1.1	11

#	ARTICLE	IF	CITATIONS
10121	Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome. <i>Frontiers in Genetics</i> , 2019, 10, 59.	1.1	10
10122	Comparative Transcriptome Analysis between Ornamental Apple Species Provides Insights into Mechanism of Double Flowering. <i>Agronomy</i> , 2019, 9, 112.	1.3	3
10123	Insights into the antineoplastic mechanism of <i>Chelidonium majus</i> via systems pharmacology approach. <i>Quantitative Biology</i> , 2019, 7, 42-53.	0.3	1
10124	Introducing THOR, a Model Microbiome for Genetic Dissection of Community Behavior. <i>MBio</i> , 2019, 10, .	1.8	48
10125	Characterization of the cecum microbiome from wild and captive rock ptarmigans indigenous to Arctic Norway. <i>PLoS ONE</i> , 2019, 14, e0213503.	1.1	18
10126	Grape seed proanthocyanidins inhibit proliferation of pancreatic cancer cells by modulating microRNA expression. <i>Oncology Letters</i> , 2019, 17, 2777-2787.	0.8	10
10127	Identification of Novel Interaction Partners of Ets-1: Focus on DNA Repair. <i>Genes</i> , 2019, 10, 206.	1.0	1
10128	Ets1-Mediated Acetylation of FoxO1 Is Critical for Gluconeogenesis Regulation during Feed-Fast Cycles. <i>Cell Reports</i> , 2019, 26, 2998-3010.e5.	2.9	30
10129	Genome-wide analyses reveal genes subject to positive selection in <i>Toxoplasma gondii</i> . <i>Gene</i> , 2019, 699, 73-79.	1.0	1
10130	Network analysis of DUSP12 partners in the nucleus under genotoxic stress. <i>Journal of Proteomics</i> , 2019, 197, 42-52.	1.2	3
10131	Clinical value screening, prognostic significance and key pathway identification of miR-204-5p in endometrial carcinoma: A study based on the Cancer Genome Atlas (TCGA), and bioinformatics analysis. <i>Pathology Research and Practice</i> , 2019, 215, 1003-1011.	1.0	15
10132	A widely distributed diheme enzyme from Burkholderia that displays an atypically stable bis-Fe(IV) state. <i>Nature Communications</i> , 2019, 10, 1101.	5.8	20
10133	Cu Transport by the Extended Family of CcoA-like Transporters (CalT) in Proteobacteria. <i>Scientific Reports</i> , 2019, 9, 1208.	1.6	10
10134	Broad and Protective Influenza B Virus Neuraminidase Antibodies in Humans after Vaccination and their Clonal Persistence as Plasma Cells. <i>MBio</i> , 2019, 10, .	1.8	24
10135	Differential Expression of mRNAs in the Brain Tissues of Patients with Alzheimer's Disease Based on GEO Expression Profile and Its Clinical Significance. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	31
10136	Comprehensive Analysis of Aberrantly Expressed ceRNA network in gastric cancer with and without <i>H.pylori</i> infection. <i>Journal of Cancer</i> , 2019, 10, 853-863.	1.2	33
10137	A network approach to prioritizing susceptibility genes for genome-wide association studies. <i>Genetic Epidemiology</i> , 2019, 43, 477-491.	0.6	7
10138	Distinguishing the optimal binding mechanism of an E3 ubiquitin ligase: Covalent versus noncovalent inhibition. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12859-12869.	1.2	4

#	ARTICLE	IF	CITATIONS
10139	Comprehensive analyses of DNA methylation and gene expression profiles of Kawasaki disease. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13001-13011.	1.2	14
10140	Leveraging Big Data to Transform Drug Discovery. <i>Methods in Molecular Biology</i> , 2019, 1939, 91-118.	0.4	27
10141	How to increase our belief in discovered statistical interactions via large-scale association studies?. <i>Human Genetics</i> , 2019, 138, 293-305.	1.8	12
10142	Microbial community composition and network analyses in arid soils of the Patagonian Monte under grazing disturbance reveal an important response of the community to soil particle size. <i>Applied Soil Ecology</i> , 2019, 138, 223-232.	2.1	44
10143	Gene grouping strategy for network modeling from a small time-series dataset: An illustrative analysis of human organogenesis. <i>BioSystems</i> , 2019, 179, 24-29.	0.9	0
10144	Correlation between volatile profiles and microbial communities: A metabonomic approach to study Jiang-flavor liquor Daqu. <i>Food Research International</i> , 2019, 121, 422-432.	2.9	134
10145	Network analysis and mechanisms of action of Chinese herb-related natural compounds in lung cancer cells. <i>Phytomedicine</i> , 2019, 58, 152893.	2.3	25
10146	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. <i>Nature Communications</i> , 2019, 10, 1092.	5.8	151
10147	Utilisation of Ambient Laser Desorption Ionisation Mass Spectrometry (ALDI-MS) Improves Lipid-Based Microbial Species Level Identification. <i>Scientific Reports</i> , 2019, 9, 3006.	1.6	23
10148	Six novel immunoglobulin genes as biomarkers for better prognosis in triple-negative breast cancer by gene co-expression network analysis. <i>Scientific Reports</i> , 2019, 9, 4484.	1.6	32
10149	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. <i>Scientific Reports</i> , 2019, 9, 4302.	1.6	21
10150	Global Ubiquitome Profiling Revealed the Roles of Ubiquitinated Proteins in Metabolic Pathways of Tea Leaves in Responding to Drought Stress. <i>Scientific Reports</i> , 2019, 9, 4286.	1.6	29
10151	Integrative microRNA-mRNA Analysis of Muscle Tissues in Qianhua Mutton Merino and Small Tail Han Sheep Reveals Key Roles for oar-miR-655-3p and oar-miR-381-5p. <i>DNA and Cell Biology</i> , 2019, 38, 423-435.	0.9	17
10152	Modeling genotypes in their microenvironment to predict single- and multi-cellular behavior. <i>GigaScience</i> , 2019, 8, .	3.3	14
10153	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 2019, 10, 155.	1.1	48
10154	Prognostic and Clinicopathological Significance of SERTAD1 in Various Types of Cancer Risk: A Systematic Review and Retrospective Analysis. <i>Cancers</i> , 2019, 11, 337.	1.7	10
10155	A survey of web resources and tools for the study of TCM network pharmacology. <i>Quantitative Biology</i> , 2019, 7, 17-29.	0.3	21
10156	Comprehensive analysis of the GATA transcription factor gene family in breast carcinoma using gene microarrays, online databases and integrated bioinformatics. <i>Scientific Reports</i> , 2019, 9, 4467.	1.6	16

#	ARTICLE	IF	CITATIONS
10157	Constructing the Microbial Association Network from Large-Scale Time Series Data Using Granger Causality. <i>Genes</i> , 2019, 10, 216.	1.0	10
10158	Differentially expressed genes ASPN, COL1A1, FN1, VCAN and MUC5AC are potential prognostic biomarkers for gastric cancer. <i>Oncology Letters</i> , 2019, 17, 3191-3202.	0.8	54
10159	Inhibition of Microbial Methylation via <i>arsM</i> in the Rhizosphere: Arsenic Speciation in the Soil to Plant Continuum. <i>Environmental Science &amp; Technology</i> , 2019, 53, 3451-3463.	4.6	32
10160	Identification of Key Genes and Pathways in Post-traumatic Stress Disorder Using Microarray Analysis. <i>Frontiers in Psychology</i> , 2019, 10, 302.	1.1	16
10161	Genome-wide Analysis of bZIP Transcription Factors in wheat and Functional Characterization of a TabZIP under Abiotic Stress. <i>Scientific Reports</i> , 2019, 9, 4608.	1.6	96
10162	ANAC017 Coordinates Organellar Functions and Stress Responses by Reprogramming Retrograde Signaling. <i>Plant Physiology</i> , 2019, 180, 634-653.	2.3	72
10163	netDx: interpretable patient classification using integrated patient similarity networks. <i>Molecular Systems Biology</i> , 2019, 15, e8497.	3.2	65
10164	SNP mutation-related genes in breast cancer for monitoring and prognosis of patients: A study based on the TCGA database. <i>Cancer Medicine</i> , 2019, 8, 2303-2312.	1.3	31
10165	Candidate genes involved in metastasis of colon cancer identified by integrated analysis. <i>Cancer Medicine</i> , 2019, 8, 2338-2347.	1.3	24
10166	Whole blood transcriptome analysis reveals footprints of cattle adaptation to subarctic conditions. <i>Animal Genetics</i> , 2019, 50, 217-227.	0.6	9
10167	Identifying Hub Genes for Heat Tolerance in Water Buffalo ( <i>Bubalus bubalis</i> ) Using Transcriptome Data. <i>Frontiers in Genetics</i> , 2019, 10, 209.	1.1	26
10168	Identification of lncRNAs associated with early-stage breast cancer and their prognostic implications. <i>Molecular Oncology</i> , 2019, 13, 1342-1355.	2.1	43
10169	Proteome profiling of carbapenem-resistant <i>K. pneumoniae</i> clinical isolate (NDM-4): Exploring the mechanism of resistance and potential drug targets. <i>Journal of Proteomics</i> , 2019, 200, 102-110.	1.2	23
10170	Radical-mediated C-S bond cleavage in C2 sulfonate degradation by anaerobic bacteria. <i>Nature Communications</i> , 2019, 10, 1609.	5.8	46
10171	Transcriptome networks identify mechanisms of viral and nonviral asthma exacerbations in children. <i>Nature Immunology</i> , 2019, 20, 637-651.	7.0	106
10172	Orphan genes are involved in drought adaptations and ecoclimatic-oriented selections in domesticated cowpea. <i>Journal of Experimental Botany</i> , 2019, 70, 3101-3110.	2.4	15
10173	Genome-wide identification and analyses of bHLH family genes in <i>Brassica napus</i> . <i>Canadian Journal of Plant Science</i> , 2019, 99, 589-598.	0.3	8
10174	Temperature-induced embryonic diapause in blue-breasted quail ( <i>Coturnix chinensis</i> ) correlates with decreased mitochondrial-respiratory network and increased stress-response network. <i>Poultry Science</i> , 2019, 98, 2977-2988.	1.5	11



#	ARTICLE	IF	CITATIONS
10175	Xenbase: Facilitating the Use of <i>Xenopus</i> to Model Human Disease. <i>Frontiers in Physiology</i> , 2019, 10, 154.	1.3	61
10176	Downregulation of long noncoding RNA LINC00683 associated with unfavorable prognosis in prostate cancer based on TCGA. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 14165-14174.	1.2	11
10177	Competing endogenous RNA network and prognostic nomograms for hepatocellular carcinoma patients who underwent R0 resection. <i>Journal of Cellular Physiology</i> , 2019, 234, 20342-20353.	2.0	8
10178	Information Loss in Network Pharmacology. <i>Molecular Informatics</i> , 2019, 38, 1900032.	1.4	6
10179	Downregulation of CENPF Remodels Prostate Cancer Cells and Alters Cellular Metabolism. <i>Proteomics</i> , 2019, 19, 1900038.	1.3	22
10180	Genome-wide identification of BOR genes in poplar and their roles in response to various environmental stimuli. <i>Environmental and Experimental Botany</i> , 2019, 164, 101-113.	2.0	16
10181	Characterization of circular RNA expression profiles in cumulus cells from patients with polycystic ovary syndrome. <i>Fertility and Sterility</i> , 2019, 111, 1243-1251.e1.	0.5	38
10182	Promoting waste activated sludge reduction by linear alkylbenzene sulfonates: Surfactant dose control extracellular polymeric substances solubilization and microbial community succession. <i>Journal of Hazardous Materials</i> , 2019, 374, 74-82.	6.5	30
10183	The significance of methionine cycle enzymes in plant virus infections. <i>Current Opinion in Plant Biology</i> , 2019, 50, 67-75.	3.5	34
10184	Comparative Transcriptomics Reveal Key Sheep ( <i>Ovis aries</i> ) Hypothalamus LncRNAs that Affect Reproduction. <i>Animals</i> , 2019, 9, 152.	1.0	24
10185	Integrative Analysis Reveals Subtype-Specific Regulatory Determinants in Triple Negative Breast Cancer. <i>Cancers</i> , 2019, 11, 507.	1.7	10
10186	Combing the Hairball: Improving Visualization of miRNA-Target Interaction Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 279-289.	0.4	0
10187	Isotopic Labeling and Quantitative Proteomics of Acetylation on Histones and Beyond. <i>Methods in Molecular Biology</i> , 2019, 1977, 43-70.	0.4	12
10188	Huangqi Fuzheng decoction exerts antitumor activity by inhibiting cell growth and inducing cell death in osteosarcoma. <i>Biomedicine and Pharmacotherapy</i> , 2019, 114, 108854.	2.5	2
10189	GCR1 and GPA1 coupling regulates nitrate, cell wall, immunity and light responses in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2019, 9, 5838.	1.6	23
10190	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. <i>Scientific Reports</i> , 2019, 9, 5953.	1.6	55
10191	Buffalo milk transcriptome: A comparative analysis of early, mid and late lactation. <i>Scientific Reports</i> , 2019, 9, 5993.	1.6	28
10192	A joint molecular networking study of a <i>Smenospongia</i> sponge and a cyanobacterial bloom revealed new antiproliferative chlorinated polyketides. <i>Organic Chemistry Frontiers</i> , 2019, 6, 1762-1774.	2.3	26



#	ARTICLE	IF	CITATIONS
10193	The auxin response factor gene family in allopolyploid <i>Brassica napus</i> . <i>PLoS ONE</i> , 2019, 14, e0214885.	1.1	27
10194	Actinobacteria Isolated From <i>Laminaria ochroleuca</i> : A Source of New Bioactive Compounds. <i>Frontiers in Microbiology</i> , 2019, 10, 683.	1.5	54
10195	Exploring the microbiota and metabolites of traditional rice beer varieties of Assam and their functionalities. <i>3 Biotech</i> , 2019, 9, 174.	1.1	19
10196	NMR metabolomics for evaluating passage number and harvesting effects on mammalian cell metabolome. <i>Analytical Biochemistry</i> , 2019, 576, 20-32.	1.1	9
10197	Identifying gene modules of thyroid cancer associated with pathological stage by weighted gene co-expression network analysis. <i>Gene</i> , 2019, 704, 142-148.	1.0	16
10198	HDAC5 catalytic activity suppresses cardiomyocyte oxidative stress and NRF2 target gene expression. <i>Journal of Biological Chemistry</i> , 2019, 294, 8640-8652.	1.6	27
10199	Explorative analysis of the gene expression profile during liver regeneration of mouse: a microarray-based study. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2019, 47, 1113-1121.	1.9	4
10200	Genotype-phenotype relations of the von Hippel-Lindau tumor suppressor inferred from a large-scale analysis of disease mutations and interactors. <i>PLoS Computational Biology</i> , 2019, 15, e1006478.	1.5	24
10201	Comparative analysis of homologous aminopeptidase PepN from pathogenic and non-pathogenic mycobacteria reveals divergent traits. <i>PLoS ONE</i> , 2019, 14, e0215123.	1.1	5
10202	Systems Biology Reveals NR2F6 and TGFB1 as Key Regulators of Feed Efficiency in Beef Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 230.	1.1	41
10203	Prolonged Bat Call Exposure Induces a Broad Transcriptional Response in the Male Fall Armyworm ( <i>Spodoptera frugiperda</i> ; Lepidoptera: Noctuidae) Brain. <i>Frontiers in Behavioral Neuroscience</i> , 2019, 13, 36.	1.0	15
10204	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. <i>Diagnostics</i> , 2019, 9, 39.	1.3	3
10205	Genome-Wide Identification and Characterization of the PERK Gene Family in <i>Gossypium hirsutum</i> Reveals Gene Duplication and Functional Divergence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1750.	1.8	41
10206	Identification of Important Invasion-Related Genes in Non-functional Pituitary Adenomas. <i>Journal of Molecular Neuroscience</i> , 2019, 68, 565-589.	1.1	8
10207	Integrated analysis of gene expression changes associated with coronary artery disease. <i>Lipids in Health and Disease</i> , 2019, 18, 92.	1.2	12
10208	Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. <i>Microbiome</i> , 2019, 7, 57.	4.9	146
10209	Identification of key pathways and genes in nasopharyngeal carcinoma using bioinformatics analysis. <i>Oncology Letters</i> , 2019, 17, 4683-4694.	0.8	9
10210	Multitranscriptome analyses reveal prioritized genes specifically associated with liver fibrosis progression independent of etiology. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, G744-G754.	1.6	20

#	ARTICLE	IF	CITATIONS
10211	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. <i>Blood</i> , 2019, 133, 2651-2663.	0.6	15
10212	The genome of the giant Nomura's jellyfish sheds light on the early evolution of active predation. <i>BMC Biology</i> , 2019, 17, 28.	1.7	38
10213	Exome sequencing and bioinformatic approaches reveals rare sequence variants involved in cell signalling and elastic fibre homeostasis: new evidence in the development of ectopic calcification. <i>Cellular Signalling</i> , 2019, 59, 131-140.	1.7	15
10214	ITLN1 identified by comprehensive bioinformatic analysis as a hub candidate biological target in human epithelial ovarian cancer. <i>Cancer Management and Research</i> , 2019, Volume 11, 2379-2392.	0.9	8
10215	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	1.1	27
10216	Effect of disease-associated SLC9A9 mutations on protein-protein interaction networks: implications for molecular mechanisms for ADHD and autism. <i>ADHD Attention Deficit and Hyperactivity Disorders</i> , 2019, 11, 91-105.	1.7	12
10217	Metabolic Reprogramming in Astrocytes Distinguishes Region-Specific Neuronal Susceptibility in Huntington Mice. <i>Cell Metabolism</i> , 2019, 29, 1258-1273.e11.	7.2	97
10218	IL13 Is Essential for Survival and Early Cerebellar Programming in a Critical Neonatal Window. <i>Neuron</i> , 2019, 102, 770-785.e7.	3.8	25
10219	Liver proteomics unravel the metabolic pathways related to Feed Efficiency in beef cattle. <i>Scientific Reports</i> , 2019, 9, 5364.	1.6	43
10220	The prognostic signature of the somatic mutations in Ewing sarcoma: from a network view. <i>Japanese Journal of Clinical Oncology</i> , 2019, 49, 604-613.	0.6	2
10221	New Insight on Solute Carrier Family 27 Member 6 (SLC27A6) in Tumoral and Non-Tumoral Breast Cells. <i>International Journal of Medical Sciences</i> , 2019, 16, 366-375.	1.1	18
10222	Multivariate analyses of root phenotype and dynamic transcriptome underscore valuable root traits and water-deficit responsive gene networks in maize. <i>Plant Direct</i> , 2019, 3, e00130.	0.8	8
10223	A Network Module for the Perseus Software for Computational Proteomics Facilitates Proteome Interaction Graph Analysis. <i>Journal of Proteome Research</i> , 2019, 18, 2052-2064.	1.8	60
10224	Dynamic changes to lipid mediators support transitions among macrophage subtypes during muscle regeneration. <i>Nature Immunology</i> , 2019, 20, 626-636.	7.0	108
10225	Time-Resolved Systems Medicine Reveals Viral Infection-Modulating Host Targets. <i>Systems Medicine (New Rochelle, N Y)</i> , 2019, 2, 1-9.	1.4	14
10226	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	3.1	57
10227	Long-term manure application increases soil organic matter and aggregation, and alters microbial community structure and keystone taxa. <i>Soil Biology and Biochemistry</i> , 2019, 134, 187-196.	4.2	302
10228	Transcription factors involved in the regulatory networks governing the Calvin-Benson-Bassham cycle. <i>Tree Physiology</i> , 2019, 39, 1159-1172.	1.4	3

#	ARTICLE	IF	CITATIONS
10229	Proteomics profiling of arginine methylation defines PRMT5 substrate specificity. <i>Science Signaling</i> , 2019, 12, .	1.6	114
10230	miR-431-5p Knockdown Protects Against Angiotensin II-Induced Hypertension and Vascular Injury. <i>Hypertension</i> , 2019, 73, 1007-1017.	1.3	21
10231	Implicating Dysbiosis of the Gut Fungal Microbiome in Uveitis, an Inflammatory Disease of the Eye. , 2019, 60, 1384.		32
10232	Biological Networks: Tools, Methods, and Analysis. , 2019, , 255-286.		1
10233	In silico identification of key genes and signaling pathways targeted by a panel of signature microRNAs in prostate cancer. <i>Medical Oncology</i> , 2019, 36, 43.	1.2	6
10234	Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. <i>Nature Communications</i> , 2019, 10, 1523.	5.8	7,886
10235	The mechanical effects of CRT promoting autophagy via mitochondrial calcium uniporter down-regulation and mitochondrial dynamics alteration. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 3833-3842.	1.6	10
10236	The Megalocytivirus RBIV Induces Apoptosis and MHC Class I Presentation in Rock Bream ( <i>Oplegnathus</i> ) Tj ETQq1 1,0.784314,rgBT /Qv 2.2 17	2.2	17
10237	Integrating Molecular Network and Culture Media Variation to Explore the Production of Bioactive Metabolites by <i>Vibrio diabolicus</i> AISM3. <i>Marine Drugs</i> , 2019, 17, 196.	2.2	3
10238	Disease association of human tumor suppressor genes. <i>Molecular Genetics and Genomics</i> , 2019, 294, 931-940.	1.0	5
10239	Transcriptomics of the grape berry shrivel ripening disorder. <i>Plant Molecular Biology</i> , 2019, 100, 285-301.	2.0	19
10240	Transcriptomic Diversification of Granulosa Cells during Follicular Development in Chicken. <i>Scientific Reports</i> , 2019, 9, 5462.	1.6	34
10241	Analysis of polymorphisms in genes associated with the FA/BRCA pathway in three patients with multiple primary malignant neoplasms. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2019, 47, 1101-1112.	1.9	9
10242	Dynamic interaction network inference from longitudinal microbiome data. <i>Microbiome</i> , 2019, 7, 54.	4.9	59
10243	Identification of the Biomarkers and Pathological Process of Osteoarthritis: Weighted Gene Co-expression Network Analysis. <i>Frontiers in Physiology</i> , 2019, 10, 275.	1.3	38
10244	Data Mining and Validation of AMPK Pathway as a Novel Candidate Role Affecting Intramuscular Fat Content in Pigs. <i>Animals</i> , 2019, 9, 137.	1.0	12
10245	Identification of lncRNA-miRNA-mRNA regulatory network associated with epithelial ovarian cancer cisplatin-resistant. <i>Journal of Cellular Physiology</i> , 2019, 234, 19886-19894.	2.0	44
10246	G Protein $\beta$ subunit 7 loss contributes to progression of clear cell renal cell carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 20002-20012.	2.0	25

#	ARTICLE	IF	CITATIONS
10247	A lymph node metastasis-related protein-coding genes combining with long noncoding RNA signature for breast cancer survival prediction. <i>Journal of Cellular Physiology</i> , 2019, 234, 20036-20045.	2.0	14
10248	Network Walking charts transcriptional dynamics of nitrogen signaling by integrating validated and predicted genome-wide interactions. <i>Nature Communications</i> , 2019, 10, 1569.	5.8	92
10249	The Impact of Chronic Heat Stress on the Growth, Survival, Feeding, and Differential Gene Expression in the Sea Urchin <i>Strongylocentrotus intermedius</i> . <i>Frontiers in Genetics</i> , 2019, 10, 301.	1.1	28
10250	IFITM3 knockdown reduces the expression of CCND1 and CDK4 and suppresses the growth of oral squamous cell carcinoma cells. <i>Cellular Oncology (Dordrecht)</i> , 2019, 42, 477-490.	2.1	23
10251	The potential application of genome editing by using CRISPR/Cas9, and its engineered and ortholog variants for studying the transcription factors involved in the maintenance of phosphate homeostasis in model plants. <i>Seminars in Cell and Developmental Biology</i> , 2019, 96, 77-90.	2.3	14
10252	Dynamics of genome reorganization during human cardiogenesis reveal an RBM20-dependent splicing factory. <i>Nature Communications</i> , 2019, 10, 1538.	5.8	104
10253	Long non-coding RNAs play regulatory roles in acetaminophen-induced liver injury. <i>Journal of Digestive Diseases</i> , 2019, 20, 308-317.	0.7	3
10254	Transcriptome landscape of the early <i>Brassica napus</i> seed. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 639-650.	4.1	33
10255	Comprehensive analysis of miRNA profiles reveals the role of <i>Schistosoma japonicum</i> miRNAs at different developmental stages. <i>Veterinary Research</i> , 2019, 50, 23.	1.1	11
10256	Antiproliferative Effects of the Natural Oxadiazine Nocuolin A Are Associated With Impairment of Mitochondrial Oxidative Phosphorylation. <i>Frontiers in Oncology</i> , 2019, 9, 224.	1.3	13
10257	Candidate genes and potential mechanisms for chemoradiotherapy sensitivity in locally advanced rectal cancer. <i>Oncology Letters</i> , 2019, 17, 4494-4504.	0.8	3
10258	Weighted gene coexpression network analysis identifies specific transcriptional modules and hub genes related to intramuscular fat traits in chicken breast muscle. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13625-13639.	1.2	11
10259	Differential gene regulatory pathways and co-expression networks associated with fire blight infection in apple ( <i>Malus domestica</i> ). <i>Horticulture Research</i> , 2019, 6, 35.	2.9	20
10260	MYRF haploinsufficiency causes 46,XY and 46,XX disorders of sex development: bioinformatics consideration. <i>Human Molecular Genetics</i> , 2019, 28, 2319-2329.	1.4	25
10261	Prognostic risk model construction and molecular marker identification in glioblastoma multiforme based on mRNA/microRNA/long non-coding RNA analysis using random survival forest method. <i>Neoplasma</i> , 2019, 66, 459-469.	0.7	11
10262	Reticulate evolution in eukaryotes: Origin and evolution of the nitrate assimilation pathway. <i>PLoS Genetics</i> , 2019, 15, e1007986.	1.5	21
10263	Ligand fishing with cellular membrane-coated cellulose filter paper: a new method for screening of potential active compounds from natural products. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 1989-2000.	1.9	12
10264	Comprehensive analysis of dysregulated lncRNAs, miRNAs and mRNAs with associated ceRNA network in esophageal squamous cell carcinoma. <i>Gene</i> , 2019, 696, 206-218.	1.0	29

#	ARTICLE	IF	CITATIONS
10265	Differential effects, on oncogenic pathway signalling, by derivatives of the HNF4 $\beta$ inhibitor BI6015. <i>British Journal of Cancer</i> , 2019, 120, 488-498.	2.9	12
10266	Identification of Potential Key Genes and Pathways in Early-Onset Colorectal Cancer Through Bioinformatics Analysis. <i>Cancer Control</i> , 2019, 26, 107327481983126.	0.7	46
10267	MicroRNAs in Female Malignancies. <i>Cancer Informatics</i> , 2019, 18, 117693511982874.	0.9	11
10268	Combined analysis of dissimilar promoter accessibility and gene expression profiles identifies tissue-specific genes and actively repressed networks. <i>Epigenetics and Chromatin</i> , 2019, 12, 16.	1.8	61
10269	BioNetApp: An interactive visual data analysis platform for molecular expressions. <i>PLoS ONE</i> , 2019, 14, e0211277.	1.1	4
10270	Identification and Expression Analysis of Long Noncoding RNAs in Fat-Tail of Sheep Breeds. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1263-1276.	0.8	47
10271	Comparative Genomic Analyses Reveal Core-Genome-Wide Genes Under Positive Selection and Major Regulatory Hubs in Outlier Strains of <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 53.	1.5	36
10272	Variation in Membrane Trafficking Linked to SNARE AtSYP51 Interaction With Aquaporin NIP1;1. <i>Frontiers in Plant Science</i> , 2018, 9, 1949.	1.7	36
10273	Neuroprotective effect of grape seed extract on brain ischemia: a proteomic approach. <i>Metabolic Brain Disease</i> , 2019, 34, 889-907.	1.4	7
10274	Comprehensive analysis of differentially expressed profiles of long non-coding RNAs and messenger RNAs in kaolin-induced hydrocephalus. <i>Gene</i> , 2019, 697, 184-193.	1.0	8
10275	A transcriptomic (RNA-seq) analysis of genes responsive to both cadmium and arsenic stress in rice root. <i>Science of the Total Environment</i> , 2019, 666, 445-460.	3.9	67
10276	Circular RNAs are temporospatially regulated throughout development and ageing in the rat. <i>Scientific Reports</i> , 2019, 9, 2564.	1.6	74
10277	Discovery and structural analysis of a phloretin hydrolase from the opportunistic human pathogen <i>Mycobacterium abscessus</i> . <i>FEBS Journal</i> , 2019, 286, 1959-1971.	2.2	7
10278	Comparative Metagenomics and Network Analyses Provide Novel Insights Into the Scope and Distribution of $\beta$ -Lactamase Homologs in the Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 146.	1.5	18
10279	Global In-Silico Scenario of tRNA Genes and Their Organization in Virus Genomes. <i>Viruses</i> , 2019, 11, 180.	1.5	36
10280	Long-term application of nitrogen, not phosphate or potassium, significantly alters the diazotrophic community compositions and structures in a Mollisol in northeast China. <i>Research in Microbiology</i> , 2019, 170, 147-155.	1.0	26
10281	An Advanced Strategy for Comprehensive Profiling of ADP-ribosylation Sites Using Mass Spectrometry-based Proteomics*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1010a-1026.	2.5	113
10282	Reannotation of the Ribonucleotide Reductase in a Cyanophage Reveals Life History Strategies Within the Virioplankton. <i>Frontiers in Microbiology</i> , 2019, 10, 134.	1.5	19

#	ARTICLE	IF	CITATIONS
10283	Expression profiling and regulatory network of cucumber microRNAs and their putative target genes in response to cucumber green mottle mosaic virus infection. <i>Archives of Virology</i> , 2019, 164, 1121-1134.	0.9	20
10284	Aberrantly DNA Methylated-Differentially Expressed Genes and Pathways in Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2019, 10, 355-366.	1.2	50
10285	Long noncoding RNAs predict the survival of patients with colorectal cancer as revealed by constructing an endogenous RNA network using bioinformation analysis. <i>Cancer Medicine</i> , 2019, 8, 863-873.	1.3	29
10286	Effects of CPAP on the transcriptional signatures in patients with obstructive sleep apnea via coexpression network analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9277-9290.	1.2	6
10287	Impacts of Arsenic and Antimony Co-Contamination on Sedimentary Microbial Communities in Rivers with Different Pollution Gradients. <i>Microbial Ecology</i> , 2019, 78, 589-602.	1.4	45
10288	Comparison between dopaminergic and non-dopaminergic neurons in the VTA following chronic nicotine exposure during pregnancy. <i>Scientific Reports</i> , 2019, 9, 445.	1.6	9
10289	The Placental Transcriptome in Late Gestational Hypoxia Resulting in Murine Intrauterine Growth Restriction Parallels Increased Risk of Adult Cardiometabolic Disease. <i>Scientific Reports</i> , 2019, 9, 1243.	1.6	13
10290	Genome-Wide Characterization of Arabian Peninsula Populations: Shedding Light on the History of a Fundamental Bridge between Continents. <i>Molecular Biology and Evolution</i> , 2019, 36, 575-586.	3.5	45
10291	Ulcerative colitis: functional analysis of the in-depth proteome. <i>Clinical Proteomics</i> , 2019, 16, 4.	1.1	25
10292	Comparative transcriptome analysis of mammary epithelial cells at different stages of lactation reveals wide differences in gene expression and pathways regulating milk synthesis between Jersey and Kashmiri cattle. <i>PLoS ONE</i> , 2019, 14, e0211773.	1.1	39
10293	Disentangling the Effects of Monounsaturated Fatty Acids from Other Components of a Mediterranean Diet on Serum Metabolite Profiles: A Randomized Fully Controlled Dietary Intervention in Healthy Subjects at Risk of the Metabolic Syndrome. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1801095.	1.5	34
10294	Comparative transcriptome analysis reveals new molecular pathways for cucumber genes related to sex determination. <i>Plant Reproduction</i> , 2019, 32, 193-216.	1.3	25
10295	Inferring pathogen-host interactions between <i>Leptospira interrogans</i> and <i>Homo sapiens</i> using network theory. <i>Scientific Reports</i> , 2019, 9, 1434.	1.6	20
10296	A Systems Pharmacology Approach for Identifying the Multiple Mechanisms of Action of the Wei Pi Xiao Decoction for the Treatment of Gastric Precancerous Lesions. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-15.	0.5	32
10297	Discovery of novel glycerolated quinazolinones from <i>Streptomyces</i> sp. MBT27. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 483-492.	1.4	22
10298	Design, execution, and analysis of CRISPR-Cas9-based deletions and genetic interaction networks in the fungal pathogen <i>Candida albicans</i> . <i>Nature Protocols</i> , 2019, 14, 955-975.	5.5	25
10299	Transcriptomic analysis of cultivated cotton <i>Gossypium hirsutum</i> provides insights into host responses upon whitefly-mediated transmission of cotton leaf curl disease. <i>PLoS ONE</i> , 2019, 14, e0210011.	1.1	28
10300	Metabolic Alterations in Male-Sterile Potato as Compared to Male-Fertile. <i>Metabolites</i> , 2019, 9, 24.	1.3	14



#	ARTICLE	IF	CITATIONS
10301	Transcriptomic profiles of muscle, heart, and spleen in reaction to circadian heat stress in Ethiopian highland and lowland male chicken. <i>Cell Stress and Chaperones</i> , 2019, 24, 175-194.	1.2	11
10302	Response of soil bacterial community to bioaugmentation with a plant residue-immobilized bacterial consortium for crude oil removal. <i>Chemosphere</i> , 2019, 222, 831-838.	4.2	73
10303	Transcriptional profiling and localization of GUL-1, a COT-1 pathway component, in <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2019, 126, 1-11.	0.9	11
10304	Transcriptomic and metabolomic analysis of ZmYUC1 mutant reveals the role of auxin during early endosperm formation in maize. <i>Plant Science</i> , 2019, 281, 133-145.	1.7	36
10305	Identification of molecular biomarkers for ovarian cancer using computational approaches. <i>Carcinogenesis</i> , 2019, 40, 742-748.	1.3	10
10306	Impact of in vitro driven expression signatures of CD133 stem cell marker and tumor stroma on clinical outcomes in gastric cancers. <i>BMC Cancer</i> , 2019, 19, 119.	1.1	7
10307	Molecular Dynamics Simulations of A27S and K120A Mutated PTP1B Reveals Selective Binding of the Bidentate Inhibitor. <i>BioMed Research International</i> , 2019, 2019, 1-11.	0.9	1
10308	Effects of protease and phytase supplements on small intestinal microbiota and amino acid digestibility in broiler chickens. <i>Poultry Science</i> , 2019, 98, 2906-2918.	1.5	42
10309	Defining Key Genes Regulating Morphogenesis of Apocrine Sweat Gland in Sheepskin. <i>Frontiers in Genetics</i> , 2018, 9, 739.	1.1	15
10310	Identification of Gene Expression Changes Associated With Uterine Receptivity in Mice. <i>Frontiers in Physiology</i> , 2019, 10, 125.	1.3	17
10311	Solvolysis Artifacts: Leucettazoles as Cryptic Macrocyclic Alkaloid Dimers from a Southern Australian Marine Sponge, <i>Leucetta</i> sp.. <i>Marine Drugs</i> , 2019, 17, 106.	2.2	2
10312	Identification of critical genes associated with spinal cord injury based on the gene expression profile of spinal cord tissues from <i>trkB.T1</i> knockout mice. <i>Molecular Medicine Reports</i> , 2019, 19, 2013-2020.	1.1	3
10313	Functional Characterization of the <i>ycjQRS</i> Gene Cluster from <i>Escherichia coli</i> : A Novel Pathway for the Transformation of <i>d</i> -Gulosides to <i>d</i> -Glucosides. <i>Biochemistry</i> , 2019, 58, 1388-1399.	1.2	4
10314	Serotonin Transporter Deficiency is Associated with Dysbiosis and Changes in Metabolic Function of the Mouse Intestinal Microbiome. <i>Scientific Reports</i> , 2019, 9, 2138.	1.6	46
10315	Proteomics and Visual Health Research: Proteome of the Human Sclera Using High-Resolution Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 98-110.	1.0	8
10316	World Influence of Infectious Diseases From Wikipedia Network Analysis. <i>IEEE Access</i> , 2019, 7, 26073-26087.	2.6	16
10317	Mechanisms of in utero cortisol effects on the newborn heart revealed by transcriptomic modeling. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2019, 316, R323-R337.	0.9	11
10318	Genome-wide analysis of DNA methylation in relation to socioeconomic status during development and early adulthood. <i>American Journal of Physical Anthropology</i> , 2019, 169, 3-11.	2.1	90



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10319	Ontogeny of symbiont community structure in two carotenoid-rich, viviparous marine sponges: comparison of microbiomes and analysis of culturable pigmented heterotrophic bacteria. <i>Environmental Microbiology Reports</i> , 2019, 11, 249-261.	1.0	27
10320	Genetic and Environmental Determinants of Immune Response to Cutaneous Melanoma. <i>Cancer Research</i> , 2019, 79, 2684-2696.	0.4	45
10321	Genome-Wide Identification and Characterization of SQUAMOSA Promoter-Binding Protein (SBP) Genes Involved in the Flowering Development of Citrus Clementina. <i>Biomolecules</i> , 2019, 9, 66.	1.8	20
10322	Identification of key genes and signaling pathways during Sendai virus infection in vitro. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 13-22.	0.8	1
10323	In silico identification of copper-binding proteins of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> for their probable role in plant-pathogen interactions. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 187-195.	1.3	14
10324	Identification of the molecular relationship between intravenous leiomyomatosis and uterine myoma using RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 1442.	1.6	13
10325	Co-Expression Network Analysis and Hub Gene Selection for High-Quality Fiber in Upland Cotton ( <i>Gossypium hirsutum</i> ) Using RNA Sequencing Analysis. <i>Genes</i> , 2019, 10, 119.	1.0	29
10326	Integrated bioinformatics analysis of key genes involved in progress of colon cancer. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e00588.	0.6	33
10327	An autophagy-related long non-coding RNA signature for glioma. <i>FEBS Open Bio</i> , 2019, 9, 653-667.	1.0	82
10328	Bacterial community structure of two Mediterranean agricultural soils amended with spent coffee grounds. <i>Applied Soil Ecology</i> , 2019, 137, 12-20.	2.1	13
10329	Immune Cell Types and Secreted Factors Contributing to Inflammation-to-Cancer Transition and Immune Therapy Response. <i>Cell Reports</i> , 2019, 26, 1965-1977.e4.	2.9	28
10330	Analysis of organizational power networks through a holistic approach using consensus strategies. <i>Heliyon</i> , 2019, 5, e01172.	1.4	8
10331	Genome-wide analysis of LXXLL-mediated DAX1/SHP nuclear receptor interaction network and rational design of stapled LXXLL-based peptides to target the specific network profile. <i>International Journal of Biological Macromolecules</i> , 2019, 129, 13-22.	3.6	13
10332	Linking gene expression and oenological traits: Comparison between <i>Torulaspora delbrueckii</i> and <i>Saccharomyces cerevisiae</i> strains. <i>International Journal of Food Microbiology</i> , 2019, 294, 42-49.	2.1	27
10333	Quantitative proteomic analysis of deer antler stem cells as a model of mammalian organ regeneration. <i>Journal of Proteomics</i> , 2019, 195, 98-113.	1.2	12
10334	Selecting a Single Stereocenter: The Molecular Nuances That Differentiate Î²-Hexuronidases in the Human Gut Microbiome. <i>Biochemistry</i> , 2019, 58, 1311-1317.	1.2	12
10335	Targeting SYK signaling in myeloid cells protects against liver fibrosis and hepatocarcinogenesis. <i>Oncogene</i> , 2019, 38, 4512-4526.	2.6	27
10336	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	9.4	201

#	ARTICLE	IF	CITATIONS
10337	Genotoxicity of zinc oxide nanoparticles: an <i>in vivo</i> and <i>in silico</i> study. <i>Toxicology Research</i> , 2019, 8, 277-286.	0.9	18
10338	Quantitative phosphoproteomics reveals mitotic function of the ATR activator ETAA1. <i>Journal of Cell Biology</i> , 2019, 218, 1235-1249.	2.3	45
10339	Upregulation of DNA Metabolism-Related Genes Contributes to Radioresistance of Glioblastoma. <i>Human Gene Therapy Clinical Development</i> , 2019, 30, 74-87.	3.2	7
10340	Organellar carbon metabolism is coordinated with distinct developmental phases of secondary xylem. <i>New Phytologist</i> , 2019, 222, 1832-1845.	3.5	11
10341	Analyzing a co-occurrence gene-interaction network to identify disease-gene association. <i>BMC Bioinformatics</i> , 2019, 20, 70.	1.2	27
10342	Transforming Growth Factor Beta has Dual Effects on MMP9 and uPA Expression in HTR-8/SVneo Human Trophoblastic Cell Line. <i>Acta Biologica Colombiana</i> , 2019, 24, 26-37.	0.1	1
10343	Inflation vs. Exhaustion of Antiviral CD8+ T-Cell Populations in Persistent Infections: Two Sides of the Same Coin?. <i>Frontiers in Immunology</i> , 2019, 10, 197.	2.2	18
10344	Tracing the Pathways of Waters and Protons in Photosystem II and Cytochrome c Oxidase. <i>Inorganics</i> , 2019, 7, 14.	1.2	15
10345	Blubber transcriptome responses to repeated ACTH administration in a marine mammal. <i>Scientific Reports</i> , 2019, 9, 2718.	1.6	17
10346	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. <i>Communications Biology</i> , 2019, 2, 77.	2.0	50
10347	Analysis of key candidate genes and pathways of endometriosis pathophysiology by a genomics-bioinformatics approach. <i>Gynecological Endocrinology</i> , 2019, 35, 576-581.	0.7	9
10348	BRN2 suppresses apoptosis, reprograms DNA damage repair, and is associated with a high somatic mutation burden in melanoma. <i>Genes and Development</i> , 2019, 33, 310-332.	2.7	35
10349	Post-transcriptional adaptation of the aquatic plant <i>Spirodela polyrhiza</i> under stress and hormonal stimuli. <i>Plant Journal</i> , 2019, 98, 1120-1133.	2.8	13
10350	Genus-Wide Comparative Genomics Analysis of <i>Neisseria</i> to Identify New Genes Associated with Pathogenicity and Niche Adaptation of <i>Neisseria</i> Pathogens. <i>International Journal of Genomics</i> , 2019, 2019, 1-19.	0.8	17
10351	Identification of RNA Expression Profiles in Thyroid Cancer to Construct a Competing Endogenous RNA (ceRNA) Network of mRNAs, Long Noncoding RNAs (lncRNAs), and microRNAs (miRNAs). <i>Medical Science Monitor</i> , 2019, 25, 1140-1154.	0.5	31
10352	Cognition-Enhancing Vagus Nerve Stimulation Alters the Epigenetic Landscape. <i>Journal of Neuroscience</i> , 2019, 39, 2407-18.	1.7	27
10353	RNA-Seq Revealed Expression of Many Novel Genes Associated With <i>Leishmania donovani</i> Persistence and Clearance in the Host Macrophage. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 17.	1.8	28
10354	The Long Non-coding RNA NRIR Drives IFN-Response in Monocytes: Implication for Systemic Sclerosis. <i>Frontiers in Immunology</i> , 2019, 10, 100.	2.2	58

#	ARTICLE	IF	CITATIONS
10355	Altered Gene Regulatory Networks Are Associated With the Transition From C3 to Crassulacean Acid Metabolism in <i>Erycina</i> (Oncidiinae: Orchidaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 2000.	1.7	30
10356	A New Microbial Pathway for Organophosphonate Degradation Catalyzed by Two Previously Misannotated Non-Heme-Iron Oxygenases. <i>Biochemistry</i> , 2019, 58, 1627-1647.	1.2	28
10357	Proteomics Reveals Profound Metabolic Changes in the Alcohol Use Disorder Brain. <i>ACS Chemical Neuroscience</i> , 2019, 10, 2364-2373.	1.7	26
10358	An integrative systems genetic analysis of mammalian lipid metabolism. <i>Nature</i> , 2019, 567, 187-193.	13.7	101
10359	Identification of long non-coding RNA HERC2P2 as a tumor suppressor in glioma. <i>Carcinogenesis</i> , 2019, 40, 956-964.	1.3	13
10360	Development of novel predictive miRNA/target gene pathways for colorectal cancer distance metastasis to the liver using a bioinformatic approach. <i>PLoS ONE</i> , 2019, 14, e0211968.	1.1	19
10361	Characterization of lncRNA-miRNA-mRNA Network to Reveal Potential Functional ceRNAs in Bovine Skeletal Muscle. <i>Frontiers in Genetics</i> , 2019, 10, 91.	1.1	39
10362	PRMT5 Modulates Splicing for Genome Integrity and Preserves Proteostasis of Hematopoietic Stem Cells. <i>Cell Reports</i> , 2019, 26, 2316-2328.e6.	2.9	75
10363	Chronic copper treatment prevents the liver critical balance transcription response induced by acetaminophen. <i>Journal of Trace Elements in Medicine and Biology</i> , 2019, 53, 113-119.	1.5	4
10364	The tea leaf microbiome shows specific responses to chemical pesticides and biocontrol applications. <i>Science of the Total Environment</i> , 2019, 667, 33-40.	3.9	47
10365	Circular RNA biogenesis is decreased in postmortem cortical gray matter in schizophrenia and may alter the bioavailability of associated miRNA. <i>Neuropsychopharmacology</i> , 2019, 44, 1043-1054.	2.8	55
10366	Structural insight into the serotonin (5-HT) receptor family by molecular docking, molecular dynamics simulation and systems pharmacology analysis. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 1138-1156.	2.8	30
10367	Transcriptomic and genomic structural variation analyses on grape cultivars reveal new insights into the genotype-dependent responses to water stress. <i>Scientific Reports</i> , 2019, 9, 2809.	1.6	17
10368	The susceptibility of sea-island cotton recombinant inbred lines to <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> infection is characterized by altered expression of long noncoding RNAs. <i>Scientific Reports</i> , 2019, 9, 2894.	1.6	19
10369	Identifying Windows of Susceptibility by Temporal Gene Analysis. <i>Scientific Reports</i> , 2019, 9, 2740.	1.6	9
10370	Transcriptome analysis reveals the impact of arbuscular mycorrhizal symbiosis on <i>Sesbania cannabina</i> expose to high salinity. <i>Scientific Reports</i> , 2019, 9, 2780.	1.6	17
10371	Clustering analysis to identify key genes associated with motor neuron excitability following spinal cord injury. <i>International Journal of Neuroscience</i> , 2019, 129, 856-863.	0.8	4
10372	Integrated Bioinformatics Analysis of Hub Genes and Pathways in Anaplastic Thyroid Carcinomas. <i>International Journal of Endocrinology</i> , 2019, 2019, 1-9.	0.6	14

#	ARTICLE	IF	CITATIONS
10373	Identification of differentially expressed proteins in the injured lung from zinc chloride smoke inhalation based on proteomics analysis. <i>Respiratory Research</i> , 2019, 20, 36.	1.4	16
10374	Differences in First-Trimester Maternal Metabolomic Profiles in Pregnancies Conceived From Fertility Treatments. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 1005-1019.	1.8	15
10375	N6-Methyladenosine Landscape of Glioma Stem-Like Cells: METTL3 Is Essential for the Expression of Actively Transcribed Genes and Sustenance of the Oncogenic Signaling. <i>Genes</i> , 2019, 10, 141.	1.0	82
10376	Investigating Common Pathogenic Mechanisms between Homo sapiens and Different Strains of Candida albicans for Drug Design: Systems Biology Approach via Two-Sided NGS Data Identification. <i>Toxins</i> , 2019, 11, 119.	1.5	3
10377	Involvement of heat shock protein 40 in the wing dimorphism of the house cricket Acheta domesticus. <i>Journal of Insect Physiology</i> , 2019, 114, 35-44.	0.9	6
10378	The evolution of gene regulatory networks controlling Arabidopsis thaliana L. trichome development. <i>BMC Plant Biology</i> , 2019, 19, 53.	1.6	40
10379	Phytochrome A Regulates Carbon Flux in Dark Grown Tomato Seedlings. <i>Frontiers in Plant Science</i> , 2019, 10, 152.	1.7	13
10380	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	5.5	833
10381	Comprehensive mass spectrometry-guided phenotyping of plant specialized metabolites reveals metabolic diversity in the cosmopolitan plant family Rhamnaceae. <i>Plant Journal</i> , 2019, 98, 1134-1144.	2.8	59
10382	Linking Terpene Synthases to Sesquiterpene Metabolism in Grapevine Flowers. <i>Frontiers in Plant Science</i> , 2019, 10, 177.	1.7	27
10383	Intractome Curation and Analysis for Stroke and Spinal Cord Injury Using Semiautomatic Annotations. , 2019, , 151-166.		1
10384	MicroRNA-196a is regulated by ER and is a prognostic biomarker in ER+ breast cancer. <i>British Journal of Cancer</i> , 2019, 120, 621-632.	2.9	29
10385	Insight of Captagon Abuse by Chemogenomics Knowledgebase-guided Systems Pharmacology Target Mapping Analyses. <i>Scientific Reports</i> , 2019, 9, 2268.	1.6	10
10386	Genetic analysis of a novel antioxidant multi-target iron chelator, M30 protecting against chemotherapy-induced alopecia in mice. <i>BMC Cancer</i> , 2019, 19, 149.	1.1	9
10387	Machine learning analysis of gene expression data reveals novel diagnostic and prognostic biomarkers and identifies therapeutic targets for soft tissue sarcomas. <i>PLoS Computational Biology</i> , 2019, 15, e1006826.	1.5	75
10388	Novel Zebrafish Mono- $\pm$ 2,8-sialyltransferase (ST8Sia VIII): An Evolutionary Perspective of $\pm$ 2,8-Sialylation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 622.	1.8	7
10389	Integrated analysis of competing endogenous RNA networks revealing five prognostic biomarkers associated with colorectal cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 11256-11264.	1.2	18
10390	microRNA expression profile in porcine oocytes with different developmental competence derived from large or small follicles. <i>Molecular Reproduction and Development</i> , 2019, 86, 426-439.	1.0	17

#	ARTICLE	IF	CITATIONS
10391	Resolving Cell Fate Decisions during Somatic Cell Reprogramming by Single-Cell RNA-Seq. <i>Molecular Cell</i> , 2019, 73, 815-829.e7.	4.5	79
10392	Predicting MicroRNA Target Genes and Identifying Hub Genes in IIA Stage Colon Cancer Patients Using Bioinformatics Analysis. <i>BioMed Research International</i> , 2019, 2019, 1-13.	0.9	7
10393	Therapeutic Targeting of CD146/MCAM Reduces Bone Metastasis in Prostate Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 1049-1062.	1.5	17
10394	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. <i>Frontiers in Immunology</i> , 2019, 10, 212.	2.2	34
10395	A Novel Discovery: Holistic Efficacy at the Special Organ Level of Pungent Flavored Compounds from Pungent Traditional Chinese Medicine. <i>International Journal of Molecular Sciences</i> , 2019, 20, 752.	1.8	10
10396	Molecular Networking-Based Analysis of Cytotoxic Saponins from Sea Cucumber <i>Holothuria atra</i> . <i>Marine Drugs</i> , 2019, 17, 86.	2.2	29
10397	Investigation of circular RNAs and related genes in pulmonary fibrosis based on bioinformatics analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 11022-11032.	1.2	14
10398	Tumor infiltrating mast cells determine oncogenic HIF-2 $\alpha$ -conferred immune evasion in clear cell renal cell carcinoma. <i>Cancer Immunology, Immunotherapy</i> , 2019, 68, 731-741.	2.0	39
10399	DNA damage repair alterations modulate M2 polarization of microglia to remodel the tumor microenvironment via the p53-mediated MDK expression in glioma. <i>EBioMedicine</i> , 2019, 41, 185-199.	2.7	77
10400	ST-Steiner: a spatio-temporal gene discovery algorithm. <i>Bioinformatics</i> , 2019, 35, 3433-3440.	1.8	10
10401	Construction of Parkinson's disease marker-based weighted protein-protein interaction network for prioritization of co-expressed genes. <i>Gene</i> , 2019, 697, 67-77.	1.0	17
10402	Visualization and Analysis of Epiproteome Dynamics. <i>Journal of Molecular Biology</i> , 2019, 431, 1519-1539.	2.0	10
10403	Social network analysis in humanitarian logistics research. <i>Journal of Humanitarian Logistics and Supply Chain Management</i> , 2019, 9, 492-514.	1.7	10
10404	Long noncoding RNA DNMT3OS promotes prostate stromal cells transformation via the miR-29a/29b/COL3A1 and miR-361/TGF $\beta$ 1 axes. <i>Aging</i> , 2019, 11, 9442-9460.	1.4	25
10405	Anoxygenic Phototrophs Span Geochemical Gradients and Diverse Morphologies in Terrestrial Geothermal Springs. <i>MSystems</i> , 2019, 4, .	1.7	24
10406	Identification of key biomarkers and potential molecular mechanisms in lung cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 4429-4440.	0.8	14
10407	Shielding the Next Generation: Symbiotic Bacteria from a Reproductive Organ Protect Bobtail Squid Eggs from Fungal Fouling. <i>MBio</i> , 2019, 10, .	1.8	30
10408	Bioinformatics-based identification of key pathways and candidate genes for estrogen-induced intrahepatic cholestasis using DNA microarray analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 303-311.	1.1	2

#	ARTICLE	IF	CITATIONS
10409	Network pharmacology-based assessment to elucidate the molecular mechanism of anti-diabetic action of <i>Tinospora cordifolia</i> . <i>Clinical Phytoscience</i> , 2019, 5, .	0.8	40
10410	Key genes associated with pancreatic cancer and their association with outcomes: A bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1343-1352.	1.1	31
10411	The human DEPhOsphorylation Database DEPOD: 2019 update. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	42
10412	Mechanisms of <i>Atractylodis Macrocephalae Rhizoma</i> against Chronic Gastritis. , 2019, , .		0
10413	Anti-rheumatoid Arthritis Mechanisms of <i>Angelicae Pubescentis Radix</i> . , 2019, , .		0
10414	Origraph: Interactive Network Wrangling. , 2019, , .		14
10415	Multi-omics Analysis of Primary Cell Culture Models Reveals Genetic and Epigenetic Basis of Intratumoral Phenotypic Diversity. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 576-589.	3.0	10
10416	A Data Analysis Pipeline for Identifying Periodic Processes during <i>Drosophila</i> Development. , 2019, , .		0
10417	Healing Functions of <i>Carthami Flos</i> against Contusion and Other Potential Damages. , 2019, , .		0
10418	RuleVis: Constructing Patterns and Rules for Rule-Based Models. , 2019, , .		2
10419	Making the invisible hyper-visible: Knowledge production and the gendered power nexus in critical urban studies. <i>Human Geography(United Kingdom)</i> , 2019, 12, 36-50.	0.4	5
10420	Varying Mutational Classes Illuminate Differential Genetic Patterns Between Schizophrenia and Bipolar Disorder. , 2019, , .		0
10421	Healing Functions of <i>Carthami Flos</i> against Contusion and Other Potential Damages. , 2019, , .		0
10422	Therapeutic Mechanisms of <i>Persicae Semen</i> towards Healing Processes. , 2019, , .		0
10423	Natural Genetic Variation Screen in <i>Drosophila</i> Identifies Wnt Signaling, Mitochondrial Metabolism, and Redox Homeostasis Genes as Modifiers of Apoptosis. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3995-4005.	0.8	17
10424	A Bioinformatics Approach to Explore MicroRNAs as Tools to Bridge Pathways Between Plants and Animals. Is DNA Damage Response (DDR) a Potential Target Process?. <i>Frontiers in Plant Science</i> , 2019, 10, 1535.	1.7	9
10425	Integrated Bioinformatics Analysis Identifies Hub Genes Associated with the Pathogenesis and Prognosis of Esophageal Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	21
10426	Vildagliptin, a dipeptidyl peptidase-4 inhibitor, attenuated endothelial dysfunction through miRNAs in diabetic rats. <i>Archives of Medical Science</i> , 2021, 17, 1378-1387.	0.4	7



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10427	Antimicrobial Effects of Conditioned Medium From Amniotic Progenitor Cells in vitro and in vivo: Toward Tissue Regenerative Therapies for Bovine Mastitis. <i>Frontiers in Veterinary Science</i> , 2019, 6, 443.	0.9	13
10428	The <i>cbb<sub>3</sub></i> -type cytochrome oxidase assembly factor CcoG is a widely distributed cupric reductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21166-21175.	3.3	17
10429	Identification of key genes and pathways in calcific aortic valve disease by bioinformatics analysis. <i>Journal of Thoracic Disease</i> , 2019, 11, 5417-5426.	0.6	17
10430	Greenlip Abalone ( <i>Haliotis laevigata</i> ) Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3067-3078.	0.8	14
10431	Identifying miRNA synergism using multiple-intervention causal inference. <i>BMC Bioinformatics</i> , 2019, 20, 613.	1.2	14
10432	ODE Network Model for Nonlinear and Complex Agricultural Nutrient Solution System. , 2019, , .		4
10433	Screening and Identification of Molecular Targets Involved in Preventing Gastric Precancerous Lesions in Chronic Atrophic Gastritis by Qilianshupi Decoction. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-13.	0.5	5
10434	<i>Lotus japonicus</i> Symbiosis Genes Impact Microbial Interactions between Symbionts and Multikingdom Commensal Communities. <i>MBio</i> , 2019, 10, .	1.8	41
10435	Molecular profiling of stem cell-like female germ line cells in <i>Drosophila</i> delineates networks important for stemness and differentiation. <i>Biology Open</i> , 2019, 8, .	0.6	6
10436	CHEMICAL ANALYSIS OF LITSEA CUBEBA ESSENTIAL OIL HARVESTED FROM ARUNACHAL PRADESH, INDIA AND ESTIMATION OF MOSQUITO REPELLENT ACTIVITY WITH REFERENCE TO NETWORK ANALYSIS. <i>Asian Journal of Pharmaceutical and Clinical Research</i> , 2019, , 241-244.	0.3	1
10437	Topology Analysis of Protein-protein Interaction Network and Identification of Gene Ontology for Obstructive Sleep Apnea and Associated Diseases Using Bioinformatics Tools. , 2019, , .		0
10438	Global Proteomic Analysis of Breast Cancer Cell Plasma Membrane Electroporation. , 2019, , .		2
10439	A linked data graph approach to integration of immunological data. , 2019, 2019, 1742-1749.		0
10440	Human brain cell type-specific gene co-expression associated with autism spectrum disorder. , 2019, , .		1
10441	A knowledge driven mutual information-based analytical framework for the identification of rumen metabolites. , 2019, , .		1
10442	Visualizing multifunctional PPI network with Gene Ontology annotation. , 2019, , .		0
10443	Construction of a lncRNA-miRNA-mRNA network to determine the regulatory roles of lncRNAs in psoriasis. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4011-4021.	0.8	16
10444	Habitat Heterogeneity and Connectivity: Effects on the Planktonic Protist Community Structure at Two Adjacent Coastal Sites (the Lagoon and the Gulf of Venice, Northern Adriatic Sea, Italy) Revealed by Metabarcoding. <i>Frontiers in Microbiology</i> , 2019, 10, 2736.	1.5	18



#	ARTICLE	IF	CITATIONS
10445	Extent and characteristics of immune infiltration in clear cell renal cell carcinoma and the prognostic value. <i>Translational Andrology and Urology</i> , 2019, 8, 609-618.	0.6	17
10446	Identifying functional evolution processes according to the pathological stages of colorectal cancer. , 2019, , .		0
10447	NOESIS: A Framework for Complex Network Data Analysis. <i>Complexity</i> , 2019, 2019, 1-14.	0.9	4
10448	A new grid- and modularity-based layout algorithm for complex biological networks. <i>PLoS ONE</i> , 2019, 14, e0221620.	1.1	4
10449	Reconstruction and analysis of competitive endogenous RNA network reveals regulatory role of long non-coding RNAs in hepatic fibrosis. <i>Molecular Medicine Reports</i> , 2019, 20, 4091-4100.	1.1	5
10450	Next generation sequencing and proteomics in plant virology: how is Colombia doing?. <i>Acta Biologica Colombiana</i> , 2019, 24, 423-438.	0.1	3
10451	The four-microRNA signature identified by bioinformatics analysis predicts the prognosis of nasopharyngeal carcinoma patients. <i>Oncology Reports</i> , 2019, 42, 1767-1780.	1.2	22
10452	Global Transcriptomic Analysis of the <i>Candida albicans</i> Response to Treatment with a Novel Inhibitor of Filamentation. <i>MSphere</i> , 2019, 4, .	1.3	18
10453	Optimising cattle grazing distribution on rangeland: a systematic review and network analysis. <i>Rangeland Journal</i> , 2019, 41, 441.	0.4	7
10454	Untargeted metabolomic profiling of <i>Sphagnum fallax</i> reveals novel antimicrobial metabolites. <i>Plant Direct</i> , 2019, 3, e00179.	0.8	55
10455	Broad Substrate-Specific Phosphorylation Events Are Associated With the Initial Stage of Plant Cell Wall Recognition in <i>Neurospora crassa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2317.	1.5	25
10456	Differential Pattern of Soluble Immune Markers in Asymptomatic Dengue, West Nile and Zika Virus Infections. <i>Scientific Reports</i> , 2019, 9, 17172.	1.6	16
10457	Therapeutic strategies for diffuse midline glioma from high-throughput combination drug screening. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	129
10458	Multiple transcription factors co-regulate the <i>Mycobacterium tuberculosis</i> adaptation response to vitamin C. <i>BMC Genomics</i> , 2019, 20, 887.	1.2	9
10459	Whole-transcriptome RNA sequencing reveals the global molecular responses and ceRNA regulatory network of mRNAs, lncRNAs, miRNAs and circRNAs in response to copper toxicity in <i>Ziyang Xiangcheng</i> ( <i>Citrus junos</i> Sieb. Ex Tanaka). <i>BMC Plant Biology</i> , 2019, 19, 509.	1.6	44
10460	Biomarker discovery in inflammatory bowel diseases using network-based feature selection. <i>PLoS ONE</i> , 2019, 14, e0225382.	1.1	17
10461	Applying Semantic Network Analysis to Develop User Experience Assessment Model for Smart TV. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 3307.	1.3	1
10462	Identification of Dysregulated Competitive Endogenous RNA Networks Driven by Copy Number Variations in Malignant Gliomas. <i>Frontiers in Genetics</i> , 2019, 10, 1055.	1.1	17

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10463	The New Genetic Landscape of Cushing's Disease: Deubiquitinases in the Spotlight. <i>Cancers</i> , 2019, 11, 1761.	1.7	27
10464	Evolution of <i>Streptococcus pneumoniae</i> Serotype 3 in England and Wales: A Major Vaccine Evader. <i>Genes</i> , 2019, 10, 845.	1.0	52
10465	Single-Stranded DNA Viruses in Antarctic Cryoconite Holes. <i>Viruses</i> , 2019, 11, 1022.	1.5	31
10466	The impact of a prescribed journal list of disciplinary publishing. <i>Proceedings of the Association for Information Science and Technology</i> , 2019, 56, 620-621.	0.3	0
10467	Assessing the potential for assisted gene flow using past introduction of Norway spruce in southern Sweden: Local adaptation and genetic basis of quantitative traits in trees. <i>Evolutionary Applications</i> , 2019, 12, 1946-1959.	1.5	36
10468	An integrative methodology based on protein-protein interaction networks for identification and functional annotation of disease-relevant genes applied to channelopathies. <i>BMC Bioinformatics</i> , 2019, 20, 565.	1.2	8
10469	Analysis of miRNA signatures in CSF identifies upregulation of miR-21 and miR-146a/b in patients with multiple sclerosis and active lesions. <i>Journal of Neuroinflammation</i> , 2019, 16, 220.	3.1	48
10470	Comparative acetylome analysis reveals the potential roles of lysine acetylation for DON biosynthesis in <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2019, 20, 841.	1.2	13
10471	A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots ( <i>Nicotiana glauca</i> ). <i>Plant Physiology</i> , 2019, 171, 422-432.	1.2	22
10472	LncRNA SNHG8 is identified as a key regulator of acute myocardial infarction by RNA-seq analysis. <i>Lipids in Health and Disease</i> , 2019, 18, 201.	1.2	28
10473	Temporal Dynamics of the Soil Metabolome and Microbiome During Simulated Anaerobic Soil Disinfestation. <i>Frontiers in Microbiology</i> , 2019, 10, 2365.	1.5	53
10474	A Meta-Analysis of Comparative Transcriptomic Data Reveals a Set of Key Genes Involved in the Tolerance to Abiotic Stresses in Rice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5662.	1.8	24
10475	Strong T <sub>H</sub> 1-biased CD4 T cell responses are associated with diminished SIV vaccine efficacy. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	14
10476	Disparate responses to salinity across species and organizational levels in anchialine shrimps. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	5
10477	Systematic analysis identifies three-lncRNA signature as a potentially prognostic biomarker for lung squamous cell carcinoma using bioinformatics strategy. <i>Translational Lung Cancer Research</i> , 2019, 8, 614-635.	1.3	29
10478	Gene Expression and Fatty Acid Profiling in Longissimus thoracis Muscle, Subcutaneous Fat, and Liver of Light Lambs in Response to Concentrate or Alfalfa Grazing. <i>Frontiers in Genetics</i> , 2019, 10, 1070.	1.1	5
10479	Protein Interactions Network of Hepatitis E Virus RNA and Polymerase With Host Proteins. <i>Frontiers in Microbiology</i> , 2019, 10, 2501.	1.5	14
10480	Integrated Metabolomics-DNA Methylation Analysis Reveals Significant Long-Term Tissue-Dependent Directional Alterations in Aminoacyl-tRNA Biosynthesis in the Left Ventricle of the Heart and Hippocampus Following Proton Irradiation. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 77.	1.6	13

#	ARTICLE	IF	CITATIONS
10481	Comprehensive investigation of key biomarkers and pathways in hepatitis B virus-related hepatocellular carcinoma. <i>Journal of Cancer</i> , 2019, 10, 5689-5704.	1.2	28
10482	Expression and Functional Analysis of Hecpudin from Mandarin Fish ( <i>Siniperca chuatsi</i> ). <i>International Journal of Molecular Sciences</i> , 2019, 20, 5602.	1.8	22
10483	Genome-Wide Identification and Characterization of FBA Gene Family in Polyploid Crop <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5749.	1.8	14
10484	Network Pharmacology-Based Investigation into the Mechanisms of <i>Quyushengxin</i> Formula for the Treatment of Ulcerative Colitis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-22.	0.5	18
10485	Distribution, Interaction and Functional Profiles of Epiphytic Bacterial Communities from the Rocky Intertidal Seaweeds, South Africa. <i>Scientific Reports</i> , 2019, 9, 19835.	1.6	62
10486	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. <i>MBio</i> , 2019, 10, .	1.8	56
10487	Integrative Bioinformatics Approaches to Map Potential Novel Genes and Pathways Involved in Ovarian Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 391.	2.0	72
10488	Putative circumsporozoite protein (CSP) of <i>Plasmodium vivax</i> is considerably distinct from the well-known CSP and plays a role in the protein ubiquitination pathway. <i>Gene: X</i> , 2019, 4, 100024.	2.3	1
10489	Serum protein profiles suggest a possible link between qi deficiency constitution and Pi-qi-deficiency syndrome of chronic superficial gastritis. <i>Journal of Traditional Chinese Medical Sciences</i> , 2019, 6, 308-314.	0.1	0
10490	Modeling and Graph Analysis for Enhancing Resilience in Smart Homes. <i>Procedia Computer Science</i> , 2019, 160, 197-205.	1.2	5
10491	Characterization of the genomically encoded fosfomycin resistance enzyme from <i>Mycobacterium abscessus</i> . <i>MedChemComm</i> , 2019, 10, 1948-1957.	3.5	6
10492	A network-based approach reveals novel invasion and Maurer's clefts-related proteins in <i>Plasmodium falciparum</i> . <i>Molecular Omics</i> , 2019, 15, 431-441.	1.4	4
10493	Proteomic and Transcriptomic Changes in Hibernating Grizzly Bears Reveal Metabolic and Signaling Pathways that Protect against Muscle Atrophy. <i>Scientific Reports</i> , 2019, 9, 19976.	1.6	19
10494	Identification of circulating microRNA signatures as potential biomarkers in the serum of elk infected with chronic wasting disease. <i>Scientific Reports</i> , 2019, 9, 19705.	1.6	11
10495	ZDOG: zooming in on dominating genes with mutations in cancer pathways. <i>BMC Bioinformatics</i> , 2019, 20, 740.	1.2	1
10496	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. <i>Cell Reports</i> , 2019, 29, 4568-4582.e5.	2.9	114
10497	Air-side ammonia stripping coupled to anaerobic digestion indirectly impacts anaerobic microbiome. <i>Microbial Biotechnology</i> , 2019, 12, 1403-1416.	2.0	19
10498	Comparative analysis of ascorbate peroxidases (APXs) from selected plants with a special focus on <i>Oryza sativa</i> employing public databases. <i>PLoS ONE</i> , 2019, 14, e0226543.	1.1	7

#	ARTICLE	IF	CITATIONS
10499	Network Analyses and Data Integration of Proteomics and Metabolomics From Leaves of Two Contrasting Varieties of Sugarcane in Response to Drought. <i>Frontiers in Plant Science</i> , 2019, 10, 1524.	1.7	41
10500	A new method for mining information of co-expression network based on multi-cancers integrated data. <i>BMC Medical Genomics</i> , 2019, 12, 155.	0.7	6
10501	DUF3669, a ðœdomain of unknown functionâ€•within ZNF746 and ZNF777, oligomerizes and contributes to transcriptional repression. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 60.	1.0	10
10502	A novel graph theoretical approach for modeling microbiomes and inferring microbial ecological relationships. <i>BMC Genomics</i> , 2019, 20, 945.	1.2	10
10503	Genomic insights on heterogeneous resistance to vancomycin and teicoplanin in Methicillin-resistant <i>Staphylococcus aureus</i> : A first report from South India. <i>PLoS ONE</i> , 2019, 14, e0227009.	1.1	24
10504	Serum tryptophan-derived quinolinate and indole-3-acetate are associated with carotid intima-media thickness and its evolution in HIV-infected treated adults. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz516.	0.4	10
10505	Prognostic significance and molecular mechanisms of adenosine triphosphate-binding cassette subfamily C members in gastric cancer. <i>Medicine (United States)</i> , 2019, 98, e18347.	0.4	17
10506	Bioinformatics analysis of key biomarkers and pathways in KSHV infected endothelial cells. <i>Medicine (United States)</i> , 2019, 98, e16277.	0.4	5
10507	Identification of a novel regulatory pathway for PPARÎ± by RNA-seq characterization of the endothelial cell lipid peroxidative injury transcriptome. <i>Open Biology</i> , 2019, 9, 190141.	1.5	4
10508	Diagnostic Value Investigation and Bioinformatics Analysis of miR-31 in Patients with Lymph Node Metastasis of Colorectal Cancer. <i>Analytical Cellular Pathology</i> , 2019, 2019, 1-10.	0.7	14
10509	A Wrapper Feature Subset Selection Method Based on Randomized Search and Multilayer Structure. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	14
10510	BEST: a web server for brain expression Spatio-temporal pattern analysis. <i>BMC Bioinformatics</i> , 2019, 20, 632.	1.2	13
10511	Uncovering the Resistance Mechanism of <i>Mycobacterium tuberculosis</i> to Rifampicin Due to RNA Polymerase H451D/Y/R Mutations From Computational Perspective. <i>Frontiers in Chemistry</i> , 2019, 7, 819.	1.8	19
10512	Comparative Genomics Analysis of Ciliates Provides Insights on the Evolutionary History Within ðœNassophoreaâ€•Synhymeniaâ€•Phyllopharyngeaâ€•Assemblage. <i>Frontiers in Microbiology</i> , 2019, 10, 2819.	1.5	31
10513	Down-Regulation of Flagellar, Fimbriae, and Pili Proteins in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> (NDM-4) Clinical Isolates: A Novel Linkage to Drug Resistance. <i>Frontiers in Microbiology</i> , 2019, 10, 2865.	1.5	18
10514	Long Non-Coding RNA MAGI2-AS3 is a New Player with a Tumor Suppressive Role in High Grade Serous Ovarian Carcinoma. <i>Cancers</i> , 2019, 11, 2008.	1.7	27
10515	The mTOR Signaling Pathway Activity and Vitamin D Availability Control the Expression of Most Autism Predisposition Genes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6332.	1.8	21
10516	The Arabidopsis Transcriptome Responds Specifically and Dynamically to High Light Stress. <i>Cell Reports</i> , 2019, 29, 4186-4199.e3.	2.9	119

#	ARTICLE	IF	CITATIONS
10517	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. <i>Science</i> , 2019, 366, .	6.0	329
10518	Master Regulators of Signaling Pathways: An Application to the Analysis of Gene Regulation in Breast Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 1180.	1.1	19
10519	A network pharmacology approach to reveal the protective mechanism of <i>Salvia miltiorrhiza</i> - <i>Dalbergia odorifera</i> coupled-herbs on coronary heart disease. <i>Scientific Reports</i> , 2019, 9, 19343.	1.6	18
10520	Expression alteration of microRNAs in Nucleus Accumbens is associated with chronic stress and antidepressant treatment in rats. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 271.	1.5	12
10521	Comprehensive analysis of the lncRNA-associated ceRNA network identifies neuroinflammation biomarkers for Alzheimer's disease. <i>Molecular Omics</i> , 2019, 15, 459-469.	1.4	18
10522	Global transcriptome analysis of rat hypothalamic arcuate nucleus demonstrates reversal of hypothalamic gliosis following surgically and diet induced weight loss. <i>Scientific Reports</i> , 2019, 9, 16161.	1.6	7
10523	A Proteomic Network Approach across the Kidney Stone Disease Reveals Endoplasmic Reticulum Stress and Crystal-Cell Interaction in the Kidney. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-13.	1.9	11
10524	MicroRNA-101 Protects Against Cardiac Remodeling Following Myocardial Infarction via Downregulation of Runx-Related Transcription Factor 1. <i>Journal of the American Heart Association</i> , 2019, 8, e013112.	1.6	30
10525	CircRNA expression profile and functional analysis in testicular tissue of patients with non-obstructive azoospermia. <i>Reproductive Biology and Endocrinology</i> , 2019, 17, 100.	1.4	32
10526	Differentially expressed tRFs in CD5 positive relapsed & refractory diffuse large B cell lymphoma and the bioinformatic analysis for their potential clinical use. <i>Biology Direct</i> , 2019, 14, 23.	1.9	14
10527	Microarray Gene Expression Dataset Re-analysis Reveals Variability in Influenza Infection and Vaccination. <i>Frontiers in Immunology</i> , 2019, 10, 2616.	2.2	24
10528	Computational Inference of Gene Co-Expression Networks for the identification of Lung Carcinoma Biomarkers: An Ensemble Approach. <i>Genes</i> , 2019, 10, 962.	1.0	4
10529	Phylostratigraphic Analysis Shows the Earliest Origination of the Abiotic Stress Associated Genes in <i>A. thaliana</i> . <i>Genes</i> , 2019, 10, 963.	1.0	11
10530	Transcriptomic and Co-Expression Network Profiling of Shoot Apical Meristem Reveal Contrasting Response to Nitrogen Rate between <i>Indica</i> and <i>Japonica</i> Rice Subspecies. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5922.	1.8	12
10531	PCV2 Regulates Cellular Inflammatory Responses through Dysregulating Cellular miRNA-mRNA Networks. <i>Viruses</i> , 2019, 11, 1055.	1.5	11
10532	BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	24
10533	Soil Property and Plant Diversity Determine Bacterial Turnover and Network Interactions in a Typical Arid Inland River Basin, Northwest China. <i>Frontiers in Microbiology</i> , 2019, 10, 2655.	1.5	13
10534	7-Deazaguanine modifications protect phage DNA from host restriction systems. <i>Nature Communications</i> , 2019, 10, 5442.	5.8	63

#	ARTICLE	IF	CITATIONS
10535	Unraveling cis and trans regulatory evolution during cotton domestication. <i>Nature Communications</i> , 2019, 10, 5399.	5.8	58
10536	Topological properties and inÂvitro identification of essential nodes of the Paclitaxel and Vincristine interactomes in PC-3 cells. <i>Biomedical Journal</i> , 2019, 42, 307-316.	1.4	4
10537	The transcriptional regulator CBX2 and ovarian function: A whole genome and whole transcriptome approach. <i>Scientific Reports</i> , 2019, 9, 17033.	1.6	12
10538	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	2.4	35
10539	Methodology of predicting novel key regulators in ovarian cancer network: a network theoretical approach. <i>BMC Cancer</i> , 2019, 19, 1129.	1.1	20
10540	&lt;p&gt;The Prognosis Of Peroxiredoxin Family In Breast Cancer&lt;/p&gt;. <i>Cancer Management and Research</i> , 2019, Volume 11, 9685-9699.	0.9	24
10541	Integrative Computational Framework for Understanding Metabolic Modulation in Leishmania. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 336.	2.0	4
10542	Identification of Circulating Serum Multi-MicroRNA Signatures in Human DLBCL Models. <i>Scientific Reports</i> , 2019, 9, 17161.	1.6	25
10543	Verification of hub genes in the expression profile of aortic dissection. <i>PLoS ONE</i> , 2019, 14, e0224922.	1.1	10
10544	Up-Regulation of hsa_circ_0000517 Predicts Adverse Prognosis of Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 1105.	1.3	36
10545	Multi-dimensional computational pipeline for large-scale deep screening of compound effect assessment: an in silico case study on ageing-related compounds. <i>Npj Systems Biology and Applications</i> , 2019, 5, 42.	1.4	3
10546	Predicting novel genomic regions linked to genetic disorders using GWAS and chromosome conformation data â€“ a case study of schizophrenia. <i>Scientific Reports</i> , 2019, 9, 17940.	1.6	6
10547	Salinity reduces bacterial diversity, but increases network complexity in Tibetan Plateau lakes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	62
10548	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
10549	Analysis of key genes and their functions in placental tissue of patients with gestational diabetes mellitus. <i>Reproductive Biology and Endocrinology</i> , 2019, 17, 104.	1.4	11
10550	Transcriptome profiling of posterior kidney of brown trout, <i>Salmo trutta</i> , during proliferative kidney disease. <i>Parasites and Vectors</i> , 2019, 12, 569.	1.0	20
10551	Trypanocidal Mechanism of Action and in silico Studies of p-Coumaric Acid Derivatives. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5916.	1.8	27
10552	Transcription Factor Networks in Leaves of <i>Cichorium endivia</i> : New Insights into the Relationship between Photosynthesis and Leaf Development. <i>Plants</i> , 2019, 8, 531.	1.6	9



#	ARTICLE	IF	CITATIONS
10553	Proteomic Analysis of Radiation-Induced Acute Liver Damage in a Rabbit Model. Dose-Response, 2019, 17, 155932581988950.	0.7	4
10554	Runs of Homozygosity and NetView analyses provide new insight into the genome-wide diversity and admixture of three German cattle breeds. PLoS ONE, 2019, 14, e0225847.	1.1	18
10555	Investigating the Systems-Level Effect of Pueraria lobata for Menopause-Related Metabolic Diseases Using an Ovariectomized Rat Model and Network Pharmacological Analysis. Biomolecules, 2019, 9, 747.	1.8	7
10556	Deciphering Molecular Mechanism of the Neuropharmacological Action of Fucosterol through Integrated System Pharmacology and In Silico Analysis. Marine Drugs, 2019, 17, 639.	2.2	29
10557	Quantifying Inter-Residue Contacts through Interaction Energies. Journal of Chemical Information and Modeling, 2019, 59, 5034-5044.	2.5	10
10558	Feature selection with the Fisher score followed by the Maximal Clique Centrality algorithm can accurately identify the hub genes of hepatocellular carcinoma. Scientific Reports, 2019, 9, 17283.	1.6	37
10559	Monocytes affect bone mineral density in pre- and postmenopausal women through ribonucleoprotein complex biogenesis by integrative bioinformatics analysis. Scientific Reports, 2019, 9, 17290.	1.6	11
10560	Mining TCGA Database for Tumor Microenvironment-Related Genes of Prognostic Value in Hepatocellular Carcinoma. BioMed Research International, 2019, 2019, 1-12.	0.9	32
10561	Identification of key genes and regulators associated with carotenoid metabolism in apricot (Prunus Tj ETQq0 0 0 ggBT /Overlock 10 Tf	1.2	28
10562	Staphylococcus arlettae Genomics: Novel Insights on Candidate Antibiotic Resistance and Virulence Genes in an Emerging Opportunistic Pathogen. Microorganisms, 2019, 7, 580.	1.6	10
10563	Effects of Flaxseed and Its Components on Mammary Gland MiRNome: Identification of Potential Biomarkers to Prevent Breast Cancer Development. Nutrients, 2019, 11, 2656.	1.7	12
10564	p300/CBP inhibitor A-485 alleviates acute liver injury by regulating macrophage activation and polarization. Theranostics, 2019, 9, 8344-8361.	4.6	44
10565	Global Analysis of Enhancer Targets Reveals Convergent Enhancer-Driven Regulatory Modules. Cell Reports, 2019, 29, 2570-2578.e5.	2.9	20
10566	Identification of novel genetic variants predisposing to familial oral squamous cell carcinomas. Cell Discovery, 2019, 5, 57.	3.1	16
10567	JASPer controls interphase histone H3S10 phosphorylation by chromosomal kinase JIL-1 in Drosophila. Nature Communications, 2019, 10, 5343.	5.8	18
10568	Comorbidity of asthma and hypertension may be mediated by shared genetic dysregulation and drug side effects. Scientific Reports, 2019, 9, 16302.	1.6	20
10569	Metatranscriptomic Analysis of Multiple Environmental Stresses Identifies RAP2.4 Gene Associated with Arabidopsis Immunity to Botrytis cinerea. Scientific Reports, 2019, 9, 17010.	1.6	27
10570	A novel circRNA-miRNA-mRNA network identifies circ-YOD1 as a biomarker for coronary artery disease. Scientific Reports, 2019, 9, 18314.	1.6	60



#	ARTICLE	IF	CITATIONS
10571	Integrated Meta-omics Approaches To Understand the Microbiome of Spontaneous Fermentation of Traditional Chinese Pu-erh Tea. <i>MSystems</i> , 2019, 4, .	1.7	94
10572	Exploitation of Potentially New Antibiotics from Mangrove Actinobacteria in Maowei Sea by Combination of Multiple Discovery Strategies. <i>Antibiotics</i> , 2019, 8, 236.	1.5	14
10573	The MS-lincRNA landscape reveals a novel lincRNA BCLIN25 that contributes to tumorigenesis by upregulating ERBB2 expression via epigenetic modification and RNA-RNA interactions in breast cancer. <i>Cell Death and Disease</i> , 2019, 10, 920.	2.7	11
10574	Identification of crucial miRNAs and genes in esophageal squamous cell carcinoma by miRNA-mRNA integrated analysis. <i>Medicine (United States)</i> , 2019, 98, e16269.	0.4	24
10575	Integrative Analysis of ceRNA Network Reveals Functional lncRNAs in Intrahepatic Cholangiocarcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	12
10576	Study on the Multitarget Mechanism and Key Active Ingredients of Herba Siegesbeckiae and Volatile Oil against Rheumatoid Arthritis Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-15.	0.5	28
10577	Joint Transcriptomic Analysis of Lung Cancer and Other Lung Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 1260.	1.1	9
10578	The Transcription Factor ArcA Modulates Salmonella's Metabolism in Response to Neutrophil Hypochlorous Acid-Mediated Stress. <i>Frontiers in Microbiology</i> , 2019, 10, 2754.	1.5	17
10579	Impact of a High Protein Intake on the Plasma Metabolome in Elderly Males: 10 Week Randomized Dietary Intervention. <i>Frontiers in Nutrition</i> , 2019, 6, 180.	1.6	7
10580	RNAseq Analysis of the Response of Arabidopsis thaliana to Fractional Gravity Under Blue-Light Stimulation During Spaceflight. <i>Frontiers in Plant Science</i> , 2019, 10, 1529.	1.7	42
10581	Gigantol Targets Cancer Stem Cells and Destabilizes Tumors via the Suppression of the PI3K/AKT and JAK/STAT Pathways in Ectopic Lung Cancer Xenografts. <i>Cancers</i> , 2019, 11, 2032.	1.7	33
10582	Diversity and Functional Potential of Soil Bacterial Communities in Different Types of Farmland Shelterbelts in Mid-Western Heilongjiang, China. <i>Forests</i> , 2019, 10, 1115.	0.9	5
10583	Temporal and Spatial Differential Expression of Glutamate Receptor Genes in the Brain of Down Syndrome. , 2019, , .		0
10584	Association between ALS and retroviruses: evidence from bioinformatics analysis. <i>BMC Bioinformatics</i> , 2019, 20, 680.	1.2	7
10585	Genomewide analysis of circular RNA in pituitaries of normal and heat-stressed sows. <i>BMC Genomics</i> , 2019, 20, 1013.	1.2	10
10586	Investigating host-bacterial interactions among enteric pathogens. <i>BMC Genomics</i> , 2019, 20, 1022.	1.2	7
10587	Network analysis exposes core functions in major lifestyles of fungal and oomycete plant pathogens. <i>BMC Genomics</i> , 2019, 20, 1020.	1.2	26
10588	Root system traits impact early fire blight susceptibility in apple ( <i>Malus domestica</i> ). <i>BMC Plant Biology</i> , 2019, 19, 579.	1.6	12

#	ARTICLE	IF	CITATIONS
10589	Differential alternative splicing regulation among hepatocellular carcinoma with different risk factors. <i>BMC Medical Genomics</i> , 2019, 12, 175.	0.7	11
10590	CDK1 and CCNB1 as potential diagnostic markers of rhabdomyosarcoma: validation following bioinformatics analysis. <i>BMC Medical Genomics</i> , 2019, 12, 198.	0.7	24
10591	Systematic analysis of gene expression profiles reveals prognostic stratification and underlying mechanisms for muscle-invasive bladder cancer. <i>Cancer Cell International</i> , 2019, 19, 337.	1.8	12
10592	Identification of diagnostic biomarkers in patients with gestational diabetes mellitus based on transcriptome gene expression and methylation correlation analysis. <i>Reproductive Biology and Endocrinology</i> , 2019, 17, 112.	1.4	12
10593	The regulatory effect of microRNA-21a-3p on the promotion of telocyte angiogenesis mediated by PI3K (p110I $\alpha$ )/AKT/mTOR in LPS induced mice ARDS. <i>Journal of Translational Medicine</i> , 2019, 17, 427.	1.8	26
10594	Genetic perturbations of disease risk genes in mice capture transcriptomic signatures of late-onset Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2019, 14, 50.	4.4	31
10595	Nuclear factor erythroid 2-related factor 2 and its relationship with cellular response in nickel exposure: a systems biology analysis. <i>BMC Pharmacology &amp; Toxicology</i> , 2019, 20, 78.	1.0	5
10596	PyRates: A Python framework for rate-based neural simulations. <i>PLoS ONE</i> , 2019, 14, e0225900.	1.1	11
10597	Comparison of tumour and serum specific microRNA changes dissecting their role in pancreatic ductal adenocarcinoma: a meta-analysis. <i>BMC Cancer</i> , 2019, 19, 1175.	1.1	16
10598	EGFR mutation: novel prognostic factor associated with immune infiltration in lower-grade glioma; an exploratory study. <i>BMC Cancer</i> , 2019, 19, 1184.	1.1	34
10599	Global analysis of lysine succinylation in patchouli plant leaves. <i>Horticulture Research</i> , 2019, 6, 133.	2.9	17
10600	In silico prediction of high-resolution Hi-C interaction matrices. <i>Nature Communications</i> , 2019, 10, 5449.	5.8	46
10601	Acyl ethanolamides in Diabetes and Diabetic Nephropathy: Novel targets from untargeted plasma metabolomic profiles of South Asian Indian men. <i>Scientific Reports</i> , 2019, 9, 18117.	1.6	12
10602	Statistical characteristics of amino acid covariance as possible descriptors of viral genomic complexity. <i>Scientific Reports</i> , 2019, 9, 18410.	1.6	7
10603	<i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> communication in biofilm infections: insights through network and database construction. <i>Critical Reviews in Microbiology</i> , 2019, 45, 712-728.	2.7	20
10604	Integration of Gene Expression Profile Data of Human Epicardial Adipose Tissue from Coronary Artery Disease to Verification of Hub Genes and Pathways. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	14
10605	Acquisition of Invasiveness by Breast Adenocarcinoma Cells Engages Established Hallmarks and Novel Regulatory Mechanisms. <i>Cancer Genomics and Proteomics</i> , 2019, 16, 505-518.	1.0	2
10606	Identification of Homeobox Genes Associated with Lignification and Their Expression Patterns in Bamboo Shoots. <i>Biomolecules</i> , 2019, 9, 862.	1.8	15

#	ARTICLE	IF	CITATIONS
10607	Effect of Ethylene on Cell Wall and Lipid Metabolism during Alleviation of Postharvest Chilling Injury in Peach. <i>Cells</i> , 2019, 8, 1612.	1.8	51
10608	Profiles of Long Non-Coding RNAs and mRNA Expression in Human Macrophages Regulated by Interleukin-27. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6207.	1.8	12
10609	An Integrated Pan-Cancer Analysis and Structure-Based Virtual Screening of GPR15. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6226.	1.8	15
10610	Mechanistic Insights into the Effect of Ligands on Structural Stability and Selectivity of Sulfotransferase 2A1 (SULT2A1). <i>ACS Omega</i> , 2019, 4, 22021-22034.	1.6	18
10611	3 $\beta$ , 6 $\beta$ -dichloro-5 $\alpha$ -cholestane facilitates neuronal development through modulating TrkA signaling regulated proteins in primary hippocampal neuron. <i>Scientific Reports</i> , 2019, 9, 18919.	1.6	11
10612	Circulating proteomic signature of early death in heart failure patients with reduced ejection fraction. <i>Scientific Reports</i> , 2019, 9, 19202.	1.6	21
10613	Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver. <i>Scientific Reports</i> , 2019, 9, 19195.	1.6	46
10614	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25900-25908.	3.3	165
10615	Evolution and Diversity of Assembly-Line Polyketide Synthases. <i>Chemical Reviews</i> , 2019, 119, 12524-12547.	23.0	178
10616	Pan-cancer molecular subtypes revealed by mass-spectrometry-based proteomic characterization of more than 500 human cancers. <i>Nature Communications</i> , 2019, 10, 5679.	5.8	358
10617	Construction of an miRNA-mRNA regulatory network in colorectal cancer with bioinformatics methods. <i>Anti-Cancer Drugs</i> , 2019, 30, 588-595.	0.7	8
10618	Inflammation Promotes Progression of Pancreatic Cancer Through WNT/ $\beta$ -Catenin Pathway-Dependent Manner. <i>Pancreas</i> , 2019, 48, 1003-1014.	0.5	16
10619	A Circulating miRNA-Based Scoring System Established by WGCNA to Predict Colon Cancer. <i>Analytical Cellular Pathology</i> , 2019, 2019, 1-7.	0.7	7
10620	PAX8 expression in high-grade serous ovarian cancer positively regulates attachment to ECM via Integrin $\beta$ 3. <i>Cancer Cell International</i> , 2019, 19, 303.	1.8	27
10621	Transcriptome Analysis of Wheat Roots Reveals a Differential Regulation of Stress Responses Related to Arbuscular Mycorrhizal Fungi and Soil Disturbance. <i>Biology</i> , 2019, 8, 93.	1.3	22
10622	Interactions of pharmaceutical companies with world countries, cancers and rare diseases from Wikipedia network analysis. <i>PLoS ONE</i> , 2019, 14, e0225500.	1.1	1
10623	Induction of an Alternative mRNA 5' Leader Enhances Translation of the Ciliopathy Gene Inpp5e and Resistance to Oncolytic Virus Infection. <i>Cell Reports</i> , 2019, 29, 4010-4023.e5.	2.9	15
10624	Cisplatin treatment of testicular cancer patients introduces long-term changes in the epigenome. <i>Clinical Epigenetics</i> , 2019, 11, 179.	1.8	18

#	ARTICLE	IF	CITATIONS
10625	Global Transcriptomic Analysis of the Canine corpus luteum (CL) During the First Half of Diestrus and Changes Induced by in vivo Inhibition of Prostaglandin Synthase 2 (PTGS2/COX2). <i>Frontiers in Endocrinology</i> , 2019, 10, 715.	1.5	6
10626	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 2558.	1.5	16
10627	Distinct Coastal Microbiome Populations Associated With Autochthonous- and Allochthonous-Like Dissolved Organic Matter. <i>Frontiers in Microbiology</i> , 2019, 10, 2579.	1.5	16
10628	Spatial sorting enables comprehensive characterization of liver zonation. <i>Nature Metabolism</i> , 2019, 1, 899-911.	5.1	125
10629	Characteristic dysbiosis of gut microbiota of Chinese patients with diarrhea-predominant irritable bowel syndrome by an insight into the pan-microbiome. <i>Chinese Medical Journal</i> , 2019, 132, 889-904.	0.9	32
10630	Screening and identification of key biomarkers in nasopharyngeal carcinoma. <i>Medicine (United States)</i> , 2019, 98, e17997.	0.4	18
10631	Two precision medicine predictive tools for six malignant solid tumors: from gene-based research to clinical application. <i>Journal of Translational Medicine</i> , 2019, 17, 405.	1.8	19
10632	Identification of a Tumor Microenvironment-Related Eight-Gene Signature for Predicting Prognosis in Lower-Grade Gliomas. <i>Frontiers in Genetics</i> , 2019, 10, 1143.	1.1	29
10633	Culture-Dependent and -Independent Analyses Reveal the Diversity, Structure, and Assembly Mechanism of Benthic Bacterial Community in the Ross Sea, Antarctica. <i>Frontiers in Microbiology</i> , 2019, 10, 2523.	1.5	19
10634	Oncoviruses Can Drive Cancer by Rewiring Signaling Pathways Through Interface Mimicry. <i>Frontiers in Oncology</i> , 2019, 9, 1236.	1.3	28
10635	Nordic Artificial Intelligence Research and Development. <i>Communications in Computer and Information Science</i> , 2019, , .	0.4	1
10636	Bioinformatics analysis of differentially expressed genes involved in human developmental chondrogenesis. <i>Medicine (United States)</i> , 2019, 98, e16240.	0.4	6
10637	Identification of Key Genes and Prognostic Value Analysis in Hepatocellular Carcinoma by Integrated Bioinformatics Analysis. <i>International Journal of Genomics</i> , 2019, 2019, 1-21.	0.8	16
10638	Metabolic rewiring of the hypertensive kidney. <i>Science Signaling</i> , 2019, 12, .	1.6	40
10639	Using lexicography to characterise relations between species mentions in the biodiversity literature. , 2019, , .		0
10640	Systems pharmacology based approach to investigate the in-vivo therapeutic efficacy of <i>Albizia lebbbeck</i> (L.) in experimental model of Parkinson's disease. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 352.	3.7	14
10641	Molecular Insights into miRNA-Driven Resistance to 5-Fluorouracil and Oxaliplatin Chemotherapy: miR-23b Modulates the Epithelial-Mesenchymal Transition of Colorectal Cancer Cells. <i>Journal of Clinical Medicine</i> , 2019, 8, 2115.	1.0	24
10642	Marine Bacteria from Rocas Atoll as a Rich Source of Pharmacologically Active Compounds. <i>Marine Drugs</i> , 2019, 17, 671.	2.2	10

#	ARTICLE	IF	CITATIONS
10643	Transcriptome-wide Profiling of Cerebral Cavernous Malformations Patients Reveal Important Long noncoding RNA molecular signatures. <i>Scientific Reports</i> , 2019, 9, 18203.	1.6	14
10644	Differential gene expression among three sex types reveals a MALE STERILITY 1 (CpMS1) for sex differentiation in papaya. <i>BMC Plant Biology</i> , 2019, 19, 545.	1.6	12
10645	<p>&lt;p>&gt;Activation of ATM-c-IAP1 Pathway Mediates the Protective Effects of Estradiol in Human Vascular Endothelial Cells Exposed to Intermittent Hypoxia&lt;/p>&lt;/p>. <i>Nature and Science of Sleep</i> , 2019, Volume 11, 357-366.	1.4	0
10646	The Differential Role of Central and Bridge Symptoms in Deactivating Psychopathological Networks. <i>Frontiers in Psychology</i> , 2019, 10, 2448.	1.1	45
10647	Transcriptome of Chicken Liver Tissues Reveals the Candidate Genes and Pathways Responsible for Adaptation into Two Different Climatic Conditions. <i>Animals</i> , 2019, 9, 1076.	1.0	10
10648	Cracks Reinforce the Interactions among Soil Bacterial Communities in the Coal Mining Area of Loess Plateau, China. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 4892.	1.2	12
10649	A Bioinformatic Approach for the Identification of Molecular Determinants of Resistance/Sensitivity to Cancer Thermo-therapy. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-13.	1.9	7
10650	&lt;p>&lt;p>&gt;Integrated Analysis To Identify Molecular Biomarkers Of High-Grade Serous Ovarian Cancer&lt;/p>&lt;/p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 10057-10075.	1.0	4
10651	<p><p>< p>Weighted Gene Co-Expression Network Analysis Identified Cancer Cell Proliferation as a Common Phenomenon During Perineural Invasion</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 10361-10374.	1.0	12
10652	Common Neurodegeneration-Associated Proteins Are Physiologically Expressed by Human B Lymphocytes and Are Interconnected via the Inflammation/Autophagy-Related Proteins TRAF6 and SQSTM1. <i>Frontiers in Immunology</i> , 2019, 10, 2704.	2.2	13
10653	Transcriptome Meta-Analysis Deciphers a Dysregulation in Immune Response-Associated Gene Signatures during Sepsis. <i>Genes</i> , 2019, 10, 1005.	1.0	26
10654	Quantitative Proteomic Analysis Uncovers the Mediation of Endoplasmic Reticulum Stress-Induced Autophagy in DHAV-1-Infected DEF Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6160.	1.8	12
10655	DeSUMOylase SENP7-Mediated Epithelial Signaling Triggers Intestinal Inflammation via Expansion of Gamma-Delta T Cells. <i>Cell Reports</i> , 2019, 29, 3522-3538.e7.	2.9	43
10656	Alterations of the interactome of Bcl-2 proteins in breast cancer at the transcriptional, mutational and structural level. <i>PLoS Computational Biology</i> , 2019, 15, e1007485.	1.5	42
10657	Biological Network Approach for the Identification of Regulatory Long Non-Coding RNAs Associated With Metabolic Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 1130.	1.1	34
10658	Dissecting the Role of NF- $\kappa$ B Protein Family and Its Regulators in Rheumatoid Arthritis Using Weighted Gene Co-Expression Network. <i>Frontiers in Genetics</i> , 2019, 10, 1163.	1.1	18
10659	Bioinformatic analysis of peripheral blood RNA-sequencing sensitively detects the cause of late graft loss following overt hyperglycemia in pig-to-nonhuman primate islet xenotransplantation. <i>Scientific Reports</i> , 2019, 9, 18835.	1.6	4
10660	Transcriptome sequencing of <i>Saccharina japonica</i> sporophytes during whole developmental periods reveals regulatory networks underlying alginate and mannitol biosynthesis. <i>BMC Genomics</i> , 2019, 20, 975.	1.2	32

#	ARTICLE	IF	CITATIONS
10661	Dysregulation of MicroRNA Regulatory Network in Lower Extremities Arterial Disease. <i>Frontiers in Genetics</i> , 2019, 10, 1200.	1.1	22
10662	A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. <i>Nature Neuroscience</i> , 2019, 22, 2087-2097.	7.1	591
10663	Peripheral blood mononuclear cell transcriptomes reveal an over-representation of down-regulated genes associated with immunity in HIV-exposed uninfected infants. <i>Scientific Reports</i> , 2019, 9, 18124.	1.6	8
10664	Comparative Network Pharmacology Analysis of Classical TCM Prescriptions for Chronic Liver Disease. <i>Frontiers in Pharmacology</i> , 2019, 10, 1353.	1.6	25
10665	Whole Genome Expression Analyses of miRNAs and mRNAs Suggest the Involvement of miR-320a and miR-155-3p and their Targeted Genes in Lithium Response in Bipolar Disorder. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6040.	1.8	28
10666	Soil pH is the primary factor driving the distribution and function of microorganisms in farmland soils in northeastern China. <i>Annals of Microbiology</i> , 2019, 69, 1461-1473.	1.1	125
10667	A generic workflow for Single Locus Sequence Typing (SLST) design and subspecies characterization of microbiota. <i>Scientific Reports</i> , 2019, 9, 19834.	1.6	12
10668	An integrated metabolomics and 16S rRNA gene sequencing approach exploring the molecular pathways and potential targets behind the effects of <i>Radix Scrophulariae</i> . <i>RSC Advances</i> , 2019, 9, 33354-33367.	1.7	3
10669	Screening of molecular targets and construction of a ceRNA network for oxaliplatin resistance in colorectal cancer. <i>RSC Advances</i> , 2019, 9, 31413-31424.	1.7	2
10670	Sparganin A alleviates blood stasis syndrome and its key targets by molecular docking. <i>RSC Advances</i> , 2019, 9, 37978-37985.	1.7	4
10671	&lt;p&gt;Super-Enhancer-Associated Hub Genes In Chronic Myeloid Leukemia Identified Using Weighted Gene Co-Expression Network Analysis&lt;/p&gt;. <i>Cancer Management and Research</i> , 2019, Volume 11, 10705-10718.	0.9	13
10672	De novo sequencing of the transcriptome reveals regulators of the floral transition in <i>Fargesia macclureana</i> (Poaceae). <i>BMC Genomics</i> , 2019, 20, 1035.	1.2	8
10673	Metabolomic and metallomic profile differences between Veterans and Civilians with Pulmonary Sarcoidosis. <i>Scientific Reports</i> , 2019, 9, 19584.	1.6	13
10674	Utilizing network pharmacology to explore the underlying mechanism of <i>Radix Salviae</i> in diabetic retinopathy. <i>Chinese Medicine</i> , 2019, 14, 58.	1.6	23
10675	A systems biology approach uncovers a gene co-expression network associated with cell wall degradability in maize. <i>PLoS ONE</i> , 2019, 14, e0227011.	1.1	2
10676	Dynamic perspectives into the mechanisms of mutation-induced p53 DNA binding loss and inactivation using active perturbation theory: Structural and molecular insights toward the design of potent reactivators in cancer therapy. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 951-966.	1.2	18
10677	Understanding and predicting disease relationships through similarity fusion. <i>Bioinformatics</i> , 2019, 35, 1213-1220.	1.8	13
10678	Resistance mechanism of the oncogenic $\Delta 23$ deletion mutation in <i>BRAF</i> kinase to dabrafenib and vemurafenib revealed by molecular dynamics simulations and binding free energy calculations. <i>Chemical Biology and Drug Design</i> , 2019, 93, 177-187.	1.5	6



#	ARTICLE	IF	CITATIONS
10679	Shared co-expression networks in frontal cortex of the normal aged brain and schizophrenia. <i>Schizophrenia Research</i> , 2019, 204, 253-261.	1.1	6
10680	Comparative comprehension on the anti-rheumatic Chinese herbal medicine <i>Siegesbeckiae Herba</i> : Combined computational predictions and experimental investigations. <i>Journal of Ethnopharmacology</i> , 2019, 228, 200-209.	2.0	22
10681	Global Networks of Symbiodinium-Bacteria Within the Coral Holobiont. <i>Microbial Ecology</i> , 2019, 77, 794-807.	1.4	43
10682	IL-17A is functionally relevant and a potential therapeutic target in bullous pemphigoid. <i>Journal of Autoimmunity</i> , 2019, 96, 104-112.	3.0	85
10683	Revealing Clusters of Connected Pathways Through Multisource Data Integration in Huntington's Disease and Spastic Ataxia. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 26-37.	3.9	18
10684	Seed mucilage interacts with soil microbial community and physiochemical processes to affect seedling emergence on desert sand dunes. <i>Plant, Cell and Environment</i> , 2019, 42, 591-605.	2.8	18
10686	Preliminary results from structural systems biology approach in <i>Tetrahymena thermophila</i> reveal novel perspectives for this toxicological model. <i>Archives of Microbiology</i> , 2019, 201, 51-59.	1.0	8
10687	A novel phylogenetic tree based on the presence of protein domains in selected actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 101-107.	0.7	7
10688	Integrated proteomic analysis of tumor necrosis factor $\alpha$ and interleukin $1\beta$ -induced endothelial inflammation. <i>Journal of Proteomics</i> , 2019, 192, 89-101.	1.2	17
10689	Computational systems pharmacology analysis of cannabidiol: a combination of chemogenomics-knowledgebase network analysis and integrated in silico modeling and simulation. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 374-386.	2.8	34
10690	Identification of differentially expressed genes and signaling pathways using bioinformatics in interstitial lung disease due to tyrosine kinase inhibitors targeting the epidermal growth factor receptor. <i>Investigational New Drugs</i> , 2019, 37, 384-400.	1.2	8
10691	<i>Oryza sativa</i> class III peroxidase (OsPRX38) overexpression in <i>Arabidopsis thaliana</i> reduces arsenic accumulation due to apoplastic lignification. <i>Journal of Hazardous Materials</i> , 2019, 362, 383-393.	6.5	88
10692	MicroRNA-488 inhibits progression of colorectal cancer via inhibition of the mitogen-activated protein kinase pathway by targeting claudin-2. <i>American Journal of Physiology - Cell Physiology</i> , 2019, 316, C33-C47.	2.1	30
10693	Modulation of specific cell cycle phases in human embryonic stem cells by lncRNA RNA decoys. <i>Journal of Molecular Recognition</i> , 2019, 32, e2763.	1.1	5
10694	Integrated analysis of in vitro data and the adverse outcome pathway framework for prioritization and regulatory applications: An exploratory case study using publicly available data on piperonyl butoxide and liver models. <i>Toxicology in Vitro</i> , 2019, 54, 23-32.	1.1	11
10695	A comparative system-level analysis of the neurodegenerative diseases. <i>Journal of Cellular Physiology</i> , 2019, 234, 5215-5229.	2.0	6
10696	Changes in the urinary extracellular vesicle proteome are associated with nephronophthisis-related ciliopathies. <i>Journal of Proteomics</i> , 2019, 192, 27-36.	1.2	22
10697	A novel seven-lncRNA signature for prognosis prediction in hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 213-223.	1.2	55



#	ARTICLE	IF	CITATIONS
10698	Insights into the role of amino acid oxidase mutations in amyotrophic lateral sclerosis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 2180-2197.	1.2	11
10699	Downregulation of AC061961.2, LINGO1 and RP11-13E1.5 is associated with dilated cardiomyopathy progression. <i>Journal of Cellular Physiology</i> , 2019, 234, 4460-4471.	2.0	20
10700	Covalent vs. Non-Covalent Inhibition: Tackling Drug Resistance in EGFR – A Thorough Dynamic Perspective. <i>Chemistry and Biodiversity</i> , 2019, 16, e1800518.	1.0	8
10701	Cross-ID: Analysis and Visualization of Complex XL-MS-Driven Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2019, 18, 642-651.	1.8	13
10702	Identification and epigenetic analysis of divergent long non-coding RNAs in multilineage differentiation of human Neural Progenitor Cells. <i>RNA Biology</i> , 2019, 16, 13-24.	1.5	16
10703	Genome-Wide Identification and Comparative Analysis for OPT Family Genes in Panax ginseng and Eleven Flowering Plants. <i>Molecules</i> , 2019, 24, 15.	1.7	20
10704	The bacterial and fungal microbiome of the skin of healthy dogs and dogs with atopic dermatitis and the impact of topical antimicrobial therapy, an exploratory study. <i>Veterinary Microbiology</i> , 2019, 229, 90-99.	0.8	46
10705	Genomic characterization of cervical cancer based on human papillomavirus status. <i>Gynecologic Oncology</i> , 2019, 152, 629-637.	0.6	31
10706	Erythrocyte PUFAs, circulating acylcarnitines, and metabolic syndrome risk: a prospective study in Chinese. <i>Journal of Lipid Research</i> , 2019, 60, 421-429.	2.0	10
10707	The underlying pathophysiology association between the Type 2 diabetic and hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 10835-10841.	2.0	12
10708	Camphor white oil induces tumor regression through cytotoxic T cell-dependent mechanisms. <i>Molecular Carcinogenesis</i> , 2019, 58, 722-734.	1.3	22
10709	Exogenous interleukin-1 $\beta$ signaling negatively impacts acquired chemoresistance and alters cell adhesion molecule expression pattern in colorectal carcinoma cells HCT116. <i>Cytokine</i> , 2019, 114, 38-46.	1.4	4
10710	Structural Evidence for Dimer-Interface-Driven Regulation of the Type II Cysteine Desulfurase, SufS. <i>Biochemistry</i> , 2019, 58, 687-696.	1.2	20
10711	Identifying Driver Interfaces Enriched for Somatic Missense Mutations in Tumors. <i>Methods in Molecular Biology</i> , 2019, 1907, 51-72.	0.4	4
10712	Unraveling gut microbiota in Parkinson's disease and atypical parkinsonism. <i>Movement Disorders</i> , 2019, 34, 396-405.	2.2	252
10713	Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect. <i>DNA Research</i> , 2019, 26, 119-130.	1.5	21
10714	Mapping the Ku Interactome Using Proximity-Dependent Biotin Identification in Human Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1064-1077.	1.8	33
10715	Using OmicsNet for Network Integration and 3D Visualization. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e69.	25.8	44

#	ARTICLE	IF	CITATIONS
10716	Dual Regulatory Functions of SUFU and Targetome of GLI2 in SHH Subgroup Medulloblastoma. <i>Developmental Cell</i> , 2019, 48, 167-183.e5.	3.1	39
10717	Iron-associated protein interaction networks reveal the key functional modules related to survival and virulence of <i>Pasteurella multocida</i> . <i>Microbial Pathogenesis</i> , 2019, 127, 257-266.	1.3	4
10718	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 145, 19-39.	1.4	15
10719	A standardization process for mental model analysis in socio-ecological systems. <i>Environmental Modelling and Software</i> , 2019, 112, 108-111.	1.9	7
10720	River Ganges water as reservoir of microbes with antibiotic and metal ion resistance genes: High throughput metagenomic approach. <i>Environmental Pollution</i> , 2019, 246, 443-451.	3.7	105
10721	Full title: Identification of potential drug targets against carbapenem resistant Enterobacteriaceae (CRE) strains using in silico gene network analysis. <i>Gene Reports</i> , 2019, 14, 129-137.	0.4	6
10722	Profile analysis of circRNAs induced by porcine endemic diarrhea virus infection in porcine intestinal epithelial cells. <i>Virology</i> , 2019, 527, 169-179.	1.1	36
10723	Novel Modified Vaccinia Virus Ankara Vector Expressing Anti-apoptotic Gene B13R Delays Apoptosis and Enhances Humoral Responses. <i>Journal of Virology</i> , 2019, 93, .	1.5	10
10724	Tools for 3D Interactome Visualization. <i>Journal of Proteome Research</i> , 2019, 18, 753-758.	1.8	26
10725	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 447-458.	5.9	68
10726	Prediction of MicroRNAs in the Epstein-Barr Virus Reveals Potential Targets for the Viral Self-Regulation. <i>Indian Journal of Microbiology</i> , 2019, 59, 73-80.	1.5	2
10727	Interrogation of genome-wide networks in biology: comparison of knowledge-based and statistical methods. <i>International Journal of Advances in Engineering Sciences and Applied Mathematics</i> , 2019, 11, 119-137.	0.7	5
10728	Bacterial community analysis of marine recirculating aquaculture system bioreactors for complete nitrogen removal established from a commercial inoculum. <i>Aquaculture</i> , 2019, 503, 198-206.	1.7	53
10729	MicroRNA-384 inhibits the progression of esophageal squamous cell carcinoma through blockade of the LIMK1/cofilin signaling pathway by binding to LIMK1. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 751-761.	2.5	10
10730	Comparative transcriptome analysis identifies genes associated with papilla development in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 255-263.	0.4	4
10731	The phosphoenolpyruvate carboxylase gene family identification and expression analysis under abiotic and phytohormone stresses in <i>Solanum lycopersicum</i> L. <i>Gene</i> , 2019, 690, 11-20.	1.0	27
10732	Combining genome-wide association analyses and gene interaction networks to reveal new genes associated with carcass traits, meat quality and fatty acid profiles in pigs. <i>Livestock Science</i> , 2019, 220, 180-189.	0.6	8
10733	Culturomics-Based Taxonomic Diversity of Bacterial Communities in the Hot Springs of Saudi Arabia. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 17-27.	1.0	13

#	ARTICLE	IF	CITATIONS
10734	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019, 29, 223-235.	2.4	46
10735	Single-cell RNA-Seq of follicular lymphoma reveals malignant B-cell types and coexpression of T-cell immune checkpoints. <i>Blood</i> , 2019, 133, 1119-1129.	0.6	99
10736	A Blueprint for Systems Biology. <i>Clinical Chemistry</i> , 2019, 65, 342-344.	1.5	6
10737	Clinically Relevant Post-Translational Modification Analysesâ€”Maturing Workflows and Bioinformatics Tools. <i>International Journal of Molecular Sciences</i> , 2019, 20, 16.	1.8	50
10738	E2F7, EREG, miR-451a and miR-106b-5p are associated with the cervical cancer development. <i>Archives of Gynecology and Obstetrics</i> , 2019, 299, 1089-1098.	0.8	23
10739	Interactome of the yeast RNA polymerase III transcription machinery constitutes several chromatin modifiers and regulators of the genes transcribed by RNA polymerase II. <i>Gene</i> , 2019, 702, 205-214.	1.0	8
10740	Genome reconstruction of a novel carbohydrate digesting bacterium from the chicken caecal microflora. <i>Meta Gene</i> , 2019, 20, 100543.	0.3	11
10741	Differential co-occurrence relationships shaping ecotype diversification within <i>Thaumarchaeota</i> populations in the coastal ocean water column. <i>ISME Journal</i> , 2019, 13, 1144-1158.	4.4	80
10742	Identification of potential miRNAâ€”mRNA regulatory network contributing to pathogenesis of HBV-related HCC. <i>Journal of Translational Medicine</i> , 2019, 17, 7.	1.8	103
10743	Effects of the Wastewater Flow Rate on Interactions between the Genus <i>Nitrosomonas</i> and Diverse Populations in an Activated Sludge Microbiome. <i>Microbes and Environments</i> , 2019, 34, 89-94.	0.7	6
10744	IRAK3 gene silencing prevents cardiac rupture and ventricular remodeling through negative regulation of the NF- $\kappa$ B signaling pathway in a mouse model of acute myocardial infarction. <i>Journal of Cellular Physiology</i> , 2019, 234, 11722-11733.	2.0	19
10745	Mapping loci controlling fatty acid profiles, oil and protein content by genome-wide association study in <i>Brassica napus</i> . <i>Crop Journal</i> , 2019, 7, 217-226.	2.3	19
10746	Alterations in serum amino-acid profile in the progression of colorectal cancer: associations with systemic inflammation, tumour stage and patient survival. <i>British Journal of Cancer</i> , 2019, 120, 238-246.	2.9	54
10747	Evolutionary dynamics of specialisation in herbivorous stick insects. <i>Ecology Letters</i> , 2019, 22, 354-364.	3.0	8
10748	RNA-seq Analysis of the SCN1A-KO Model based on CRISPR/Cas9 Genome Editing Technology. <i>Neuroscience</i> , 2019, 398, 1-11.	1.1	15
10749	PPIExp: A Web-Based Platform for Integration and Visualization of Proteinâ€”Protein Interaction Data and Spatiotemporal Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 633-641.	1.8	8
10751	TriPOINT: a software tool to prioritize important genes in pathways and their non-coding regulators. <i>Bioinformatics</i> , 2019, 35, 2686-2689.	1.8	0
10752	Genome-Wide Expression Profiling Unveils Autoimmune Response Signatures in the Perivascular Adipose Tissue of Abdominal Aortic Aneurysm. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 237-249.	1.1	35

#	ARTICLE	IF	CITATIONS
10753	The protein interaction networks of mucolipins and two-pore channels. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 1111-1123.	1.9	28
10754	Function and Compensatory Mechanisms Among the Components of the Chloroplastic Redox Network. <i>Critical Reviews in Plant Sciences</i> , 2019, 38, 1-28.	2.7	14
10755	Molecular Correlates of Metastasis by Systematic Pan-Cancer Analysis Across The Cancer Genome Atlas. <i>Molecular Cancer Research</i> , 2019, 17, 476-487.	1.5	28
10756	A Competing Endogenous RNA Network Reveals Novel Potential lncRNA, miRNA, and mRNA Biomarkers in the Prognosis of Human Colon Adenocarcinoma. <i>Journal of Surgical Research</i> , 2019, 235, 22-33.	0.8	47
10757	Integrated analysis of pseudogene <i>RP11-564D11.3</i> expression and its potential roles in hepatocellular carcinoma. <i>Epigenomics</i> , 2019, 11, 267-280.	1.0	17
10758	Analysis of Brassica napus dehydrins and their Co-Expression regulatory networks in relation to cold stress. <i>Gene Expression Patterns</i> , 2019, 31, 7-17.	0.3	19
10759	CXCR6 protects from inflammation and fibrosis in NEMOLPC-KO mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 391-402.	1.8	14
10760	Integrative meta-analysis of publically available microarray datasets of several epithelial cell lines identifies biological processes affected by silver nanoparticles exposure. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2019, 216, 67-74.	1.3	6
10761	Transcriptome monitoring visualizes growth stage-dependent nutrient status dynamics in rice under field conditions. <i>Plant Journal</i> , 2019, 97, 1048-1060.	2.8	21
10762	Identification and characterization of the zebra finch ( <i>Taeniopygia guttata</i> ) sperm proteome. <i>Journal of Proteomics</i> , 2019, 193, 192-204.	1.2	10
10763	Flax rhamnogalacturonan lyases: phylogeny, differential expression and modeling of protein structure. <i>Physiologia Plantarum</i> , 2019, 167, 173-187.	2.6	19
10764	Multi-tissue integration of transcriptomic and specialized metabolite profiling provides tools for assessing the common bean ( <i>Phaseolus vulgaris</i> ) metabolome. <i>Plant Journal</i> , 2019, 97, 1132-1153.	2.8	33
10765	Reduced plasma levels of small HDL particles transporting fibrinolytic proteins in pulmonary arterial hypertension. <i>Thorax</i> , 2019, 74, 380-389.	2.7	34
10766	Profiling of indole metabolic pathway in thermo-sensitive Bainong male sterile line in wheat ( <i>Triticum</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	1.4	14
10767	A molecular dynamics based investigation reveals the role of rare Ribonuclease 4 variants in amyotrophic lateral sclerosis susceptibility. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2019, 813, 1-12.	0.4	6
10768	Dissecting the Genomic Diversification of Late Embryogenesis Abundant (LEA) Protein Gene Families in Plants. <i>Genome Biology and Evolution</i> , 2019, 11, 459-471.	1.1	102
10769	A Network Analysis of Biomarkers for Type 2 Diabetes. <i>Diabetes</i> , 2019, 68, 281-290.	0.3	28
10770	Assembly of the $\beta$ 24-Integrin Interactome Based on Proximal Biotinylation in the Presence and Absence of Heterodimerization*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 277-293.	2.5	19

#	ARTICLE	IF	CITATIONS
10771	Adaptive shifts of bacterioplankton communities in response to nitrogen enrichment in a highly polluted river. <i>Environmental Pollution</i> , 2019, 245, 290-299.	3.7	55
10772	Esrrb plays important roles in maintaining self-renewal of trophoblast stem cells (TSCs) and reprogramming somatic cells to induced TSCs. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 463-473.	1.5	19
10773	Fragile X syndrome and connective tissue dysregulation. <i>Clinical Genetics</i> , 2019, 95, 262-267.	1.0	25
10774	Repurposing of Approved Cardiovascular Drugs against Ischemic Cerebrovascular Disease by Disease-Associated Network-Assisted Prediction. <i>Chemical and Pharmaceutical Bulletin</i> , 2019, 67, 32-40.	0.6	4
10775	Genetic engineering of indica rice with AtDREB1A gene for enhanced abiotic stress tolerance. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 136, 173-188.	1.2	11
10776	Proteins Altered by Surgical Weight Loss Highlight Biomarkers of Insulin Resistance in the Community. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 107-115.	1.1	20
10777	Rare copy number variation in extremely impulsively violent males. <i>Genes, Brain and Behavior</i> , 2019, 18, e12536.	1.1	9
10778	Systems pharmacology approach to investigate the molecular mechanisms of herb <i>Rhodiola rosea</i> L. radix. <i>Drug Development and Industrial Pharmacy</i> , 2019, 45, 456-464.	0.9	10
10779	Genes and transcription factors related to the adverse effects of maternal type I diabetes mellitus on fetal development. <i>Molecular and Cellular Probes</i> , 2019, 43, 64-71.	0.9	0
10780	Comprehensive analysis of tumor immune infiltration associated with endogenous competitive RNA networks in lung adenocarcinoma. <i>Pathology Research and Practice</i> , 2019, 215, 159-170.	1.0	36
10781	Block alignment: New representation and comparison method to study evolution of genomes. <i>Genomics</i> , 2019, 111, 1590-1603.	1.3	1
10782	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632.	1.8	1,228
10783	Phylogenetic, molecular evolution and structural analyses of the WFDC1/prostate stromal protein 20 (ps20). <i>Gene</i> , 2019, 686, 125-140.	1.0	3
10784	Metabolite systems profiling identifies exploitable weaknesses in retinoblastoma. <i>FEBS Letters</i> , 2019, 593, 23-41.	1.3	11
10785	Identification and characterization of circular RNAs involved in mechanical force-induced periodontal ligament stem cells. <i>Journal of Cellular Physiology</i> , 2019, 234, 10166-10177.	2.0	34
10786	Ten Years with New Delhi Metallo- $\beta$ -lactamase-1 (NDM-1): From Structural Insights to Inhibitor Design. <i>ACS Infectious Diseases</i> , 2019, 5, 9-34.	1.8	123
10787	Sunflower resistance to multiple downy mildew pathotypes revealed by recognition of conserved effectors of the oomycete <i>Plasmopara halstedii</i> . <i>Plant Journal</i> , 2019, 97, 730-748.	2.8	74
10788	Bioprospecting Reveals Class III $\gamma$ -Transaminases Converting Bulky Ketones and Environmentally Relevant Polyamines. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	17

#	ARTICLE	IF	CITATIONS
10789	Probing the Dynamic Mechanism of Uncommon Allosteric Inhibitors Optimized to Enhance Drug Selectivity of SHP2 with Therapeutic Potential for Cancer Treatment. <i>Applied Biochemistry and Biotechnology</i> , 2019, 188, 260-281.	1.4	11
10790	New insights into host adaptation to swine respiratory disease revealed by genetic differentiation and RNA sequencing analyses. <i>Evolutionary Applications</i> , 2019, 12, 535-548.	1.5	7
10791	Alterations in the gut microbiota and metabolite profiles of thyroid carcinoma patients. <i>International Journal of Cancer</i> , 2019, 144, 2728-2745.	2.3	72
10792	Comparative Nuclear Proteomics Analysis Provides Insight into the Mechanism of Signaling and Immune Response to Blast Disease Caused by <i>Magnaporthe oryzae</i> in Rice. <i>Proteomics</i> , 2019, 19, e1800188.	1.3	11
10793	Low expression of PDK1 inhibits renal cell carcinoma cell proliferation, migration, invasion and epithelial mesenchymal transition through inhibition of the PI3K-PDK1-Akt pathway. <i>Cellular Signalling</i> , 2019, 56, 1-14.	1.7	21
10794	<i>Complement C7</i> is a novel risk gene for Alzheimer's disease in Han Chinese. <i>National Science Review</i> , 2019, 6, 257-274.	4.6	55
10795	Node-Link or Adjacency Matrices: Old Question, New Insights. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019, 25, 2940-2952.	2.9	35
10796	Comparative transcriptome analysis of Ethiopian indigenous chickens from low and high altitudes under heat stress condition reveals differential immune response. <i>Animal Genetics</i> , 2019, 50, 42-53.	0.6	23
10797	ERR $\alpha$ promotes breast cancer cell dissemination to bone by increasing RANK expression in primary breast tumors. <i>Oncogene</i> , 2019, 38, 950-964.	2.6	25
10798	Wnt and BMP signaling pathways cooperatively induce the differentiation of multiple myeloma mesenchymal stem cells into osteoblasts by upregulating EMX2. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6515-6527.	1.2	22
10799	Long non-coding RNAs influence the transcriptome in pulmonary arterial hypertension: the role of <i>PAXIP1-AS1</i> . <i>Journal of Pathology</i> , 2019, 247, 357-370.	2.1	40
10800	Plasmatic and chamber-specific modulation of cardiac microRNAs in an acute model of DOX-induced cardiotoxicity. <i>Biomedicine and Pharmacotherapy</i> , 2019, 110, 1-8.	2.5	25
10801	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	5.2	90
10802	Interactome mapping defines BRG1, a component of the SWI/SNF chromatin remodeling complex, as a new partner of the transcriptional regulator CTCF. <i>Journal of Biological Chemistry</i> , 2019, 294, 861-873.	1.6	38
10803	<i>Anxa2</i> gene silencing attenuates obesity-induced insulin resistance by suppressing the NF- $\kappa$ B signaling pathway. <i>American Journal of Physiology - Cell Physiology</i> , 2019, 316, C223-C234.	2.1	25
10804	<i>E. coli</i> gene regulatory networks are inconsistent with gene expression data. <i>Nucleic Acids Research</i> , 2019, 47, 85-92.	6.5	60
10805	Tumor-suppressive effects of microRNA-181d-5p on non-small-cell lung cancer through the CDKN3-mediated Akt signaling pathway in vivo and in vitro. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 316, L918-L933.	1.3	22
10806	Investigation of the Underlying Genes and Mechanism of Macrophage-Enriched Ruptured Atherosclerotic Plaques Using Bioinformatics Method. <i>Journal of Atherosclerosis and Thrombosis</i> , 2019, 26, 636-658.	0.9	25



#	ARTICLE	IF	CITATIONS
10807	Rbf Activates the Myogenic Transcriptional Program to Promote Skeletal Muscle Differentiation. <i>Cell Reports</i> , 2019, 26, 702-719.e6.	2.9	26
10808	Vitamin D-mediated attenuation of miR-155 in human macrophages infected with dengue virus: Implications for the cytokine response. <i>Infection, Genetics and Evolution</i> , 2019, 69, 12-21.	1.0	42
10809	Organoid-Induced Differentiation of Conventional T Cells from Human Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2019, 24, 376-389.e8.	5.2	142
10810	Ochratoxin A Exposure Impairs Porcine Granulosa Cell Growth via the PI3K/AKT Signaling Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2679-2690.	2.4	36
10811	Identification of target genes in cancer diseases using protein-protein interaction networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2019, 8, 1.	1.2	3
10812	Decoding the enigma of antiviral crisis: Does one target molecule regulate all?. <i>Cytokine</i> , 2019, 115, 13-23.	1.4	32
10813	Microarray Data Analysis of Molecular Mechanism Associated with Stroke Progression. <i>Journal of Molecular Neuroscience</i> , 2019, 67, 424-433.	1.1	6
10814	Functional divergence of annotated l-isoaspartate O-methyltransferases in an $\hat{\pm}$ -proteobacterium. <i>Journal of Biological Chemistry</i> , 2019, 294, 2854-5714.	1.6	6
10815	Dysfunctional Mechanism of Liver Cancer Mediated by Transcription Factor and Non-coding RNA. <i>Current Bioinformatics</i> , 2019, 14, 100-107.	0.7	20
10816	Structural and Phylogenetic Diversity of Anaerobic Carbon-Monoxide Dehydrogenases. <i>Frontiers in Microbiology</i> , 2018, 9, 3353.	1.5	41
10817	Qualitative assessment of functional module detectors on microarray and RNASeq data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2019, 8, 1.	1.2	12
10818	Isolation of anticancer and anti-trypanosome secondary metabolites from the endophytic fungus <i>Aspergillus flocculus</i> via bioactivity guided isolation and MS based metabolomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1106-1107, 71-83.	1.2	72
10819	An analysis of plasma reveals proteins in the acute phase response pathway to be candidate diagnostic biomarkers for depression. <i>Psychiatry Research</i> , 2019, 272, 404-410.	1.7	14
10820	Analysis of viral and bacterial communities in groundwater associated with contaminated land. <i>Science of the Total Environment</i> , 2019, 656, 1413-1426.	3.9	18
10821	Pathological priming causes developmental gene network heterochronicity in autistic subject-derived neurons. <i>Nature Neuroscience</i> , 2019, 22, 243-255.	7.1	209
10822	New mechanistic insights of clear cell renal cell carcinoma from integrated miRNA and mRNA expression profiling studies. <i>Biomedicine and Pharmacotherapy</i> , 2019, 111, 821-834.	2.5	13
10823	Co-expression networks provide insights into molecular mechanisms of postharvest temperature modulation of apple fruit to reduce superficial scald. <i>Postharvest Biology and Technology</i> , 2019, 149, 27-41.	2.9	18
10824	Elevated gibberellin enhances lignin accumulation in celery ( <i>Apium graveolens</i> L.) leaves. <i>Protoplasma</i> , 2019, 256, 777-788.	1.0	23



#	ARTICLE	IF	CITATIONS
10825	Biomarker Discovery for Immunotherapy of Pituitary Adenomas: Enhanced Robustness and Prediction Ability by Modern Computational Tools. <i>International Journal of Molecular Sciences</i> , 2019, 20, 151.	1.8	24
10826	Gene Expression Pathways across Multiple Tissues in Antineutrophil Cytoplasmic Antibody-associated Vasculitis Reveal Core Pathways of Disease Pathology. <i>Journal of Rheumatology</i> , 2019, 46, 609-615.	1.0	10
10827	Visualizing Post-Translational Modifications in Protein Interaction Networks Using PTMOracle. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e71.	25.8	3
10828	A novel long noncoding RNA AK016739 inhibits osteoblast differentiation and bone formation. <i>Journal of Cellular Physiology</i> , 2019, 234, 11524-11536.	2.0	30
10829	Building Bridges Between Structural and Network-Based Systems Biology. <i>Molecular Biotechnology</i> , 2019, 61, 221-229.	1.3	10
10830	Long noncoding RNA AK089579 inhibits epithelial-mesenchymal transition of peritoneal mesothelial cells by competitively binding to microRNA-296-3p via DOK2 in peritoneal fibrosis. <i>FASEB Journal</i> , 2019, 33, 5112-5125.	0.2	18
10831	Alteration in gut microbiota associated with hepatitis B and non-hepatitis virus related hepatocellular carcinoma. <i>Gut Pathogens</i> , 2019, 11, 1.	1.6	143
10832	A Century of Topological Coevolution of Complex Infrastructure Networks in an Alpine City. <i>Complexity</i> , 2019, 2019, 1-16.	0.9	19
10833	Bioinformatics-Based Approaches Predict That <i>MIR-17-5P</i> Functions in the Pathogenesis of Seasonal Allergic Rhinitis Through Regulating <i>ABCA1</i> and <i>CD69</i> . <i>American Journal of Rhinology and Allergy</i> , 2019, 33, 269-276.	1.0	8
10834	Systematic evaluation of <i>C. elegans</i> lincRNAs with CRISPR knockout mutants. <i>Genome Biology</i> , 2019, 20, 7.	3.8	25
10835	Protein modeling, molecular network and molecular dynamics study of newly sequenced interleukin-18 ( <i>IL-18</i> ) gene in <i>Mus musculus</i> . <i>Journal of Cellular Physiology</i> , 2019, 234, 14285-14295.	2.0	4
10836	Analysis of Protein Structures Using Residue Interaction Networks. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2019, , 55-69.	0.6	2
10837	Discovery and profiling of small RNAs from <i>Puccinia triticina</i> by deep sequencing and identification of their potential targets in wheat. <i>Functional and Integrative Genomics</i> , 2019, 19, 391-407.	1.4	37
10838	Epigenetically modulated <i>FOXM1</i> suppresses dendritic cell maturation in pancreatic cancer and colon cancer. <i>Molecular Oncology</i> , 2019, 13, 873-893.	2.1	43
10839	How Histone Deacetylase Inhibitors Alter the Secondary Metabolites of <i>Botryosphaeria mamanae</i> , an Endophytic Fungus Isolated from <i>Bixa orellana</i> . <i>Chemistry and Biodiversity</i> , 2019, 16, e1800485.	1.0	21
10840	Identification of molecular marker associated with ovarian cancer prognosis using bioinformatics analysis and experiments. <i>Journal of Cellular Physiology</i> , 2019, 234, 11023-11036.	2.0	58
10841	Integration of miRNA and mRNA Expression Data for Understanding Etiology of Gynecologic Cancers. <i>Methods in Molecular Biology</i> , 2019, 1912, 323-338.	0.4	7
10842	Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. <i>Cell Reports</i> , 2019, 26, 496-506.e3.	2.9	21

#	ARTICLE	IF	CITATIONS
10843	CCL22 is a biomarker of cartilage injury and plays a functional role in chondrocyte apoptosis. <i>Cytokine</i> , 2019, 115, 32-44.	1.4	12
10844	SWATH based quantitative proteomics analysis reveals Hfq2 play an important role on pleiotropic physiological functions in <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2019, 195, 1-10.	1.2	14
10845	Combined Single-Cell Profiling of lncRNAs and Functional Screening Reveals that H19 Is Pivotal for Embryonic Hematopoietic Stem Cell Development. <i>Cell Stem Cell</i> , 2019, 24, 285-298.e5.	5.2	96
10846	Functional annotation of orthologs in metagenomes: a case study of genes for the transformation of oceanic dimethylsulfoniopropionate. <i>ISME Journal</i> , 2019, 13, 1183-1197.	4.4	24
10847	A gene expression map of shoot domains reveals regulatory mechanisms. <i>Nature Communications</i> , 2019, 10, 141.	5.8	96
10848	Translation control of the immune checkpoint in cancer and its therapeutic targeting. <i>Nature Medicine</i> , 2019, 25, 301-311.	15.2	184
10849	PopCluster: an algorithm to identify genetic variants with ethnicity-dependent effects. <i>Bioinformatics</i> , 2019, 35, 3046-3054.	1.8	3
10850	Hepatic Gene Expression During the Perinatal Transition in the Rat. <i>Gene Expression</i> , 2019, 19, 1-13.	0.5	4
10851	The Emergence of Hubs in Complex Syntactic Networks and the DP Hypothesis: The Relevance of a Linguistic Analysis. , 2019, , 273-288.		1
10852	Identification of candidate diagnostic and prognostic biomarkers for pancreatic carcinoma. <i>EBioMedicine</i> , 2019, 40, 382-393.	2.7	93
10853	Identification of key genes and transcription factors in aging mesenchymal stem cells by DNA microarray data. <i>Gene</i> , 2019, 692, 79-87.	1.0	15
10854	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , 2019, 56, 565-583.	5.4	7
10855	Zhixiong Capsule (ZXC), a traditional Chinese patent medicine, prevents atherosclerotic plaque formation in rabbit carotid artery and the related mechanism investigation based on network pharmacology and biological research. <i>Phytomedicine</i> , 2019, 59, 152776.	2.3	9
10856	Coupled virus - bacteria interactions and ecosystem function in an engineered microbial system. <i>Water Research</i> , 2019, 152, 264-273.	5.3	31
10857	Aspartoacylase: a central nervous system enzyme. Structure, catalytic activity and regulation mechanisms. <i>Russian Chemical Reviews</i> , 2019, 88, 1-26.	2.5	7
10858	Intra-clade metabolomic profiling of MAR4 <i>Streptomyces</i> from the Macaronesia Atlantic region reveals a source of anti-biofilm metabolites. <i>Environmental Microbiology</i> , 2019, 21, 1099-1112.	1.8	31
10859	MicroRNA expression profile of HCT-8 cells in the early phase of <i>Cryptosporidium parvum</i> infection. <i>BMC Genomics</i> , 2019, 20, 37.	1.2	20
10860	Identifying Molecular Markers of Cervical Cancer Based on Competing Endogenous RNA Network Analysis. <i>Gynecologic and Obstetric Investigation</i> , 2019, 84, 350-359.	0.7	7

#	ARTICLE	IF	CITATIONS
10861	Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing. <i>BMC Genomics</i> , 2019, 20, 23.	1.2	110
10862	Identification and analysis of long non-coding RNAs in response to H5N1 influenza viruses in duck ( <i>Anas platyrhynchos</i> ). <i>BMC Genomics</i> , 2019, 20, 36.	1.2	20
10863	Aerobic midgut microbiota of sand fly vectors of zoonotic visceral leishmaniasis from northern Iran, a step toward finding potential paratransgenic candidates. <i>Parasites and Vectors</i> , 2019, 12, 10.	1.0	25
10864	Domestication and Temperature Modulate Gene Expression Signatures and Growth in the Australasian Snapper <i>Chrysophrys auratus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 105-116.	0.8	22
10865	Activation of the Bile Acid Pathway and No Observed Antimicrobial Peptide Sequences in the Skin of a Poison Frog. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 581-589.	0.8	1
10866	Characteristics of atmospheric bacterial and fungal communities in PM2.5 following biomass burning disturbance in a rural area of North China Plain. <i>Science of the Total Environment</i> , 2019, 651, 2727-2739.	3.9	71
10867	T4-type viruses: Important impacts on shaping bacterial community along a chronosequence of 2000-year old paddy soils. <i>Soil Biology and Biochemistry</i> , 2019, 128, 89-99.	4.2	18
10868	Global expression profiling and pathway analysis in two different population groups in relation to high altitude. <i>Functional and Integrative Genomics</i> , 2019, 19, 205-215.	1.4	3
10869	Comparative proteomic analysis of four biotechnological strains <i>Lactococcus lactis</i> through label-free quantitative proteomics. <i>Microbial Biotechnology</i> , 2019, 12, 265-274.	2.0	19
10870	Identifying Key Genes of Liver Cancer by Networking of Multiple Data Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 792-800.	1.9	7
10871	Integrated Succinylome and Metabolome Profiling Reveals Crucial Role of S-Ribosylhomocysteine Lyase in Quorum Sensing and Metabolism of <i>Aeromonas hydrophila</i> *. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 200-215.	2.5	45
10872	Simulated microgravity triggers characteristic morphology and stress response in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2019, 36, 85-97.	0.8	4
10873	Alteration of mesenchymal stem cells polarity by laminar shear stimulation promoting $\beta$ -catenin nuclear localization. <i>Biomaterials</i> , 2019, 190-191, 1-10.	5.7	14
10874	Resveratrol decreases the expression of genes involved in inflammation through transcriptional regulation. <i>Free Radical Biology and Medicine</i> , 2019, 130, 8-22.	1.3	37
10875	Genomic analysis of RNA-Seq and sRNA-Seq data identifies potential regulatory sRNAs and their functional roles in <i>Staphylococcus aureus</i> . <i>Genomics</i> , 2019, 111, 1431-1446.	1.3	10
10876	Molecular classification and subtype-specific drug sensitivity research of uterine carcinosarcoma under multi-omics framework. <i>Cancer Biology and Therapy</i> , 2019, 20, 227-235.	1.5	5
10877	Identification of <i>CD28</i> and <i>PTEN</i> as novel prognostic markers for cervical cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 7004-7011.	2.0	13
10878	Functional characterization of RNA fragments using high-throughput interactome screening. <i>Journal of Proteomics</i> , 2019, 193, 173-183.	1.2	6

#	ARTICLE	IF	CITATIONS
10879	Identification of Potential miRNAs Biomarkers for High-Grade Prostate Cancer by Integrated Bioinformatics Analysis. <i>Pathology and Oncology Research</i> , 2019, 25, 1445-1456.	0.9	20
10880	Evaluation of potential carcinogenicity of organic chemicals in synthetic turf crumb rubber. <i>Environmental Research</i> , 2019, 169, 163-172.	3.7	48
10881	Phenotyping analysis of the Japanese Kampo medicine maoto in healthy human subjects using wide-targeted plasma metabolomics. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 164, 119-127.	1.4	14
10882	A six-microRNA risk score model predicts prognosis in esophageal squamous cell carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 6810-6819.	2.0	18
10883	Integrative network analysis reveals biological pathways associated with Williams syndrome. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2019, 60, 585-598.	3.1	24
10884	Bacterioplankton Metacommunity Processes across Thermal Gradients: Weaker Species Sorting but Stronger Niche Segregation in Summer than in Winter in a Subtropical Bay. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	24
10885	Potential biomarkers for heart failure. <i>Journal of Cellular Physiology</i> , 2019, 234, 9467-9474.	2.0	9
10886	MatrixDB: integration of new data with a focus on glycosaminoglycan interactions. <i>Nucleic Acids Research</i> , 2019, 47, D376-D381.	6.5	93
10887	In Silico Oncology Drug Repositioning and Polypharmacology. <i>Methods in Molecular Biology</i> , 2019, 1878, 243-261.	0.4	48
10888	Zika Virus Infection of Human Mesenchymal Stem Cells Promotes Differential Expression of Proteins Linked to Several Neurological Diseases. <i>Molecular Neurobiology</i> , 2019, 56, 4708-4717.	1.9	39
10889	Multimiomics analysis on DNA methylation and the expression of both messenger RNA and microRNA in lung adenocarcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 7579-7586.	2.0	23
10890	Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019, 148, 398-406.	5.3	90
10891	Translocatome: a novel resource for the analysis of protein translocation between cellular organelles. <i>Nucleic Acids Research</i> , 2019, 47, D495-D505.	6.5	17
10892	Transcriptome analysis of grass carp provides insights into disease-related genes and novel regulation pattern of bile acid feedback in response to lithocholic acid. <i>Aquaculture</i> , 2019, 500, 613-621.	1.7	21
10893	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. <i>Science of the Total Environment</i> , 2019, 651, 2148-2157.	3.9	25
10894	LION LBD: a literature-based discovery system for cancer biology. <i>Bioinformatics</i> , 2019, 35, 1553-1561.	1.8	47
10895	Navigating Among Known Structures in Protein Space. <i>Methods in Molecular Biology</i> , 2019, 1851, 233-249.	0.4	2
10896	Plant-mediated effects of soil phosphorus on the root-associated fungal microbiota in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2019, 221, 2123-2137.	3.5	46

#	ARTICLE	IF	CITATIONS
10897	Integrated network analysis and machine learning approach for the identification of key genes of triple-negative breast cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6154-6167.	1.2	34
10898	Identification of <i>TAF1</i> , <i>HNF4A</i> , and <i>CALM2</i> as potential therapeutic target genes for liver fibrosis. <i>Journal of Cellular Physiology</i> , 2019, 234, 9045-9051.	2.0	24
10899	Systems vaccinology and big data in the vaccine development chain. <i>Immunology</i> , 2019, 156, 33-46.	2.0	57
10900	Mitochondria-mediated apoptosis was induced by oleuropein in H1299 cells involving activation of p38 MAP kinase. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 5480-5494.	1.2	23
10901	The polyproline motif of S6K2: eIF5A translational dependence and importance for protein-protein interactions. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6015-6025.	1.2	5
10902	Expression profile and potential functional differentiation of the Speedy/RINGO family in mice. <i>Gene</i> , 2019, 683, 80-86.	1.0	1
10903	Molecular and disease association of gestational diabetes mellitus affected mother and placental datasets reveal a strong link between insulin growth factor (IGF) genes in amino acid transport pathway: A network biology approach. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1577-1587.	1.2	7
10904	Identification of genes associated with survival of breast cancer patients. <i>Breast Cancer</i> , 2019, 26, 317-325.	1.3	18
10905	Profiling of miRNAs in serum of children with attention-deficit hyperactivity disorder shows significant alterations. <i>Journal of Psychiatric Research</i> , 2019, 109, 185-192.	1.5	27
10906	PaDuA: A Python Library for High-Throughput (Phospho)proteomics Data Analysis. <i>Journal of Proteome Research</i> , 2019, 18, 576-584.	1.8	15
10907	C1q and TNF related protein 1 regulates expression of inflammatory genes in vascular smooth muscle cells. <i>Genes and Genomics</i> , 2019, 41, 397-406.	0.5	16
10908	Bioinformatic Analysis Reveals Novel Immune-Associated Hub Genes in Human Membranous Nephropathy. <i>Genetic Testing and Molecular Biomarkers</i> , 2019, 23, 23-31.	0.3	6
10909	Evidence for functional interactions between the placenta and brain in pregnant mice. <i>FASEB Journal</i> , 2019, 33, 4261-4272.	0.2	26
10910	Overexpression of microRNA-98 inhibits cell proliferation and promotes cell apoptosis via claudin-1 in human colorectal carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6090-6105.	1.2	11
10911	Nonalcoholic Fatty Liver Disease Demonstrates a Pre-fibrotic and Premalignant Molecular Signature. <i>Digestive Diseases and Sciences</i> , 2019, 64, 1257-1269.	1.1	6
10912	Gene microarray analysis of expression profiles in Suberoyllanilide hydroxamic acid-treated Dendritic cells. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 392-397.	1.0	4
10913	Flt3L Treatment of Bone Marrow Donors Increases Graft Plasmacytoid Dendritic Cell Content and Improves Allogeneic Transplantation Outcomes. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, 1075-1084.	2.0	10
10914	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , 2019, 97, 1154-1167.	2.8	114

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10915	A three microRNA-based prognostic signature for small cell lung cancer overall survival. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 8723-8730.	1.2	14
10916	Py3plex: A Library for Scalable Multilayer Network Analysis and Visualization. <i>Studies in Computational Intelligence</i> , 2019, , 757-768.	0.7	6
10917	Chemical Space and Biological Target Network of Anti-Inflammatory Natural Products. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 66-73.	2.5	15
10918	Drug repositioning in epilepsy reveals novel antiseizure candidates. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 295-309.	1.7	40
10919	<i>TIGD1</i> , a gene of unknown function, involves cell cycle progression and correlates with poor prognosis in human cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9758-9767.	1.2	9
10920	Tripartite Network-Based Repurposing Method Using Deep Learning to Compute Similarities for Drug-Target Prediction. <i>Methods in Molecular Biology</i> , 2019, 1903, 317-328.	0.4	10
10921	Shared KEGG pathways of icariin-targeted genes and osteoarthritis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7741-7750.	1.2	12
10922	Machine-learning-based patient-specific prediction models for knee osteoarthritis. <i>Nature Reviews Rheumatology</i> , 2019, 15, 49-60.	3.5	119
10923	Proteome-wide Tyrosine Phosphorylation Analysis Reveals Dysregulated Signaling Pathways in Ovarian Tumors. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 448-460.	2.5	19
10924	Laser Microdissection-Based Tissue-Specific Transcriptome Analysis Reveals a Novel Regulatory Network of Genes Involved in Heat-Induced Grain Chalk in Rice Endosperm. <i>Plant and Cell Physiology</i> , 2019, 60, 626-642.	1.5	40
10925	Computer vision-based phenotyping for improvement of plant productivity: a machine learning perspective. <i>GigaScience</i> , 2019, 8, .	3.3	99
10926	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019, 4, 352-361.	5.9	78
10927	The Site-Specific Amino Acid Preferences of Homologous Proteins Depend on Sequence Divergence. <i>Genome Biology and Evolution</i> , 2019, 11, 121-135.	1.1	4
10928	Plasma proteome correlates of lipid and lipoprotein: biomarkers of metabolic diversity and inflammation in children of rural Nepal. <i>Journal of Lipid Research</i> , 2019, 60, 149-160.	2.0	6
10929	Identification of Key Residues in Proteins Through Centrality Analysis and Flexibility Prediction with RINspecter. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e66.	25.8	13
10930	The <i>Pseudomonas aeruginosa</i> Pan-Genome Provides New Insights on Its Population Structure, Horizontal Gene Transfer, and Pathogenicity. <i>Genome Biology and Evolution</i> , 2019, 11, 109-120.	1.1	223
10931	Discovery of caerulomycin/collismycin-type 2,2'-bipyridine natural products in the genomic era. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 459-468.	1.4	13
10932	Analysis of bHLH coding genes of <i>Cicer arietinum</i> during heavy metal stress using biological network. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 113-121.	1.4	14



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10933	A Genome-wide Association Study Identifying RAP1A as a Novel Susceptibility Gene for Crohn's Disease in Japanese Individuals. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 648-658.	0.6	22
10934	The intestinal microbiota associated with cardiac valve calcification differs from that of coronary artery disease. <i>Atherosclerosis</i> , 2019, 284, 121-128.	0.4	75
10935	The exploration of novel Alzheimer's therapeutic agents from the pool of FDA approved medicines using drug repositioning, enzyme inhibition and kinetic mechanism approaches. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 2513-2526.	2.5	37
10936	Correlation between EZH2 and CEP55 and lung adenocarcinoma prognosis. <i>Pathology Research and Practice</i> , 2019, 215, 292-301.	1.0	24
10937	Evidence for co-selection of antibiotic resistance genes and mobile genetic elements in metal polluted urban soils. <i>Science of the Total Environment</i> , 2019, 656, 512-520.	3.9	183
10938	Bioinformatic analysis reveals novel hub genes and pathways associated with hypertensive nephropathy. <i>Nephrology</i> , 2019, 24, 1103-1114.	0.7	8
10939	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 5459-5471.	1.2	4
10940	Interface-Based Structural Prediction of Novel Host-Pathogen Interactions. <i>Methods in Molecular Biology</i> , 2019, 1851, 317-335.	0.4	21
10941	IL-6 mediates ER expansion during hyperpolarization of alternatively activated macrophages. <i>Immunology and Cell Biology</i> , 2019, 97, 203-217.	1.0	18
10942	Detecting Amino Acid Coevolution with Bayesian Graphical Models. <i>Methods in Molecular Biology</i> , 2019, 1851, 105-122.	0.4	5
10943	Protein Kinase C Epsilon Deletion in Adipose Tissue, but Not in Liver, Improves Glucose Tolerance. <i>Cell Metabolism</i> , 2019, 29, 183-191.e7.	7.2	42
10944	Identification of key genes in prostate cancer gene expression profile by bioinformatics. <i>Andrologia</i> , 2019, 51, e13169.	1.0	12
10945	Comprehensive analysis of microRNA-messenger RNA regulatory network in gemcitabine-resistant bladder cancer cells. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6347-6360.	1.2	11
10946	Summer phyto- and bacterioplankton communities during low and high productivity scenarios in the Western Antarctic Peninsula. <i>Polar Biology</i> , 2019, 42, 159-169.	0.5	23
10947	Exploring single-domain antibody thermostability by molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3686-3696.	2.0	13
10948	Whole transcriptome analysis of the pectoralis major muscle reveals molecular mechanisms involved with white striping in broiler chickens. <i>Poultry Science</i> , 2019, 98, 590-601.	1.5	46
10949	Deciphering genome-wide WRKY gene family of <i>Triticum aestivum</i> L. and their functional role in response to Abiotic stress. <i>Genes and Genomics</i> , 2019, 41, 79-94.	0.5	31
10950	Metabolomics profiling reveals profound metabolic impairments in mice and patients with Sandhoff disease. <i>Molecular Genetics and Metabolism</i> , 2019, 126, 151-156.	0.5	15



#	ARTICLE	IF	CITATIONS
10951	Identifying and validating blood mRNA biomarkers for acute and chronic insufficient sleep in humans: a machine learning approach. <i>Sleep</i> , 2019, 42, .	0.6	35
10952	Dynamics changes in the transcription factors during early human embryonic development. <i>Journal of Cellular Physiology</i> , 2019, 234, 6489-6502.	2.0	18
10953	Prognostic value of aberrantly expressed methylation gene profiles in lung squamous cell carcinoma: A study based on The Cancer Genome Atlas. <i>Journal of Cellular Physiology</i> , 2019, 234, 6519-6528.	2.0	31
10954	Deciphering the metabolic role of AMPK in cancer multi-drug resistance. <i>Seminars in Cancer Biology</i> , 2019, 56, 56-71.	4.3	25
10955	Identification of several key genes by microarray data analysis of bovine mammary gland epithelial cells challenged with <i>Escherichia coli</i> and <i>Staphylococcus aureus</i> . <i>Gene</i> , 2019, 683, 123-132.	1.0	44
10956	Comprehensive analysis of aberrantly expressed profiles of messenger RNA in alcoholic liver disease. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 4248-4254.	1.2	1
10957	Network-based integration of mRNA and miRNA profiles reveals new target genes involved in pancreatic cancer. <i>Molecular Carcinogenesis</i> , 2019, 58, 206-218.	1.3	17
10958	Expression of retinoic acid signaling components ADH7 and ALDH1A1 is reduced in aniridia limbal epithelial cells and a siRNA primary cell based aniridia model. <i>Experimental Eye Research</i> , 2019, 179, 8-17.	1.2	20
10959	Progression from low- to high-grade in a glioblastoma model reveals the pivotal role of immunoediting. <i>Cancer Letters</i> , 2019, 442, 213-221.	3.2	18
10960	Systems genetics of nonsyndromic orofacial clefting provides insights into its complex aetiology. <i>European Journal of Human Genetics</i> , 2019, 27, 226-234.	1.4	7
10961	Effect of hepatitis B virus (HBV) <i>surface</i> gene variability on markers of replication during treated human immunodeficiency virus-HBV infection in Western Africa. <i>Liver International</i> , 2019, 39, 280-289.	1.9	2
10962	Effect of Different Soil Phosphate Sources on the Active Bacterial Microbiota Is Greater in the Rhizosphere than in the Endorhiza of Barley ( <i>Hordeum vulgare</i> L.). <i>Microbial Ecology</i> , 2019, 77, 689-700.	1.4	14
10963	Long-term application of manure over plant residues mitigates acidification, builds soil organic carbon and shifts prokaryotic diversity in acidic Ultisols. <i>Applied Soil Ecology</i> , 2019, 133, 24-33.	2.1	76
10964	Secondary structures transition of tau protein with intrinsically disordered proteins specific force field. <i>Chemical Biology and Drug Design</i> , 2019, 93, 242-253.	1.5	6
10965	Identification of characteristic genes distinguishing neural stem cells from astrocytes. <i>Gene</i> , 2019, 681, 26-35.	1.0	7
10966	Computational models for lncRNA function prediction and functional similarity calculation. <i>Briefings in Functional Genomics</i> , 2019, 18, 58-82.	1.3	141
10967	Effects of zooplankton carcasses degradation on freshwater bacterial community composition and implications for carbon cycling. <i>Environmental Microbiology</i> , 2019, 21, 34-49.	1.8	11
10968	C:N ratio shaped both taxonomic and functional structure of microbial communities in livestock and poultry breeding wastewater treatment reactor. <i>Science of the Total Environment</i> , 2019, 651, 625-633.	3.9	76

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10969	TorsinA Is Functionally Associated with Spermatogenesis. <i>Microscopy and Microanalysis</i> , 2019, 25, 221-228.	0.2	4
10970	Identification of potential mechanism and hub genes for neuropathic pain by expression-based genome-wide association study. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 4912-4923.	1.2	9
10971	Combining network topology with transcriptomic data for identifying radiosensitive gene signatures. <i>Journal of Computational Methods in Sciences and Engineering</i> , 2019, 19, 565-579.	0.1	0
10972	Contrasting Soil Bacterial and Fungal Communities between the Swamp and Upland in the Boreal Forest and their Biogeographic Distribution Patterns. <i>Wetlands</i> , 2019, 39, 441-451.	0.7	2
10973	NetShift™: a methodology for understanding driver microbes from healthy and disease microbiome datasets. <i>ISME Journal</i> , 2019, 13, 442-454.	4.4	114
10974	Discovery of SERPINA3 as a candidate urinary biomarker of lupus nephritis activity. <i>Rheumatology</i> , 2019, 58, 321-330.	0.9	20
10975	Soil Characteristics Overwhelm Cultivar Effects on the Structure and Assembly of Root-Associated Microbiomes of Modern Maize. <i>Pedosphere</i> , 2019, 29, 360-373.	2.1	37
10976	Identification of PIWI-interacting RNA modules by weighted correlation network analysis. <i>Cluster Computing</i> , 2019, 22, 707-717.	3.5	3
10977	Network Analysis of MPO and Other Relevant Proteins Involved in Diabetic Foot Ulcer and Other Diabetic Complications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 180-190.	2.2	5
10978	Hepatic accumulation of S-adenosylmethionine in hamsters with non-alcoholic fatty liver disease associated with metabolic syndrome under selenium and vitamin E deficiency. <i>Clinical Science</i> , 2019, 133, 409-423.	1.8	19
10979	Association of Inflammatory Bowel Disease with Arthritis: Evidence from In Silico Gene Expression Patterns and Network Topological Analysis. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 387-396.	2.2	7
10980	Comprehensive analysis of <i>Helicobacter pylori</i> infection-associated diseases based on miRNA-mRNA interaction network. <i>Briefings in Bioinformatics</i> , 2019, 20, 1492-1501.	3.2	26
10981	Interactive and coordinated visualization approaches for biological data analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1513-1523.	3.2	10
10982	Analysing Network Models to Make Discoveries about Biological Mechanisms. <i>British Journal for the Philosophy of Science</i> , 2019, 70, 459-484.	1.4	22
10983	Distinct telomere length and molecular signatures in seminoma and non-seminoma of testicular germ cell tumor. <i>Briefings in Bioinformatics</i> , 2019, 20, 1502-1512.	3.2	22
10984	Integrated Pathways of <i>Candida albicans</i> Revealing Potential Targets and Key Factors Accountable for Pathogenicity. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 575-584.	0.4	2
10985	Selection of biomarkers for HIV-1 latency by integrated analysis. <i>Genomics</i> , 2019, 111, 327-333.	1.3	8
10986	Systems Bioinformatics: increasing precision of computational diagnostics and therapeutics through network-based approaches. <i>Briefings in Bioinformatics</i> , 2019, 20, 806-824.	3.2	87

#	ARTICLE	IF	CITATIONS
10987	Estrogen receptor-alpha isoforms are the main estrogen receptors expressed in non-small cell lung carcinoma. <i>Steroids</i> , 2019, 142, 65-76.	0.8	10
10988	Analysis of time-course microarray data: Comparison of common tools. <i>Genomics</i> , 2019, 111, 636-641.	1.3	4
10989	Clinical Importance of a Cytokine Network in Major Burns. <i>Shock</i> , 2019, 51, 185-193.	1.0	29
10990	Computational profiling of the gut-brain axis: microflora dysbiosis insights to neurological disorders. <i>Briefings in Bioinformatics</i> , 2019, 20, 825-841.	3.2	27
10991	Insights into the role of ribonuclease 4 polymorphisms in amyotrophic lateral sclerosis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 116-130.	2.0	8
10992	LncRNA and mRNA integration network reconstruction reveals novel key regulators in esophageal squamous-cell carcinoma. <i>Genomics</i> , 2019, 111, 76-89.	1.3	26
10993	Diseases and their clinical heterogeneity – Are we ignoring the SNiPers and micRomaNagers? An illustration using Beta-thalassemia clinical spectrum and fetal hemoglobin levels. <i>Genomics</i> , 2019, 111, 67-75.	1.3	8
10994	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , 2019, 20, 1238-1249.	3.2	15
10995	Integrated Bioinformatics Analysis of Potential Biomarkers for Prostate Cancer. <i>Pathology and Oncology Research</i> , 2019, 25, 455-460.	0.9	14
10996	Extracytoplasmic function sigma factors in <i>Pseudomonas aeruginosa</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 706-721.	0.9	61
10997	Application of Atlas of Cancer Signalling Network in preclinical studies. <i>Briefings in Bioinformatics</i> , 2019, 20, 701-716.	3.2	16
10998	Identifying Bacterial Essential Genes Based on a Feature-Integrated Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1274-1279.	1.9	8
10999	Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 858-867.	1.9	1
11000	An autism-linked missense mutation in SHANK3 reveals the modularity of Shank3 function. <i>Molecular Psychiatry</i> , 2020, 25, 2534-2555.	4.1	61
11001	Onyx: A new Canvas-based tool for visualizing biomedical and health ontologies. <i>Expert Systems</i> , 2020, 37, e12380.	2.9	2
11002	Gene co-expression network approach for predicting prognostic microRNA biomarkers in different subtypes of breast cancer. <i>Genomics</i> , 2020, 112, 135-143.	1.3	22
11003	Using network analysis to explore cognitive domains in patients with unipolar versus bipolar depression: a prospective naturalistic study. <i>CNS Spectrums</i> , 2020, 25, 380-391.	0.7	13
11004	<i>RFM<sup>3</sup></i> : Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1729-1740.	1.9	9

#	ARTICLE	IF	CITATIONS
11005	Clinical trials, progression-speed differentiating features and swiftness rule of the innovative targets of first-in-class drugs. <i>Briefings in Bioinformatics</i> , 2020, 21, 649-662.	3.2	139
11006	Bayesian inference of networks across multiple sample groups and data types. <i>Biostatistics</i> , 2020, 21, 561-576.	0.9	10
11007	Protein complex prediction: A survey. <i>Genomics</i> , 2020, 112, 174-183.	1.3	38
11008	Effect of the key histone modifications on the expression of genes related to breast cancer. <i>Genomics</i> , 2020, 112, 853-858.	1.3	14
11009	Comprehensive bioinformatics analysis of trabecular meshwork gene expression data to unravel the molecular pathogenesis of primary open-angle glaucoma. <i>Acta Ophthalmologica</i> , 2020, 98, 48-57.	0.6	18
11010	Comprehensive analysis of prognostic immune-related genes in the tumor microenvironment of cutaneous melanoma. <i>Journal of Cellular Physiology</i> , 2020, 235, 1025-1035.	2.0	95
11011	Co-expression analysis provides important module and pathways of human dilated cardiomyopathy. <i>Journal of Cellular Physiology</i> , 2020, 235, 494-503.	2.0	8
11012	Pan-cancer analysis of iron metabolic landscape across the Cancer Genome Atlas. <i>Journal of Cellular Physiology</i> , 2020, 235, 1013-1024.	2.0	43
11013	Identification of a Multiplex Biomarker Panel for Hypertrophic Cardiomyopathy Using Quantitative Proteomics and Machine Learning. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 114-127.	2.5	32
11014	Identification of driver genes and somatic mutations in cell-free DNA of patients with pulmonary lymphangioleiomyomatosis. <i>International Journal of Cancer</i> , 2020, 146, 103-114.	2.3	7
11015	Degradome of soluble ADAM10 and ADAM17 metalloproteases. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 331-350.	2.4	46
11016	Biocontrol of Root Diseases and Growth Promotion of the Tuberos Plant <i>Aconitum carmichaelii</i> Induced by Actinomycetes Are Related to Shifts in the Rhizosphere Microbiota. <i>Microbial Ecology</i> , 2020, 79, 134-147.	1.4	30
11017	Targeted proteomic response to coffee consumption. <i>European Journal of Nutrition</i> , 2020, 59, 1529-1539.	1.8	2
11018	Identification and Verification of Two Novel Differentially Expressed Proteins from Non-neoplastic Mucosa and Colorectal Carcinoma Via iTRAQ Combined with Liquid Chromatography-Mass Spectrometry. <i>Pathology and Oncology Research</i> , 2020, 26, 967-976.	0.9	4
11019	MicroRNA-related markers associated with corpus luteum tropism in buffalo ( <i>Bubalus bubalis</i> ). <i>Genomics</i> , 2020, 112, 108-113.	1.3	3
11020	Genome-wide identification and analysis of the eQTL lncRNAs in multiple sclerosis based on RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1023-1037.	3.2	35
11021	A case of fatal acebutolol poisoning: an illustration of the potential of molecular networking. <i>International Journal of Legal Medicine</i> , 2020, 134, 251-256.	1.2	18
11022	Rescue of premature aging defects in Cockayne syndrome stem cells by CRISPR/Cas9-mediated gene correction. <i>Protein and Cell</i> , 2020, 11, 1-22.	4.8	54

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11023	Muscle transcriptome signature and gene regulatory network analysis in two divergent lines of a hilly bovine species <i>Mithun</i> ( <i>Bos frontalis</i> ). <i>Genomics</i> , 2020, 112, 252-262.	1.3	12
11024	Differential dynamics of hepatic protein expressions with long-term cultivated hepatitis C virus infection. <i>Journal of Microbiology, Immunology and Infection</i> , 2020, 53, 715-723.	1.5	1
11025	Grade-specific diagnostic and prognostic biomarkers in breast cancer. <i>Genomics</i> , 2020, 112, 388-396.	1.3	29
11026	Identification of transcription factors that regulate <i>ATG8</i> expression and autophagy in <i>Arabidopsis</i> . <i>Autophagy</i> , 2020, 16, 123-139.	4.3	81
11027	Integrated analysis of human transcriptome data for Rett syndrome finds a network of involved genes. <i>World Journal of Biological Psychiatry</i> , 2020, 21, 712-725.	1.3	19
11028	Integration of network models and evolutionary analysis into high-throughput modeling of protein dynamics and allosteric regulation: theory, tools and applications. <i>Briefings in Bioinformatics</i> , 2020, 21, 815-835.	3.2	58
11029	Downregulations of miR-449a and miR-145-5p Act as Prognostic Biomarkers for Endometrial Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 834-844.	0.8	20
11030	Coding and non-coding transcriptome of mesial temporal lobe epilepsy: Critical role of small non-coding RNAs. <i>Neurobiology of Disease</i> , 2020, 134, 104612.	2.1	33
11031	Time-Series Expression Analysis of Epidermal Stem Cells from High Fat Diet Mice. <i>Journal of Computational Biology</i> , 2020, 27, 769-778.	0.8	2
11032	Novel MicroRNA Biomarkers, <i>miR-142-5p</i> , <i>miR-550a</i> , <i>miR-1826</i> , and <i>miR-1201</i> , Were Identified for Primary Melanoma. <i>Journal of Computational Biology</i> , 2020, 27, 815-824.	0.8	8
11033	Organ-specific small non-coding RNA responses in domestic (Sudani) ducks experimentally infected with highly pathogenic avian influenza virus (H5N1). <i>RNA Biology</i> , 2020, 17, 112-124.	1.5	15
11034	Assessment of the genes and molecular mechanisms of B cells activation through systems biology approaches. <i>Human Antibodies</i> , 2020, 28, 83-87.	0.6	0
11035	Phytochemical comparison of different tea ( <i>Camellia sinensis</i> ) cultivars and its association with sensory quality of finished tea. <i>LWT - Food Science and Technology</i> , 2020, 117, 108595.	2.5	33
11036	A Distinct Pretreatment Immune Gene Signature in Lentigo Maligna Is Associated with Imiquimod Response. <i>Journal of Investigative Dermatology</i> , 2020, 140, 869-877.e16.	0.3	15
11037	Transcriptome analysis of <i>Idesia polycarpa</i> Maxim. var <i>vestita</i> Diels flowers during sex differentiation. <i>Journal of Forestry Research</i> , 2020, 31, 2463-2478.	1.7	2
11038	Transcriptomic Profiling of Acute Cold Stress-Induced Disease Resistance (SIDR) Genes and Pathways in the Grapevine Powdery Mildew Pathosystem. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 284-295.	1.4	7
11039	Circulatory factors associated with function and prognosis in patients with severe heart failure. <i>Clinical Research in Cardiology</i> , 2020, 109, 655-672.	1.5	19
11040	The effects of ectomycorrhizal fungi on heavy metals™ transport in <i>Pinus massoniana</i> and bacteria community in rhizosphere soil in mine tailing area. <i>Journal of Hazardous Materials</i> , 2020, 381, 121203.	6.5	65

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11041	Transcriptome analysis of axillary bud differentiation in a new dual-axillary bud genotype of sugarcane. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 685-701.	0.8	3
11042	Learning parameters of Bayesian networks from datasets with systematically missing data: A meta-analytic approach. <i>Expert Systems With Applications</i> , 2020, 141, 112956.	4.4	5
11043	Transcriptomic insight into cadmium-induced neurotoxicity in embryonic neural stem/progenitor cells. <i>Toxicology in Vitro</i> , 2020, 62, 104686.	1.1	20
11044	Identification and quantification of bacterial genomes carrying antibiotic resistance genes and virulence factor genes for aquatic microbiological risk assessment. <i>Water Research</i> , 2020, 168, 115160.	5.3	102
11045	The integrative regulatory network of circRNA and microRNA in keloid scarring. <i>Molecular Biology Reports</i> , 2020, 47, 201-209.	1.0	33
11046	Closing the gap between formats for storing layout information in systems biology. <i>Briefings in Bioinformatics</i> , 2020, 21, 1249-1260.	3.2	12
11047	Whole Proteome Analysis of GA3 Response at Panicle Stage in Grape ( <i>Vitis vinifera</i> ) cv. Thompson Seedless. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 994-1008.	2.8	0
11048	PBK as a Potential Biomarker Associated with Prognosis of Glioblastoma. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 56-64.	1.1	21
11049	PerMemDB: A database for eukaryotic peripheral membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183076.	1.4	14
11050	A genomics approach reveals the global genetic polymorphism, structure, and functional diversity of ten accessions of the marine model diatom <i>Phaeodactylum tricornutum</i> . <i>ISME Journal</i> , 2020, 14, 347-363.	4.4	50
11051	Upregulation of microRNA-141 suppresses epithelial-mesenchymal transition and lymph node metastasis in laryngeal cancer through HOXC6-dependent TGF- $\beta$ 2 signaling pathway. <i>Cellular Signalling</i> , 2020, 66, 109444.	1.7	35
11052	Developing a virus-microRNA interactome using cytoscape. <i>MethodsX</i> , 2020, 7, 100700.	0.7	3
11053	Factors regulating the compositions and distributions of dissolved organic matter in the estuaries of Jiaozhou Bay in North China. <i>Oceanologia</i> , 2020, 62, 101-110.	1.1	11
11054	Autologous micrograft accelerates endogenous wound healing response through ERK-induced cell migration. <i>Cell Death and Differentiation</i> , 2020, 27, 1520-1538.	5.0	29
11055	The pathogenicity, structural and functional exploration of human HMGB1 single nucleotide polymorphisms using <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4471-4482.	2.0	3
11056	Comparative morphological and transcriptomic responses of lowland and upland rice to root-zone hypoxia. <i>Environmental and Experimental Botany</i> , 2020, 169, 103916.	2.0	17
11057	Density-dependent oxylipin production in natural diatom communities: possible implications for plankton dynamics. <i>ISME Journal</i> , 2020, 14, 164-177.	4.4	19
11058	LEF1 supports metastatic brain colonization by regulating glutathione metabolism and increasing ROS resistance in breast cancer. <i>International Journal of Cancer</i> , 2020, 146, 3170-3183.	2.3	23



#	ARTICLE	IF	CITATIONS
11059	MicroRNAâ€9 overexpression suppresses vulnerable atherosclerotic plaque and enhances vascular remodeling through negative regulation of the p38MAPK pathway via OLR1 in acute coronary syndrome. Journal of Cellular Biochemistry, 2020, 121, 49-62.	1.2	18
11060	Construction of a circular RNAâ€microRNAâ€messengerRNA regulatory network in stomach adenocarcinoma. Journal of Cellular Biochemistry, 2020, 121, 1317-1331.	1.2	21
11061	Identification of key candidate genes in neuropathic pain by integrated bioinformatic analysis. Journal of Cellular Biochemistry, 2020, 121, 1635-1648.	1.2	48
11062	miRâ€298 plays a pivotal role in colon cancer invasiveness by targeting PTEN. Journal of Cellular Physiology, 2020, 235, 4335-4350.	2.0	17
11063	Identification of Drug Targets in Breast Cancer Metabolic Network. Journal of Computational Biology, 2020, 27, 975-986.	0.8	4
11064	Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river. Environmental Microbiology, 2020, 22, 832-849.	1.8	115
11065	Fecal microbiota transplantation results in bacterial strain displacement in patients with inflammatory bowel diseases. FEBS Open Bio, 2020, 10, 41-55.	1.0	14
11066	The apical annuli of <i>Toxoplasma gondii</i> are composed of coiledâ€coil and signalling proteins embedded in the inner membrane complex sutures. Cellular Microbiology, 2020, 22, e13112.	1.1	38
11067	Microbiota characterization of sheep milk and its association with somatic cell count using 16s rRNA gene sequencing. Journal of Animal Breeding and Genetics, 2020, 137, 73-83.	0.8	21
11068	HRLC-ESI-MS based identification of active small molecules from <i>Cissus quadrangularis</i> and likelihood of their action towards the primary targets of osteoarthritis. Journal of Molecular Structure, 2020, 1199, 127048.	1.8	13
11069	Consecutive lactate formation and chain elongation to reduce exogenous chemicals input in repeated-batch food waste fermentation. Water Research, 2020, 169, 115215.	5.3	132
11070	Identification of Biomarkers Associated with Septic Cardiomyopathy Based on Bioinformatics Analyses. Journal of Computational Biology, 2020, 27, 69-80.	0.8	11
11071	Detailed Analysis of Molecular Mechanisms in Primary and Metastatic Melanoma. Journal of Computational Biology, 2020, 27, 9-19.	0.8	5
11072	Profiling and Bioinformatic Analysis of Differentially Expressed Cytokines in Aqueous Humor of High Myopic Eyes â€ Clues for Anti-VEGF Injections. Current Eye Research, 2020, 45, 97-103.	0.7	5
11073	The MicroRNA Landscapes Profiling Reveals Potential Signatures of Necrotizing Enterocolitis in Infants. Journal of Computational Biology, 2020, 27, 30-39.	0.8	5
11074	Ubiquitin-Specific Protease 8; Mutant Corticotrope Adenomas Present Unique Secretory and Molecular Features and Shed Light on the Role of Ubiquitylation on ACTH Processing. Neuroendocrinology, 2020, 110, 119-129.	1.2	21
11075	Serial gene co-expression network approach to mine biological meanings from integrated transcriptomes of the porcine endometrium during estrous cycle. Functional and Integrative Genomics, 2020, 20, 117-131.	1.4	1
11076	New Insights on â€ GALAâ€™ Apple Fruit Development: Sugar and Acid Accumulation: A Transcriptomic Approach. Journal of Plant Growth Regulation, 2020, 39, 680-702.	2.8	12



#	ARTICLE	IF	CITATIONS
11077	Correlation network analysis shows divergent effects of a long-term, high-fat diet and exercise on early stage osteoarthritis phenotypes in mice. <i>Journal of Sport and Health Science</i> , 2020, 9, 119-131.	3.3	17
11078	Reconstruction of transcriptional regulatory networks of Fis and H-NS in <i>Escherichia coli</i> from genome-wide data analysis. <i>Genomics</i> , 2020, 112, 1264-1272.	1.3	11
11079	Human chromatin remodeler cofactor, RNA interactor, eraser and writer sperm RNAs responding to obesity. <i>Epigenetics</i> , 2020, 15, 32-46.	1.3	15
11080	MicroRNA-326 decreases tau phosphorylation and neuron apoptosis through inhibition of the JNK signaling pathway by targeting <i>VAV1</i> in Alzheimer's disease. <i>Journal of Cellular Physiology</i> , 2020, 235, 480-493.	2.0	47
11081	DNA Rchitect: an R based visualizer for network analysis of chromatin interaction data. <i>Bioinformatics</i> , 2020, 36, 644-646.	1.8	5
11082	Design, synthesis, biological evaluation and molecular dynamics simulation studies of (R)-5-methylthiazolidin-4-One derivatives as megakaryocyte protein tyrosine phosphatase 2 (PTP-MEG2) inhibitors for the treatment of type 2 diabetes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3156-3165.	2.0	5
11083	Convergent functional genomics of cocaine misuse in humans and animal models. <i>American Journal of Drug and Alcohol Abuse</i> , 2020, 46, 22-30.	1.1	12
11084	Prediction of progression of chronic atrophic gastritis with <i>Helicobacter pylori</i> and poor prognosis of gastric cancer by CYP3A4. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2020, 35, 425-432.	1.4	13
11085	Revealing liver specific microRNAs linked with carbohydrate metabolism of farmed carp, <i>Labeo rohita</i> (Hamilton, 1822). <i>Genomics</i> , 2020, 112, 32-44.	1.3	11
11086	Gene expression profiling and identification of hub genes in Nelore cattle with different marbling score levels. <i>Genomics</i> , 2020, 112, 873-879.	1.3	31
11087	Discovery and validation of methylated-differentially expressed genes in <i>Helicobacter pylori</i> -induced gastric cancer. <i>Cancer Gene Therapy</i> , 2020, 27, 473-485.	2.2	27
11088	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. <i>Genomics</i> , 2020, 112, 820-830.	1.3	15
11089	Multimapping confounds ribosome profiling analysis: A case study of the Hsp90 molecular chaperone. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 57-68.	1.5	5
11090	Imbalanced testicular metabolism induced by thyroid disorders: New evidences from quantitative proteome. <i>Endocrine</i> , 2020, 67, 209-223.	1.1	7
11091	Gene coexpression analysis offers important modules and pathway of human lung adenocarcinomas. <i>Journal of Cellular Physiology</i> , 2020, 235, 454-464.	2.0	14
11092	Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2005-2016.	1.9	11
11093	Association of urinary ionic profiles and acute kidney injury and mortality in patients after cardiac surgery. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2020, 159, 918-926.e5.	0.4	8
11094	Transcriptome profiling of muscle in Nelore cattle phenotypically divergent for the ribeye muscle area. <i>Genomics</i> , 2020, 112, 1257-1263.	1.3	13

#	ARTICLE	IF	CITATIONS
11095	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. <i>Plant Biotechnology Journal</i> , 2020, 18, 553-567.	4.1	24
11096	Non-coding RNA regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194417.	0.9	262
11097	Screening for the Biomarkers Associated with Myocardial Infarction by Bioinformatics Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 779-785.	0.8	6
11098	Association Between Plasma Diacetylspermine and Tumor Spermine Synthase With Outcome in Triple-Negative Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 607-616.	3.0	40
11099	New insights on human essential genes based on integrated analysis and the construction of the HEGIAP web-based platform. <i>Briefings in Bioinformatics</i> , 2020, 21, 1397-1410.	3.2	51
11100	Citywide Transmission of Multidrug-resistant Tuberculosis Under China's Rapid Urbanization: A Retrospective Population-based Genomic Spatial Epidemiological Study. <i>Clinical Infectious Diseases</i> , 2020, 71, 142-151.	2.9	46
11101	Prognostic Markers Identification in Glioma by Gene Expression Profile Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 81-90.	0.8	19
11102	Molecular insight into cotton leaf curl geminivirus disease resistance in cultivated cotton ( <i>Gossypium hirsutum</i> ). <i>Plant Biotechnology Journal</i> , 2020, 18, 691-706.	4.1	44
11103	Microarray Assay Reveals Ciliary Abnormalities of the Allergic Nasal Mucosa. <i>American Journal of Rhinology and Allergy</i> , 2020, 34, 50-58.	1.0	8
11104	Systematic Exploration of the High Likelihood Set of Phylogenetic Tree Topologies. <i>Systematic Biology</i> , 2020, 69, 280-293.	2.7	5
11105	Coordinated DNA Methylation and Gene Expression Data for Identification of the Critical Genes Associated with Childhood Atopic Asthma. <i>Journal of Computational Biology</i> , 2020, 27, 109-120.	0.8	10
11106	Agricultural activities affect the pattern of the resistome within the phyllosphere microbiome in peri-urban environments. <i>Journal of Hazardous Materials</i> , 2020, 382, 121068.	6.5	28
11107	Effective electrochemotherapy with curcumin in MDA-MB-231-human, triple negative breast cancer cells: A global proteomics study. <i>Bioelectrochemistry</i> , 2020, 131, 107350.	2.4	33
11108	Reactivation of super-enhancers by KLF4 in human Head and Neck Squamous Cell Carcinoma. <i>Oncogene</i> , 2020, 39, 262-277.	2.6	15
11109	Genome-Wide Analysis of HSP70 Family Protein in <i>Vigna radiata</i> and Coexpression Analysis Under Abiotic and Biotic Stress. <i>Journal of Computational Biology</i> , 2020, 27, 738-754.	0.8	0
11110	CD49 <sup>high</sup> Defines a Distinct Skin Mesenchymal Stem Cell Population Capable of Hair Follicle Epithelial Cell Maintenance. <i>Journal of Investigative Dermatology</i> , 2020, 140, 544-555.e9.	0.3	11
11111	Gene co-regulation and co-expression in the aryl hydrocarbon receptor-mediated transcriptional regulatory network in the mouse liver. <i>Archives of Toxicology</i> , 2020, 94, 113-126.	1.9	11
11112	Abstract art paintings, global image properties, and verbal descriptions: An empirical and computational investigation. <i>Acta Psychologica</i> , 2020, 202, 102936.	0.7	17

#	ARTICLE	IF	CITATIONS
11113	Sex, drugs, and sexually transmitted infections: A latent class analysis among men who have sex with men in Amsterdam and surrounding urban regions, the Netherlands. <i>Drug and Alcohol Dependence</i> , 2020, 206, 107526.	1.6	24
11114	Identification of Multiple Sclerosis key genetic factors through multi-staged data mining. <i>Multiple Sclerosis and Related Disorders</i> , 2020, 39, 101446.	0.9	4
11115	Global transcriptome analysis of porcine oocytes in correlation with follicle size. <i>Molecular Reproduction and Development</i> , 2020, 87, 102-114.	1.0	5
11116	Egg adaptive mutation patterns of H3N2 human influenza A viruses. <i>Journal of Infection</i> , 2020, 80, 232-254.	1.7	1
11117	Dissecting the Transcriptomic Basis of Phenotypic Evolution in an Aquatic Keystone Grazer. <i>Molecular Biology and Evolution</i> , 2020, 37, 475-487.	3.5	13
11118	Identification of Potential Gene Signatures Related to Sleep Deprivation. <i>Journal of Computational Biology</i> , 2020, 27, 904-913.	0.8	1
11119	Signatures of altered DNA methylation gene expression after central and peripheral nerve injury. <i>Journal of Cellular Physiology</i> , 2020, 235, 5171-5181.	2.0	12
11120	Network of lipid interconnections at the interfaces of galactolipid and phospholipid bilayers. <i>Journal of Molecular Liquids</i> , 2020, 298, 112002.	2.3	6
11121	Identification and Mobilization of a Cryptic Antibiotic Biosynthesis Gene Locus from a Human-Pathogenic <i>Nocardia</i> Isolate. <i>ACS Chemical Biology</i> , 2020, 15, 1161-1168.	1.6	10
11122	Identification of Biomolecular Information in Rotenone-Induced Cellular Model of Parkinson's Disease by Public Microarray Data Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 888-903.	0.8	4
11123	Key Regulatory Effect of Activated $\text{HIF-1}\alpha$ /VEGFA Signaling Pathway in Systemic Capillary Leak Syndrome Confirmed by Bioinformatics Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 914-922.	0.8	5
11124	Analysis of Gene Expression in Bladder Cancer: Possible Involvement of Mitosis and Complement and Coagulation Cascades Signaling Pathway. <i>Journal of Computational Biology</i> , 2020, 27, 987-998.	0.8	26
11125	Effect of simulated microgravity and ionizing radiation on expression profiles of miRNA, lncRNA, and mRNA in human lymphoblastoid cells. <i>Life Sciences in Space Research</i> , 2020, 24, 1-8.	1.2	17
11126	Identification of key microRNAs and genes associated with abdominal aortic aneurysm based on the gene expression profile. <i>Experimental Physiology</i> , 2020, 105, 160-173.	0.9	7
11127	Identification of aberrantly expressed lncRNA and the associated TF-mRNA network in hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 1491-1503.	1.2	23
11128	Patterns and processes of free-living and particle-associated bacterioplankton and archaeoplankton communities in a subtropical river-bay system in South China. <i>Limnology and Oceanography</i> , 2020, 65, S161.	1.6	48
11129	Differential metabolic and multi-tissue transcriptomic responses to fructose consumption among genetically diverse mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165569.	1.8	21
11130	Brain and blood metabolome for Alzheimer's dementia: findings from a targeted metabolomics analysis. <i>Neurobiology of Aging</i> , 2020, 86, 123-133.	1.5	83

#	ARTICLE	IF	CITATIONS
11131	Concentric vs. eccentric remodelling in heart failure with reduced ejection fraction: clinical characteristics, pathophysiology and response to treatment. <i>European Journal of Heart Failure</i> , 2020, 22, 1147-1155.	2.9	50
11132	Metabolomics of soybean green stem and foliar retention (GSFR) disease using mass spectrometry and molecular networking. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8655.	0.7	8
11133	Multicellular growth of the Basidiomycota phytopathogen fungus <i>Sporisorium reilianum</i> induced by acid conditions. <i>Folia Microbiologica</i> , 2020, 65, 511-521.	1.1	6
11134	Long-term organic fertilization improves the productivity of kiwifruit ( <i>Actinidia chinensis</i> Planch.) through increasing rhizosphere microbial diversity and network complexity. <i>Applied Soil Ecology</i> , 2020, 147, 103426.	2.1	56
11135	Protective effects of <i>Cordyceps</i> extract against UVB-induced damage and prediction of application prospects in the topical administration: An experimental validation and network pharmacology study. <i>Biomedicine and Pharmacotherapy</i> , 2020, 121, 109600.	2.5	10
11136	Prediction of modes of action of components of traditional medicinal preparations. <i>Physical Sciences Reviews</i> , 2020, 5, .	0.8	3
11137	Inferring biosynthetic and gene regulatory networks from <i>Artemisia annua</i> RNA sequencing data on a credit card-sized ARM computer. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194429.	0.9	12
11138	Antiproliferative activity and mode of action analysis of novel amino and amido substituted phenantrene and naphtho[2,1-b]thiophene derivatives. <i>European Journal of Medicinal Chemistry</i> , 2020, 185, 111833.	2.6	13
11139	Investigation of the pharmacodynamic substances in dahuang zhechong pill that inhibit energy metabolism. <i>Journal of Ethnopharmacology</i> , 2020, 251, 112332.	2.0	9
11140	Interactomic analysis of the sHSP family during tomato fruit ripening. <i>Plant Gene</i> , 2020, 21, 100208.	1.4	6
11141	Multivariate Statistical Analysis and Odor-Taste Network To Reveal Odor-Taste Associations. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 10318-10328.	2.4	21
11142	Bovine milk transcriptome analysis reveals microRNAs and RNU2 involved in mastitis. <i>FEBS Journal</i> , 2020, 287, 1899-1918.	2.2	30
11143	Identifying prognostic biomarkers in endometrial carcinoma based on ceRNA network. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 2437-2446.	1.2	15
11144	Genome-wide association study of vitamin E in sweet corn kernels. <i>Crop Journal</i> , 2020, 8, 341-350.	2.3	20
11145	Screening and Identification of Key Biomarkers in Pancreatic Cancer: Evidence from Bioinformatic Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1079-1091.	0.8	2
11146	Immune/Neural approach to characterize salivary gland neoplasms (SGN). <i>Applied Soft Computing Journal</i> , 2020, 88, 105877.	4.1	4
11147	Quantitative proteomics reveals the molecular mechanism of <i>Aeromonas hydrophila</i> in enoxacin stress. <i>Journal of Proteomics</i> , 2020, 211, 103561.	1.2	14
11148	Metabolomics of red light-induced stomatal opening in <i>Arabidopsis thaliana</i> : Coupling with abscisic acid and jasmonic acid metabolism. <i>Plant Journal</i> , 2020, 101, 1331-1348.	2.8	25

#	ARTICLE	IF	CITATIONS
11149	De novo transcriptomic analysis of light-induced flavonoid pathway, transcription factors in the flower buds of <i>Lonicera japonica</i> . <i>Trees - Structure and Function</i> , 2020, 34, 267-283.	0.9	14
11150	Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194430.	0.9	93
11151	Protein isoelectric point distribution in the interactomes across the domains of life. <i>Biophysical Chemistry</i> , 2020, 256, 106269.	1.5	10
11152	New tetrodotoxin analogs in Brazilian pufferfishes tissues and microbiome. <i>Chemosphere</i> , 2020, 242, 125211.	4.2	9
11153	Aldehyde and Volatile Organic Compound Yields in Commercial Cigarette Mainstream Smoke Are Mutually Related and Depend on the Sugar and Humectant Content in Tobacco. <i>Nicotine and Tobacco Research</i> , 2020, 22, 1748-1756.	1.4	21
11154	A NAC-type transcription factor confers aluminium resistance by regulating cell wall-associated receptor kinase 1 and cell wall pectin. <i>Plant, Cell and Environment</i> , 2020, 43, 463-478.	2.8	63
11155	CoA Synthase ( <i>COASY</i> ) Mediates Radiation Resistance via PI3K Signaling in Rectal Cancer. <i>Cancer Research</i> , 2020, 80, 334-346.	0.4	33
11156	Genome-wide association study and predictive ability for growth traits in Nellore cattle. <i>Livestock Science</i> , 2020, 231, 103861.	0.6	5
11157	Interleukin-17 Inhibition in Spondyloarthritis Is Associated With Subclinical Gut Microbiome Perturbations and a Distinctive Interleukin-25-Driven Intestinal Inflammation. <i>Arthritis and Rheumatology</i> , 2020, 72, 645-657.	2.9	51
11158	Hypothalamic transcriptome of tame and aggressive silver foxes ( <i>Vulpes vulpes</i> ) identifies gene expression differences shared across brain regions. <i>Genes, Brain and Behavior</i> , 2020, 19, e12614.	1.1	24
11159	Plant Regulomics: a data-driven interface for retrieving upstream regulators from plant multi-omics data. <i>Plant Journal</i> , 2020, 101, 237-248.	2.8	75
11160	Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292.	2.8	25
11161	tuxnet: a simple interface to process RNA sequencing data and infer gene regulatory networks. <i>Plant Journal</i> , 2020, 101, 716-730.	2.8	20
11162	Screening of significant biomarkers related with prognosis of liver cancer by lncRNA-associated ceRNAs analysis. <i>Journal of Cellular Physiology</i> , 2020, 235, 2464-2477.	2.0	32
11163	The effect of cadmium on the microRNAome, degradome and transcriptome of rice seedlings. <i>Plant Growth Regulation</i> , 2020, 90, 15-27.	1.8	7
11164	Galectin-3 Exerts a Pro-differentiating and Pro-myelinating Effect Within a Temporal Window Spanning Precursors and Pre-oligodendrocytes: Insights into the Mechanisms of Action. <i>Molecular Neurobiology</i> , 2020, 57, 976-987.	1.9	11
11165	Investigation of binding mechanism and downregulation of elacestrant for wild and L536S mutant estrogen receptor- $\alpha$ through molecular dynamics simulation and binding free energy analysis. <i>Journal of Computational Chemistry</i> , 2020, 41, 97-109.	1.5	7
11166	Machine learning techniques for protein function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 397-413.	1.5	90

#	ARTICLE	IF	CITATIONS
11167	Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194418.	0.9	39
11168	Multiple outcome meta-analysis of gene-expression data in inflammatory bowel disease. <i>Genomics</i> , 2020, 112, 1761-1767.	1.3	10
11169	Allosteric mechanism of an oximino- $\epsilon$ -piperidino- $\epsilon$ -piperidine antagonist for the CCR5 chemokine receptor. <i>Chemical Biology and Drug Design</i> , 2020, 95, 113-123.	1.5	1
11170	Complex patterns of dopamine-related gene expression in the ventral tegmental area of male zebra finches relate to dyadic interactions with long-term female partners. <i>Genes, Brain and Behavior</i> , 2020, 19, e12619.	1.1	6
11171	Insights into the chemosensory basis of flavor in table grapes. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 1405-1417.	1.7	20
11172	The Composition and Phosphorus Cycling Potential of Bacterial Communities Associated With Hyphae of <i>Penicillium</i> in Soil Are Strongly Affected by Soil Origin. <i>Frontiers in Microbiology</i> , 2019, 10, 2951.	1.5	19
11173	Brain-Derived Extracellular Vesicle microRNA Signatures Associated with In Utero and Postnatal Oxycodone Exposure. <i>Cells</i> , 2020, 9, 21.	1.8	38
11174	A Model of Hormonal Regulation of Stamen Abortion during Pre-Meiosis of <i>Litsea cubeba</i> . <i>Genes</i> , 2020, 11, 48.	1.0	12
11175	Comparative Transcriptomics Provides Insight into Floral Color Polymorphism in a <i>Pleione limprichtii</i> Orchid Population. <i>International Journal of Molecular Sciences</i> , 2020, 21, 247.	1.8	32
11176	Integrated Metabolomics and Transcriptomics Suggest the Global Metabolic Response to 2-Aminoacrylate Stress in <i>Salmonella enterica</i> . <i>Metabolites</i> , 2020, 10, 12.	1.3	11
11177	The <i>Xylella fastidiosa</i> -Resistant Olive Cultivar "Leccino" Has Stable Endophytic Microbiota during the Olive Quick Decline Syndrome (OQDS). <i>Pathogens</i> , 2020, 9, 35.	1.2	39
11178	The Diversity of Associated Microorganisms in Different Organs and Rhizospheric Soil of <i>Arctium lappa</i> L.. <i>Current Microbiology</i> , 2020, 77, 746-754.	1.0	6
11179	RHON1 Co-transcriptionally Resolves R-Loops for Arabidopsis Chloroplast Genome Maintenance. <i>Cell Reports</i> , 2020, 30, 243-256.e5.	2.9	29
11180	Data-Mining Approach on Transcriptomics and Methylomics Placental Analysis Highlights Genes in Fetal Growth Restriction. <i>Frontiers in Genetics</i> , 2019, 10, 1292.	1.1	13
11181	Bacillus Strains Associated to <i>Homoscleromorpha</i> Sponges are Highly Active Against Multidrug Resistant Bacteria. <i>Current Microbiology</i> , 2020, 77, 807-815.	1.0	24
11182	Harvesting of Prebiotic Fructooligosaccharides by Nonbeneficial Human Gut Bacteria. <i>MSphere</i> , 2020, 5, .	1.3	12
11183	CD3D is associated with immune checkpoints and predicts favorable clinical outcome in colon cancer. <i>Immunotherapy</i> , 2020, 12, 25-35.	1.0	31
11184	Exploration of key regulators driving primary feather follicle induction in goose skin. <i>Gene</i> , 2020, 731, 144338.	1.0	9



#	ARTICLE	IF	CITATIONS
11185	Signature of genome wide gene expression in classical swine fever virus infected macrophages and PBMCs of indigenous vis-a-vis crossbred pigs. <i>Gene</i> , 2020, 731, 144356.	1.0	6
11186	The Database of Cross-Linguistic Colexifications, reproducible analysis of cross-linguistic polysemies. <i>Scientific Data</i> , 2020, 7, 13.	2.4	60
11187	A unifying paradigm for transcriptional heterogeneity and squamous features in pancreatic ductal adenocarcinoma. <i>Nature Cancer</i> , 2020, 1, 59-74.	5.7	124
11188	New Benthic Cyanobacteria from Guadeloupe Mangroves as Producers of Antimicrobials. <i>Marine Drugs</i> , 2020, 18, 16.	2.2	13
11189	Epigenetic response of endothelial cells to different wall shear stress magnitudes: A report of new mechano- $\mu$ miRNAs. <i>Journal of Cellular Physiology</i> , 2020, 235, 7827-7839.	2.0	20
11190	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSP $\alpha$ TF and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	0.8	4
11191	Genetic analysis of oxidative and endoplasmic reticulum stress responses induced by cobalt toxicity in budding yeast. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129516.	1.1	10
11192	Mucosal microbial load in Crohn's disease: A potential predictor of response to faecal microbiota transplantation. <i>EBioMedicine</i> , 2020, 51, 102611.	2.7	21
11193	The bacterial community structures in response to the gut passage of earthworm ( <i>Eisenia fetida</i> ) feeding on cow dung and domestic sludge: Illumina high-throughput sequencing-based data analysis. <i>Ecotoxicology and Environmental Safety</i> , 2020, 190, 110149.	2.9	25
11194	Large-scale patterns of soil antibiotic resistome in Chinese croplands. <i>Science of the Total Environment</i> , 2020, 712, 136418.	3.9	53
11195	Outer Radial Glia-like Cancer Stem Cells Contribute to Heterogeneity of Glioblastoma. <i>Cell Stem Cell</i> , 2020, 26, 48-63.e6.	5.2	222
11196	Toxic consequences and oxidative protein carbonylation from chloropicrin exposure in human corneal epithelial cells. <i>Toxicology Letters</i> , 2020, 322, 1-11.	0.4	17
11197	Regulatory network analysis of Paneth cell and goblet cell enriched gut organoids using transcriptomics approaches. <i>Molecular Omics</i> , 2020, 16, 39-58.	1.4	31
11198	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020, 16, 59-72.	1.4	11
11199	Identification of Potential Biomarkers for Intervertebral Disc Degeneration Using the Genome-Wide Expression Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1341-1349.	0.8	2
11200	KRCC1: A potential therapeutic target in ovarian cancer. <i>FASEB Journal</i> , 2020, 34, 2287-2300.	0.2	5
11201	Rapid Affinity Purification of Tagged Plant Mitochondria (Mito-AP) for Metabolome and Proteome Analyses. <i>Plant Physiology</i> , 2020, 182, 1194-1210.	2.3	42
11202	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. <i>Neuron</i> , 2020, 105, 975-991.e7.	3.8	287



#	ARTICLE	IF	CITATIONS
11203	Algorithm-based coevolution network identification reveals key functional residues of the $\beta$ -glucuronidase subfamilies. <i>FASEB Journal</i> , 2020, 34, 1983-1995.	0.2	7
11204	Differential Gene Expression in Circulating CD14+ Monocytes Indicates the Prognosis of Critically Ill Patients with Sepsis. <i>Journal of Clinical Medicine</i> , 2020, 9, 127.	1.0	18
11205	Network pharmacology based research into the effect and mechanism of Xijiao Dihuang decoction against sepsis. <i>Biomedicine and Pharmacotherapy</i> , 2020, 122, 109777.	2.5	26
11206	Removal of antibiotic resistant bacteria and antibiotic resistance genes in wastewater effluent by UV-activated persulfate. <i>Journal of Hazardous Materials</i> , 2020, 388, 122070.	6.5	102
11207	Identification of common key genes and pathways between type 1 diabetes and multiple sclerosis using transcriptome and interactome analysis. <i>Endocrine</i> , 2020, 68, 81-92.	1.1	21
11208	Pagoamide A, a Cyclic Depsipeptide Isolated from a Cultured Marine Chlorophyte, <i>Derbesia</i> sp., Using MS/MS-Based Molecular Networking. <i>Journal of Natural Products</i> , 2020, 83, 617-625.	1.5	22
11209	Architecture of The Human Ape1 Interactome Defines Novel Cancers Signatures. <i>Scientific Reports</i> , 2020, 10, 28.	1.6	22
11210	Concurrent lipidomics and proteomics on malignant plasma cells from multiple myeloma patients: Probing the lipid metabolome. <i>PLoS ONE</i> , 2020, 15, e0227455.	1.1	17
11211	Characterizing community dynamics and exploring bacterial assemblages in two activated sludge systems. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1795-1808.	1.7	11
11212	Metabolic compounds within the porcine uterine environment are unique to the type of conceptus present during the early stages of blastocyst elongation. <i>Molecular Reproduction and Development</i> , 2020, 87, 174-190.	1.0	9
11213	Patterns of immune infiltration in lung adenocarcinoma revealed a prognosis-associated microRNA-mast cells network. <i>Human Cell</i> , 2020, 33, 205-219.	1.2	6
11214	The atherosclerosis-ameliorating effects and molecular mechanisms of BuYangHuanWu decoction. <i>Biomedicine and Pharmacotherapy</i> , 2020, 123, 109664.	2.5	35
11215	Rationalization of a traditional liver medicine using systems biology approach and its evaluation in preclinical trial. <i>Computational Biology and Chemistry</i> , 2020, 84, 107196.	1.1	9
11216	Estuarine sediments are key hotspots of intracellular and extracellular antibiotic resistance genes: A high-throughput analysis in Haihe Estuary in China. <i>Environment International</i> , 2020, 135, 105385.	4.8	55
11217	Exploring core functional microbiota related with flavor compounds involved in the fermentation of a natural fermented plain sufu (Chinese fermented soybean curd). <i>Food Microbiology</i> , 2020, 90, 103408.	2.1	56
11218	A UHPLC-MS/MS based metabolomics and chemoinformatics approach to chemically distinguish "super foods" from a variety of plant-based foods. <i>Food Chemistry</i> , 2020, 313, 126071.	4.2	18
11219	Bioturbation effect of fortified Daqu on microbial community and flavor metabolite in Chinese strong-flavor liquor brewing microecosystem. <i>Food Research International</i> , 2020, 129, 108851.	2.9	86
11220	Understanding the social evolution of the Java community in Stack Overflow: A 10-year study of developer interactions. <i>Future Generation Computer Systems</i> , 2020, 105, 446-454.	4.9	9

#	ARTICLE	IF	CITATIONS
11221	Comprehensive analysis of dysregulated lncRNAs and their competing endogenous RNA network in triple-negative breast cancer. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 429-436.	3.6	33
11222	The ingredient co-occurrence network of packaged foods distributed in the United States. <i>Journal of Food Composition and Analysis</i> , 2020, 86, 103391.	1.9	8
11223	Up-regulation of Sirt1/miR-149-5p signaling may play a role in resveratrol induced protection against ischemia via p53 in rat brain. <i>Journal of Clinical Neuroscience</i> , 2020, 72, 402-411.	0.8	40
11224	Characterizing fruit ripening in plantain and Cavendish bananas: A proteomics approach. <i>Journal of Proteomics</i> , 2020, 214, 103632.	1.2	20
11225	Omic approaches to decipher the molecular mechanisms of fibrosis, and design new anti-fibrotic strategies. <i>Seminars in Cell and Developmental Biology</i> , 2020, 101, 161-169.	2.3	11
11226	Microglial microRNAs mediate sex-specific responses to tau pathology. <i>Nature Neuroscience</i> , 2020, 23, 167-171.	7.1	79
11227	Combined EGFR and ROCK Inhibition in Triple-negative Breast Cancer Leads to Cell Death Via Impaired Autophagic Flux. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 261-277.	2.5	14
11228	Analyzing the genes and pathways related to major depressive disorder via a systems biology approach. <i>Brain and Behavior</i> , 2020, 10, e01502.	1.0	30
11229	Identification of 102 Correlations between Serum Metabolites and Habitual Diet in a Metabolomics Study of the Prostate, Lung, Colorectal, and Ovarian Cancer Trial. <i>Journal of Nutrition</i> , 2020, 150, 694-703.	1.3	27
11230	Microbiome-Guided Exploration of the Microbial Assemblage of the Exotic Beverage "Insect Tea" Native to Southwestern China. <i>Frontiers in Microbiology</i> , 2020, 10, 3087.	1.5	2
11231	Bringing data from curated pathway resources to Cytoscape with OmniPath. <i>Bioinformatics</i> , 2020, 36, 2632-2633.	1.8	30
11232	A comprehensive analysis on the effects of 1,25(OH)2D3 on primary chondrocytes cultured from patients with osteoarthritis. <i>Gene</i> , 2020, 730, 144322.	1.0	8
11233	Mice lacking uterine enhancer of zeste homolog 2 have transcriptomic changes associated with uterine epithelial proliferation. <i>Physiological Genomics</i> , 2020, 52, 81-95.	1.0	9
11234	miRNA-150-5p promotes hepatic stellate cell proliferation and sensitizes hepatocyte apoptosis during liver fibrosis. <i>Epigenomics</i> , 2020, 12, 53-67.	1.0	25
11235	Proteomic analysis of whey proteins in the colostrum and mature milk of Xinong Saanen goats. <i>Journal of Dairy Science</i> , 2020, 103, 1164-1174.	1.4	23
11236	Evaluation of miRNA Expression Profiles in Schizophrenia Using Principal-Component Analysis-Based Unsupervised Feature Extraction Method. <i>Journal of Computational Biology</i> , 2020, 27, 1253-1263.	0.8	7
11237	Regulation of color transition in purple tea ( <i>Camellia sinensis</i> ). <i>Planta</i> , 2020, 251, 35.	1.6	21
11238	Serum metabolic fingerprinting of pre-lameness dairy cows by GC-MS reveals typical profiles that can identify susceptible cows. <i>Journal of Proteomics</i> , 2020, 213, 103620.	1.2	8

#	ARTICLE	IF	CITATIONS
11239	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein-Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 1874-1882.	3.2	20
11240	Identification of prognostic genes in adrenocortical carcinoma microenvironment based on bioinformatic methods. <i>Cancer Medicine</i> , 2020, 9, 1161-1172.	1.3	44
11241	Population dynamics of methanogens and methanotrophs along the salinity gradient in Pearl River Estuary: implications for methane metabolism. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1331-1346.	1.7	34
11242	SILAC-based quantitative proteomics reveals pleiotropic, phenotypic modulation in primary murine macrophages infected with the protozoan pathogen <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2020, 213, 103617.	1.2	9
11243	Exploring a <i>Drosophila</i> Transcription Factor Interaction Network to Identify Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2020, 27, 1313-1328.	0.8	0
11244	Succession of bacterial community and methanotrophy during lake shrinkage. <i>Journal of Soils and Sediments</i> , 2020, 20, 1545-1557.	1.5	12
11245	Identification of common candidate genes and pathways for progression of ovarian, cervical and endometrial cancers. <i>Meta Gene</i> , 2020, 23, 100634.	0.3	6
11246	Species differences in immune-mediated CNS tissue injury and repair: A (neuro)inflammatory topic. <i>Glia</i> , 2020, 68, 811-829.	2.5	28
11247	Succession of phytoplankton community during intensive shrimp ( <i>Litopenaeus vannamei</i> ) cultivation and its effects on cultivation systems. <i>Aquaculture</i> , 2020, 520, 734733.	1.7	11
11248	Estrogen receptor 1 and progesterone receptor are distinct biomarkers and prognostic factors in estrogen receptor-positive breast cancer: Evidence from a bioinformatic analysis. <i>Biomedicine and Pharmacotherapy</i> , 2020, 121, 109647.	2.5	19
11249	Glioblastoma models driven by different mutations converge to the proneural subtype. <i>Cancer Letters</i> , 2020, 469, 447-455.	3.2	13
11250	Molecular mechanism of action of Liuwei Dihuang pill for the treatment of osteoporosis based on network pharmacology and molecular docking. <i>European Journal of Integrative Medicine</i> , 2020, 33, 101009.	0.8	8
11251	Generating topological protein interaction scores and data visualization with TopS. <i>Methods</i> , 2020, 184, 13-18.	1.9	5
11252	Bioinformatics-assisted, integrated omics studies on medicinal plants. <i>Briefings in Bioinformatics</i> , 2020, 21, 1857-1874.	3.2	26
11253	Gene network analysis reveals a core set of genes involved in the immune response of Japanese flounder ( <i>Paralichthys olivaceus</i> ) against <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 98, 800-809.	1.6	33
11254	Plant virus interaction mechanism and associated pathways in mosaic disease of small cardamom ( <i>Elettaria cardamomum</i> Maton) by RNA-Seq approach. <i>Genomics</i> , 2020, 112, 2041-2051.	1.3	5
11255	<i>In Silico</i> Identification of Probable Drug and Vaccine Candidates Against Antibiotic-Resistant <i>Acinetobacter baumannii</i> . <i>Microbial Drug Resistance</i> , 2020, 26, 456-467.	0.9	8
11256	The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2020, 182, 857-869.	2.3	35

#	ARTICLE	IF	CITATIONS
11257	Identification of the key differentially expressed genes and pathways involved in neutrophilia. <i>Innate Immunity</i> , 2020, 26, 270-284.	1.1	1
11258	Genetic architecture of subspecies divergence in trace mineral accumulation and elemental correlations in the rice grain. <i>Theoretical and Applied Genetics</i> , 2020, 133, 529-545.	1.8	38
11259	Identification of Marker Genes and Pathways in Patients with Primary Biliary Cholangitis. <i>Journal of Computational Biology</i> , 2020, 27, 923-933.	0.8	2
11260	Acquisition of a Unique Mesenchymal Precursor-like Blastema State Underlies Successful Adult Mammalian Digit Tip Regeneration. <i>Developmental Cell</i> , 2020, 52, 509-524.e9.	3.1	74
11261	Correlates of Nonrandom Patterns of Serotype Switching in <i>Pneumococcus</i> . <i>Journal of Infectious Diseases</i> , 2020, 221, 1669-1676.	1.9	4
11262	Soil fungal and prokaryotic community structure exhibits differential short-term responses to timber harvest in the Pacific Northwest. <i>Pedosphere</i> , 2020, 30, 109-125.	2.1	4
11263	Mapping axon initial segment structure and function by multiplexed proximity biotinylation. <i>Nature Communications</i> , 2020, 11, 100.	5.8	73
11264	Identification of potential key genes for HER-2 positive breast cancer based on bioinformatics analysis. <i>Medicine (United States)</i> , 2020, 99, e18445.	0.4	19
11265	Sex-specific and opposite modulatory aspects revealed by PPI network and pathway analysis of ischemic stroke in humans. <i>PLoS ONE</i> , 2020, 15, e0227481.	1.1	3
11266	Mining of cancer core-genes and their protein interactome using expression profiling based PPI network approach. <i>Gene Reports</i> , 2020, 18, 100583.	0.4	3
11267	Single molecule sequencing reveals response of manganese-oxidizing microbiome to different biofilter media in drinking water systems. <i>Water Research</i> , 2020, 171, 115424.	5.3	26
11268	A Comprehensive Tyrosine Phosphoproteomic Analysis Reveals Novel Components of the Platelet CLEC-2 Signaling Cascade. <i>Thrombosis and Haemostasis</i> , 2020, 120, 262-276.	1.8	22
11269	AMPK Interactome Reveals New Function in Non-homologous End Joining DNA Repair. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 467-477.	2.5	11
11270	Multi-omic Characterization of the Mode of Action of a Potent New Antimalarial Compound, JPC-3210, Against <i>Plasmodium falciparum</i> . <i>Molecular and Cellular Proteomics</i> , 2020, 19, 308-325.	2.5	30
11271	ECHO, the executable CHondrocyte: A computational model to study articular chondrocytes in health and disease. <i>Cellular Signalling</i> , 2020, 68, 109471.	1.7	13
11272	Differential Expression of Rice Valine-Glutamine Gene Family in Response to Nitric Oxide and Regulatory Circuit of OsVQ7 and OsWRKY24. <i>Rice Science</i> , 2020, 27, 10-20.	1.7	6
11273	Multi-level transcriptome sequencing identifies COL1A1 as a candidate marker in human heart failure progression. <i>BMC Medicine</i> , 2020, 18, 2.	2.3	65
11274	ELF5 modulates the estrogen receptor cistrome in breast cancer. <i>PLoS Genetics</i> , 2020, 16, e1008531.	1.5	17

#	ARTICLE	IF	CITATIONS
11275	An Integrative Transcriptome Analysis Reveals Consistently Dysregulated Long Noncoding RNAs and Their Transcriptional Regulation Relationships in Heart Failure. <i>Journal of Computational Biology</i> , 2020, 27, 958-964.	0.8	2
11276	Reflections on integrating bioinformatics into the undergraduate curriculum: The Lancaster experience. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 118-127.	0.5	8
11277	Proteomics Analysis of <i>Candida albicans</i> dnm1 Haploid Mutant Unraveled the Association between Mitochondrial Fission and Antifungal Susceptibility. <i>Proteomics</i> , 2020, 20, e1900240.	1.3	12
11278	Lipidomic profiling of dairy cattle oocytes by high performance liquid chromatography-high resolution tandem mass spectrometry for developmental competence markers. <i>Theriogenology</i> , 2020, 144, 56-66.	0.9	10
11279	Long-term nutrient inputs shift soil microbial functional profiles of phosphorus cycling in diverse agroecosystems. <i>ISME Journal</i> , 2020, 14, 757-770.	4.4	280
11280	The coding and non-coding transcriptional landscape of subependymal giant cell astrocytomas. <i>Brain</i> , 2020, 143, 131-149.	3.7	24
11281	Identification of microRNAs in skeletal muscle associated with lung cancer cachexia. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020, 11, 452-463.	2.9	40
11282	Human Rhinovirus Inhibition Through Capsid "Canyon" Perturbation: Structural Insights into The Role of a Novel Benzothioephene Derivative. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 3-13.	0.9	9
11283	Conserved and divergent expression dynamics during early patterning of the telencephalon in mouse and chick embryos. <i>Progress in Neurobiology</i> , 2020, 186, 101735.	2.8	10
11284	Transcriptome analysis of the thermosensitive genic male-sterile line provides new insights into fertility alteration in rice ( <i>Oryza sativa</i> ). <i>Genomics</i> , 2020, 112, 2119-2129.	1.3	13
11285	Metabolite database for root, tuber, and banana crops to facilitate modern breeding in understudied crops. <i>Plant Journal</i> , 2020, 101, 1258-1268.	2.8	35
11286	Expression changes in protein-coding genes and long non-coding RNAs in denatured dermis following thermal injury. <i>Burns</i> , 2020, 46, 1128-1135.	1.1	6
11287	Gut microbiome associated with APC gene mutation in patients with intestinal adenomatous polyps. <i>International Journal of Biological Sciences</i> , 2020, 16, 135-146.	2.6	42
11288	Derivation of notochordal cells from human embryonic stem cells reveals unique regulatory networks by single cell transcriptomics. <i>Journal of Cellular Physiology</i> , 2020, 235, 5241-5255.	2.0	18
11289	Clinical class 1 integron-integrase gene "A promising indicator to monitor the abundance and elimination of antibiotic resistance genes in an urban wastewater treatment plant. <i>Environment International</i> , 2020, 135, 105372.	4.8	89
11290	Protist Interactions and Community Structure During Early Autumn in the Kerguelen Region (Southern Ocean). <i>Protist</i> , 2020, 171, 125709.	0.6	25
11291	High-density chemical cross-linking for modeling protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 93-102.	3.3	56
11292	Identification of miR-210 and combination biomarkers as useful agents in early screening non-small cell lung cancer. <i>Gene</i> , 2020, 729, 144225.	1.0	6

#	ARTICLE	IF	CITATIONS
11293	Skeletal muscle transcriptional networks linked to type I myofiber grouping in Parkinson's disease. <i>Journal of Applied Physiology</i> , 2020, 128, 229-240.	1.2	18
11294	Arsenic and cadmium as predominant factors shaping the distribution patterns of antibiotic resistance genes in polluted paddy soils. <i>Journal of Hazardous Materials</i> , 2020, 389, 121838.	6.5	77
11295	The regulation mechanism of lncRNAs and mRNAs in sea cucumbers under global climate changes: Defense against thermal and hypoxic stresses. <i>Science of the Total Environment</i> , 2020, 709, 136045.	3.9	21
11296	Biogeographic patterns of microbial association networks in paddy soil within Eastern China. <i>Soil Biology and Biochemistry</i> , 2020, 142, 107696.	4.2	59
11297	Dark-Induced Senescence Causes Localized Changes in DNA Methylation. <i>Plant Physiology</i> , 2020, 182, 949-961.	2.3	11
11298	A PXY-Mediated Transcriptional Network Integrates Signaling Mechanisms to Control Vascular Development in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 319-335.	3.1	103
11299	Identifying common genome-wide risk genes for major psychiatric traits. <i>Human Genetics</i> , 2020, 139, 185-198.	1.8	40
11300	Effects of industrial effluents containing moderate levels of antibiotic mixtures on the abundance of antibiotic resistance genes and bacterial community composition in exposed creek sediments. <i>Science of the Total Environment</i> , 2020, 706, 136001.	3.9	24
11301	Network analysis reveals succession of <i>Microcystis</i> genotypes accompanying distinctive microbial modules with recurrent patterns. <i>Water Research</i> , 2020, 170, 115326.	5.3	51
11302	Exploring the Activation Mechanism of a Metabotropic Glutamate Receptor Homodimer via Molecular Dynamics Simulation. <i>ACS Chemical Neuroscience</i> , 2020, 11, 133-145.	1.7	12
11303	Temperature-mediated shifts in salamander transcriptomic responses to the amphibian-killing fungus. <i>Molecular Ecology</i> , 2020, 29, 325-343.	2.0	24
11304	Analysis of topology properties in different tissues of poplar based on gene co-expression networks. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	4
11305	Comparative Proteomics Unravels the Differences in Salt Stress Response of Own-Rooted and 110R-Grafted Thompson Seedless Grapevines. <i>Journal of Proteome Research</i> , 2020, 19, 583-599.	1.8	8
11306	Identification of differentially expressed genes between the colon and ileum of patients with inflammatory bowel disease by gene co-expression analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006051988726.	0.4	10
11307	TulsiPIN: An Interologous Protein Interactome of <i>Ocimum tenuiflorum</i> . <i>Journal of Proteome Research</i> , 2020, 19, 884-899.	1.8	7
11308	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
11309	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020, 5, 108-115.	5.9	83
11310	Deciphering crucial genes in coeliac disease by bioinformatics analysis. <i>Autoimmunity</i> , 2020, 53, 102-113.	1.2	7



#	ARTICLE	IF	CITATIONS
11311	Responses of microbial communities to a gradient of pig manure amendment in red paddy soils. <i>Science of the Total Environment</i> , 2020, 705, 135884.	3.9	43
11312	The Al-induced proteomes of epidermal and outer cortical cells in root apex of cherry tomato $\hat{\epsilon}$ LA 2710 $\hat{\epsilon}$ TM. <i>Journal of Proteomics</i> , 2020, 211, 103560.	1.2	12
11313	( $\hat{\alpha}$ )-Epicatechin metabolites promote vascular health through epigenetic reprogramming of endothelial-immune cell signaling and reversing systemic low-grade inflammation. <i>Biochemical Pharmacology</i> , 2020, 173, 113699.	2.0	29
11314	The Abinitproject: Impact, environment and recent developments. <i>Computer Physics Communications</i> , 2020, 248, 107042.	3.0	369
11315	Temporal effects of repeated application of biogas slurry on soil antibiotic resistance genes and their potential bacterial hosts. <i>Environmental Pollution</i> , 2020, 258, 113652.	3.7	31
11316	Transcriptomics of <i>Cherax quadricarinatus</i> hepatopancreas during infection with Decapod iridescent virus 1 (DIV1). <i>Fish and Shellfish Immunology</i> , 2020, 98, 832-842.	1.6	30
11317	Antimalarial herbal remedies of Bukavu and Uvira areas in DR Congo: An ethnobotanical survey. <i>Journal of Ethnopharmacology</i> , 2020, 249, 112422.	2.0	18
11318	Extended Human G-Protein Coupled Receptor Network: Cell-Type-Specific Analysis of G-Protein Coupled Receptor Signaling Pathways. <i>Journal of Proteome Research</i> , 2020, 19, 511-524.	1.8	12
11319	Identification of candidate genes and miRNAs for sensitizing resistant colorectal cancer cells to oxaliplatin and irinotecan. <i>Cancer Chemotherapy and Pharmacology</i> , 2020, 85, 153-171.	1.1	9
11320	Distinct Patterns of mRNA and lncRNA Expression Differences Between Lung Squamous Cell Carcinoma and Adenocarcinoma. <i>Journal of Computational Biology</i> , 2020, 27, 1067-1078.	0.8	14
11321	Deciphering Molecular Virulence Mechanism of <i>Mycobacterium tuberculosis</i> Dop isopeptidase Based on Its Sequence $\hat{\epsilon}$ Structure $\hat{\epsilon}$ Function Linkage. <i>Protein Journal</i> , 2020, 39, 33-45.	0.7	6
11322	A comparative study on the mechanisms of innate immune responses in mice induced by Alum and <i>Actinidia eriantha</i> polysaccharide. <i>International Journal of Biological Macromolecules</i> , 2020, 156, 1202-1216.	3.6	10
11323	Different class IIa HDACs repressive complexes regulate specific epigenetic responses related to cell survival in leiomyosarcoma cells. <i>Nucleic Acids Research</i> , 2020, 48, 646-664.	6.5	39
11324	Network analysis of medical care services. <i>Health Informatics Journal</i> , 2020, 26, 1631-1658.	1.1	9
11325	Heterogeneity of human prostate carcinoma $\hat{\epsilon}$ associated fibroblasts implicates a role for subpopulations in myeloid cell recruitment. <i>Prostate</i> , 2020, 80, 173-185.	1.2	51
11326	Candidate lncRNA $\hat{\epsilon}$ miRNA $\hat{\epsilon}$ mRNA network in predicting hepatocarcinogenesis with cirrhosis: an integrated bioinformatics analysis. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 87-96.	1.2	33
11327	Molecular characterization and expression analysis reveal the roles of Cys2/His2 zinc-finger transcription factors during flower development of <i>Brassica rapa</i> subsp. <i>chinensis</i> . <i>Plant Molecular Biology</i> , 2020, 102, 123-141.	2.0	12
11328	Dynamic architecture and regulatory implications of the miRNA network underlying the response to stress in melon. <i>RNA Biology</i> , 2020, 17, 292-308.	1.5	17



#	ARTICLE	IF	CITATIONS
11329	High Expression of <i>FGF5</i> Is an Independent Prognostic Factor for Poor Overall Survival and Relapse-Free Survival in Lung Adenocarcinoma. <i>Journal of Computational Biology</i> , 2020, 27, 948-957.	0.8	6
11330	PenQuest: a gamified attacker/defender meta model for cyber security assessment and education. <i>Journal of Computer Virology and Hacking Techniques</i> , 2020, 16, 19-61.	1.6	18
11331	Functional Translatome Proteomics Reveal Converging and Dose-Dependent Regulation by mTORC1 and eIF2 $\beta$ . <i>Molecular Cell</i> , 2020, 77, 913-925.e4.	4.5	81
11332	The planktonic protist interactome: where do we stand after a century of research?. <i>ISME Journal</i> , 2020, 14, 544-559.	4.4	111
11333	Mapping a Transcriptome-Guided Arabidopsis SAM Interactome. <i>Methods in Molecular Biology</i> , 2020, 2094, 113-118.	0.4	0
11334	Cloning and characterization of a gene encoding MIZ1, a domain of unknown function protein and its role in salt and drought stress in rice. <i>Protoplasma</i> , 2020, 257, 475-487.	1.0	18
11335	Shrimp disease progression increases the gut bacterial network complexity and abundances of keystone taxa. <i>Aquaculture</i> , 2020, 517, 734802.	1.7	49
11336	Urbanization significantly impacts the connectivity of soil microbes involved in nitrogen dynamics at a watershed scale. <i>Environmental Pollution</i> , 2020, 258, 113708.	3.7	10
11337	Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics. <i>Science of the Total Environment</i> , 2020, 706, 135395.	3.9	11
11338	Exploring bacterial community composition in Mediterranean deep-sea sediments and their role in heavy metal accumulation. <i>Science of the Total Environment</i> , 2020, 712, 135660.	3.9	26
11339	NMR-based metabolomics analysis identifies discriminatory metabolic disturbances in tissue and biofluid samples for progressive prostate cancer. <i>Clinica Chimica Acta</i> , 2020, 501, 241-251.	0.5	27
11340	Systems pharmacology-based study of Tanreqing injection in airway mucus hypersecretion. <i>Journal of Ethnopharmacology</i> , 2020, 249, 112425.	2.0	25
11341	Robust identification of differentially expressed genes from RNA-seq data. <i>Genomics</i> , 2020, 112, 2000-2010.	1.3	20
11342	Identifying potential entry inhibitors for emerging Nipah virus by molecular docking and chemical-protein interaction network. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 5108-5125.	2.0	15
11343	Genome-wide association study for carcass quality traits and growth in purebred and crossbred pigs1. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	23
11344	Manipulating the phytoplankton community has the potential to create a stable bacterioplankton community in a shrimp rearing environment. <i>Aquaculture</i> , 2020, 520, 734789.	1.7	19
11345	Characterizing the cancer-associated microbiome with small RNA sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2020, 522, 776-782.	1.0	6
11347	Circulating miRNAs and Risk of Sudden Death in Patients With Coronary Heart Disease. <i>JACC: Clinical Electrophysiology</i> , 2020, 6, 70-79.	1.3	21

#	ARTICLE	IF	CITATIONS
11348	Multinucleated polyploid cardiomyocytes undergo an enhanced adaptability to hypoxia via mitophagy. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 138, 115-135.	0.9	12
11349	Plasma miR-370-3P as a Biomarker of Sepsis-Associated Encephalopathy, the Transcriptomic Profiling Analysis of MicroRNA-Arrays From Mouse Brains. <i>Shock</i> , 2020, 54, 347-357.	1.0	41
11350	Identification of a genetic network for an ecologically relevant behavioural phenotype in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2020, 29, 502-518.	2.0	3
11351	Impact of short- and long-term electrically induced muscle exercise on gene signaling pathways, gene expression, and PGC1a methylation in men with spinal cord injury. <i>Physiological Genomics</i> , 2020, 52, 71-80.	1.0	17
11352	m <sup>6</sup> A RNA modification modulates gene expression and cancer-related pathways in clear cell renal cell carcinoma. <i>Epigenomics</i> , 2020, 12, 87-99.	1.0	44
11353	Analysis of Differentially Expressed Genes in Coronary Artery Disease by Integrated Microarray Analysis. <i>Biomolecules</i> , 2020, 10, 35.	1.8	12
11354	Depolarization-Associated CircRNA Regulate Neural Gene Expression and in Some Cases May Function as Templates for Translation. <i>Cells</i> , 2020, 9, 25.	1.8	32
11355	The Interaction between 30b-5p miRNA and MBNL1 mRNA is Involved in Vascular Smooth Muscle Cell Differentiation in Patients with Coronary Atherosclerosis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 11.	1.8	31
11356	Hypoxia-Induced miR-210 Is Necessary for Vascular Regeneration upon Acute Limb Ischemia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 129.	1.8	19
11357	Untargeted Metabolomics to Go beyond the Canonical Effect of Acetylsalicylic Acid. <i>Journal of Clinical Medicine</i> , 2020, 9, 51.	1.0	8
11358	Identifying Early Warning Signals for the Sudden Transition from Mild to Severe Tobacco Etch Disease by Dynamical Network Biomarkers. <i>Viruses</i> , 2020, 12, 16.	1.5	9
11359	Comprehensive analysis of biological networks and the eukaryotic initiation factor 4A gene as pivotal in hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4094-4107.	1.2	11
11360	A risk signature based on metastasis-associated genes to predict survival of patients with osteosarcoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3479-3490.	1.2	38
11361	Exploration the active compounds of <i>Astragali Radix</i> in treatment of adriamycin nephropathy by network pharmacology combined with transcriptomic approach. <i>Journal of Ethnopharmacology</i> , 2020, 258, 112537.	2.0	21
11362	Identification of key genes and pathways in abdominal aortic aneurysm by integrated bioinformatics analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006051989443.	0.4	9
11363	Identification of MYB Transcription Factors Regulating Theanine Biosynthesis in Tea Plant Using Omics-Based Gene Coexpression Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 918-926.	2.4	20
11364	Coevolved Positions Represent Key Functional Properties in the Trypsin-Like Serine Proteases Protein Family. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1060-1068.	2.5	8
11365	Proteome dynamics analysis identifies functional roles of SDE2 and hypoxia in DNA damage response in prostate cancer cells. <i>NAR Cancer</i> , 2020, 2, zcaa010.	1.6	7

#	ARTICLE	IF	CITATIONS
11366	Functional networks of co-expressed genes to explore iron homeostasis processes in the pathogenic yeast <i>Candida glabrata</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa027.	1.5	6
11367	Identification of potential gene drivers of cutaneous squamous cell carcinoma. <i>Medicine (United Tj ETQq1 1 0.784314 rgBT /Overloc</i>	0.4	6
11368	Prognostic value and immune cell infiltration of hypoxic phenotype-related gene signatures in glioblastoma microenvironment. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13235-13247.	1.6	12
11369	Integrative glycoproteomics reveals protein N-glycosylation aberrations and glycoproteomic network alterations in Alzheimer's disease. <i>Science Advances</i> , 2020, 6, .	4.7	56
11370	Static Growth Promotes PrrF and 2-Alkyl-4(1-H)-Quinolone Regulation of Type VI Secretion Protein Expression in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	9
11371	Blood pressure changes PVAT function and transcriptome: use of the mid-thoracic aorta coarcted rat. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2020, 319, H1313-H1324.	1.5	4
11372	Establishment and Investigation of a Multiple Gene Expression Signature to Predict Long-Term Survival in Pancreatic Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-20.	0.9	1
11373	Comprehensive Analysis of a ceRNA Network Identifies lncR-C3orf35 Associated with Poor Prognosis in Osteosarcoma. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3
11374	Potential Molecular Mechanisms of Chaihu-Shugan-San in Treatment of Breast Cancer Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-9.	0.5	11
11375	Identification of the specific microRNAs and competitive endogenous RNA mechanisms in osteoporosis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095472.	0.4	5
11376	Identification of Parkinson's disease-related pathways and potential risk factors. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095719.	0.4	6
11377	Genome-wide identification and characterization of ABA receptor PYL gene family in rice. <i>BMC Genomics</i> , 2020, 21, 676.	1.2	42
11378	The effects of exopolysaccharides and exopolysaccharide-producing <i>Lactobacillus</i> on the intestinal microbiome of zebrafish ( <i>Danio rerio</i> ). <i>BMC Microbiology</i> , 2020, 20, 300.	1.3	18
11379	Herbal pair Huangqin-Baishao: mechanisms underlying inflammatory bowel disease by combined system pharmacology and cell experiment approach. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 292.	1.2	8
11380	Comprehensive analysis of angiogenesis-related genes and pathways in early diabetic retinopathy. <i>BMC Medical Genomics</i> , 2020, 13, 142.	0.7	22
11381	Integrated analysis of immune-related genes in endometrial carcinoma. <i>Cancer Cell International</i> , 2020, 20, 477.	1.8	10
11382	RNAseq Reveals Sensitive, Concentration-Dependent Transcriptional Markers of Copper in <i>Mytilus californianus</i> Larvae and Adults. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
11383	Zika Virus Infection Results in Biochemical Changes Associated With RNA Editing, Inflammatory and Antiviral Responses in <i>Aedes albopictus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 559035.	1.5	6

#	ARTICLE	IF	CITATIONS
11384	Successional Change of the Fungal Microbiome Pine Seedling Roots Inoculated With <i>Tricholoma matsutake</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 574146.	1.5	10
11385	PUMAA: A Platform for Accessible Microbiome Analysis in the Undergraduate Classroom. <i>Frontiers in Microbiology</i> , 2020, 11, 584699.	1.5	10
11386	Identification of TYROBP and C1QB as Two Novel Key Genes With Prognostic Value in Gastric Cancer by Network Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 1765.	1.3	27
11387	Significance of Tumor Mutation Burden in Immune Infiltration and Prognosis in Cutaneous Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 573141.	1.3	63
11388	Dynamics of a Protein Interaction Network Associated to the Aggregation of polyQ-Expanded Ataxin-1. <i>Genes</i> , 2020, 11, 1129.	1.0	4
11389	Finding New Molecular Targets of Familiar Natural Products Using In Silico Target Prediction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7102.	1.8	10
11390	Hetiamacin E and F, New Amicoumacin Antibiotics from <i>Bacillus subtilis</i> PJS Using MS/MS-Based Molecular Networking. <i>Molecules</i> , 2020, 25, 4446.	1.7	15
11391	Panomicon: A web-based environment for interactive, visual analysis of multi-omics data. <i>Heliyon</i> , 2020, 6, e04618.	1.4	3
11392	Label-Free Quantitative Phosphoproteomics Reveals Signaling Dynamics Involved in Embryogenic Competence Acquisition in Sugarcane. <i>Journal of Proteome Research</i> , 2020, 19, 4145-4157.	1.8	11
11393	A system-level approach identifies HIF-2 $\beta$ as a critical regulator of chondrosarcoma progression. <i>Nature Communications</i> , 2020, 11, 5023.	5.8	14
11394	Integrated network pharmacology and molecular docking strategy to explore the mechanism of medicinal and edible <i>Astragali Radix</i> <i>Atractylodis Macrocephalae Rhizoma</i> acting on pneumonia via immunomodulation. <i>Journal of Food Biochemistry</i> , 2020, 44, e13510.	1.2	5
11395	An Integrated Analysis of mRNAs and miRNAs Microarray Profiles to Screen miRNA Signatures Involved in Nasopharyngeal Carcinoma. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382095699.	0.8	6
11396	TOP2A and CENPF are synergistic master regulators activated in cervical cancer. <i>BMC Medical Genomics</i> , 2020, 13, 145.	0.7	21
11397	Inhibitory Effect of a Human MicroRNA, miR-6133-5p, on the Fibrotic Activity of Hepatic Stellate Cells in Culture. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7251.	1.8	9
11398	Association of Virulence and Antibiotic Resistance in <i>Salmonella</i> —Statistical and Computational Insights into a Selected Set of Clinical Isolates. <i>Microorganisms</i> , 2020, 8, 1465.	1.6	16
11399	Identification of angiotensin-converting enzyme 2 (ACE2) protein as the potential biomarker in SARS-CoV-2 infection-related lung cancer using computational analyses. <i>Genomics</i> , 2020, 112, 4912-4923.	1.3	31
11400	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , 2020, 7, 326.	2.4	40
11401	Tumor Microenvironment-Associated Immune-Related Genes for the Prognosis of Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2020, 10, 544789.	1.3	11

#	ARTICLE	IF	CITATIONS
11402	Analysis of lncRNA Expression Profile during the Formation of Male Germ Cells in Chickens. <i>Animals</i> , 2020, 10, 1850.	1.0	9
11403	Multi-tissue Multi-omics Nutrigenomics Indicates Context-specific Effects of Docosahexaenoic Acid on Rat Brain. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000788.	1.5	2
11404	Characterization of immune pleiotropy of ESR1 gene in pigs. <i>Immunogenetics</i> , 2020, 72, 413-422.	1.2	1
11405	Transcriptome analysis provides insights into the effects of myo-inositol on the turbot <i>Scophthalmus maximus</i> . <i>Fish and Shellfish Immunology</i> , 2020, 106, 691-704.	1.6	14
11406	Gene network analysis of efflux pump proteins in <i>Shigella</i> spp.. <i>Gene Reports</i> , 2020, 21, 100839.	0.4	2
11407	Functional attributes and response of bacterial communities to nature-based fertilization during hydrocarbon remediation. <i>International Biodeterioration and Biodegradation</i> , 2020, 154, 105084.	1.9	7
11408	An integrative gene network-based approach to uncover the cellular and molecular infrastructures of schizophrenia. <i>Life Sciences</i> , 2020, 260, 118345.	2.0	7
11409	Identification of hub genes in unstable atherosclerotic plaque by conjoint analysis of bioinformatics. <i>Life Sciences</i> , 2020, 262, 118517.	2.0	8
11410	Glyoxalase 1 expression analysis by immunohistochemistry in breast cancer. <i>Pathology Research and Practice</i> , 2020, 216, 153257.	1.0	3
11411	Transcriptional network inference and master regulator analysis of the response to ribosome-inactivating proteins in leukemia cells. <i>Toxicology</i> , 2020, 441, 152531.	2.0	4
11412	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	5.8	90
11413	Correlation between bacterial communities and organic acids in the fermentation stage of traditional Chinese sour porridge. <i>International Journal of Food Properties</i> , 2020, 23, 1430-1440.	1.3	11
11414	The species evenness of "prey" bacteria correlated with <i>Bdellovibrio</i> -and-like-organisms (BALOs) in the microbial network supports the biomass of BALOs in a paddy soil. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	3
11415	A systems genetics approach reveals environment-dependent associations between SNPs, protein coexpression, and drought-related traits in maize. <i>Genome Research</i> , 2020, 30, 1593-1604.	2.4	10
11416	The expression of seven key genes can predict distant metastasis of colorectal cancer to the liver or lung. <i>Journal of Digestive Diseases</i> , 2020, 21, 639-649.	0.7	12
11417	Ancestral gene duplications in mosses characterized by integrated phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2022, 60, 144-159.	1.6	19
11418	Resequencing of 296 cultivated and wild lotus accessions unravels its evolution and breeding history. <i>Plant Journal</i> , 2020, 104, 1673-1684.	2.8	21
11419	Endothelial extracellular vesicles contain protective proteins and rescue ischemia-reperfusion injury in a human heart-on-chip. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	66

#	ARTICLE	IF	CITATIONS
11420	Natural killer cells in the human lung tumor microenvironment display immune inhibitory functions. , 2020, 8, e001054.		54
11421	Phenotypic characterisation of early COPD: a prospective caseâ€“control study. ERJ Open Research, 2020, 6, 00047-2020.	1.1	21
11422	Integrated genomics analysis highlights important SNPs and genes implicated in moderate-to-severe asthma based on GWAS and eQTL datasets. BMC Pulmonary Medicine, 2020, 20, 270.	0.8	20
11423	Lipid metabolism gene-wide profile and survival signature of lung adenocarcinoma. Lipids in Health and Disease, 2020, 19, 222.	1.2	34
11424	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. Cancer & Metabolism, 2020, 8, 22.	2.4	10
11425	Fibrillar evolution through the Tree of Life: Comparative genomics and microsynteny network analyses provide new insights into the evolutionary history of Fibrillar. PLoS Computational Biology, 2020, 16, e1008318.	1.5	8
11426	Drug effects on metabolic profiles of <i>Schistosoma mansoni</i> adult male parasites detected by 1H-NMR spectroscopy. PLoS Neglected Tropical Diseases, 2020, 14, e0008767.	1.3	7
11427	Hypolipidemic effect of <i>Alisma orientale</i> (Sam.) Juzep on gut microecology and liver transcriptome in diabetic rats. PLoS ONE, 2020, 15, e0240616.	1.1	19
11428	Network Analysis Prioritizes <i>DEWAX</i> and <i>ICE1</i> as the Candidate Genes for Major eQTL Hotspots in Seed Germination of <i>Arabidopsis thaliana</i> . G3: Genes, Genomes, Genetics, 2020, 10, 4215-4226.	0.8	6
11429	Whole Genome Sequence Data Provides Novel Insights Into the Genetic Architecture of Meat Quality Traits in Beef. Frontiers in Genetics, 2020, 11, 538640.	1.1	12
11430	Identification of the Significant Genes Regulated by Estrogen Receptor in Estrogen Receptor-Positive Breast Cancer and Their Expression Pattern Changes When Tamoxifen or Fulvestrant Resistance Occurs. Frontiers in Genetics, 2020, 11, 538734.	1.1	14
11431	Transcriptional Programs Underlying Cold Acclimation of Common Carp ( <i>Cyprinus carpio</i> L.). Frontiers in Genetics, 2020, 11, 556418.	1.1	15
11432	Bacterial Diversity Evolution in Maya Plaster and Stone Following a Bio-Conservation Treatment. Frontiers in Microbiology, 2020, 11, 599144.	1.5	19
11433	Investigating the Transition of Pre-Symptomatic to Symptomatic Huntingtonâ€™s Disease Status Based on Omics Data. International Journal of Molecular Sciences, 2020, 21, 7414.	1.8	19
11434	Applying a Chemogeographic Strategy for Natural Product Discovery from the Marine Cyanobacterium <i>Moorea bouillonii</i> . Marine Drugs, 2020, 18, 515.	2.2	6
11435	Comprehensive lipidomic profiling in serum and multiple tissues from a mouse model of diabetes. Metabolomics, 2020, 16, 115.	1.4	14
11436	Senescence Induced by BMI1 Inhibition Is a Therapeutic Vulnerability in H3K27M-Mutant DIPG. Cell Reports, 2020, 33, 108286.	2.9	39
11437	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. Immunity, 2020, 53, 1108-1122.e5.	6.6	228



#	ARTICLE	IF	CITATIONS
11438	Identification of the Prognostic Value of Immune-Related Genes in Esophageal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 989.	1.1	16
11439	Anti-Inflammatory Potential of Cow, Donkey and Goat Milk Extracellular Vesicles as Revealed by Metabolomic Profile. <i>Nutrients</i> , 2020, 12, 2908.	1.7	19
11440	Transmission of the Bean-Associated Cytorhabdovirus by the Whitefly <i>Bemisia tabaci</i> MEAM1. <i>Viruses</i> , 2020, 12, 1028.	1.5	26
11441	Dynamic transcriptome analysis indicates extensive and discrepant transcriptomic reprogramming of two rapeseed genotypes with contrasting NUE in response to nitrogen deficiency. <i>Plant and Soil</i> , 2020, 456, 369-390.	1.8	6
11442	Patterns of immune infiltration in stable and ruptured abdominal aortic aneurysms: A gene-expression-based retrospective study. <i>Gene</i> , 2020, 762, 145056.	1.0	13
11443	Kinless hubs are potential target genes in prostate cancer network. <i>Genomics</i> , 2020, 112, 5227-5239.	1.3	16
11444	Extracellular vesicles shuttle protective messages against heat stress in bovine granulosa cells. <i>Scientific Reports</i> , 2020, 10, 15824.	1.6	24
11445	Distinct mRNA and long non-coding RNA expression profiles of decidual natural killer cells in patients with early missed abortion. <i>FASEB Journal</i> , 2020, 34, 14264-14286.	0.2	7
11446	The evolution of coloration and opsins in tarantulas. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201688.	1.2	5
11447	HLA-DPA1 gene is a potential predictor with prognostic values in multiple myeloma. <i>BMC Cancer</i> , 2020, 20, 915.	1.1	14
11448	Gene coexpression network analysis reveals a novel metabolic mechanism of <i>Clostridium acetobutylicum</i> responding to phenolic inhibitors from lignocellulosic hydrolysates. <i>Biotechnology for Biofuels</i> , 2020, 13, 163.	6.2	16
11449	Functional gene categories differentiate maize leaf drought-related microbial epiphytic communities. <i>PLoS ONE</i> , 2020, 15, e0237493.	1.1	6
11450	Transcriptomic Profiling of the Adaptive and Innate Immune Responses of Atlantic Salmon to <i>Renibacterium salmoninarum</i> Infection. <i>Frontiers in Immunology</i> , 2020, 11, 567838.	2.2	19
11451	Functional Analysis of the teosinte branched 1 Gene in the Tetraploid Switchgrass ( <i>Panicum virgatum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	18
11452	Identification and Distribution of Novel Cressdnaviruses and Circular Molecules in Four Penguin Species in South Georgia and the Antarctic Peninsula. <i>Viruses</i> , 2020, 12, 1029.	1.5	10
11453	ROS production and mitochondrial dysfunction driven by PU.1-regulated NOX4-p22phox activation in A $\beta$ 2-induced retinal pigment epithelial cell injury. <i>Theranostics</i> , 2020, 10, 11637-11655.	4.6	22
11454	<p>Identification of FADS1 Through Common Gene Expression Profiles for Predicting Survival in Patients with Bladder Cancer</p>. <i>Cancer Management and Research</i> , 2020, Volume 12, 8325-8339.	0.9	11
11455	<p>Identification of G2 and S Phase-Expressed-1 as a Potential Biomarker in Patients with Prostate Cancer</p>. <i>Cancer Management and Research</i> , 2020, Volume 12, 9259-9269.	0.9	4



#	ARTICLE	IF	CITATIONS
11456	Metabolic Health Status Contributes to Transcriptome Alternation in Human Visceral Adipose Tissue During Obesity. <i>Obesity</i> , 2020, 28, 2153-2162.	1.5	10
11457	Predicted therapeutic targets for COVID-19 disease by inhibiting SARS-CoV-2 and its related receptors. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100407.	1.9	65
11458	Flooding on Beef and Swine Farms: A Scoping Review of Effects in the Midwestern United States. <i>Preventive Veterinary Medicine</i> , 2020, 184, 105158.	0.7	3
11459	Safety assessment of drug combinations used in COVID-19 treatment: in silico toxicogenomic data-mining approach. <i>Toxicology and Applied Pharmacology</i> , 2020, 406, 115237.	1.3	15
11460	Proteomic Profiles of Thyroid Gland and Gene Expression of the Hypothalamicâ€Pituitaryâ€Thyroid Axis Are Modulated by Exposure to AgNPs during Prepubertal Rat Stages. <i>Chemical Research in Toxicology</i> , 2020, 33, 2605-2622.	1.7	7
11461	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimerâ€™s disease. <i>Nature Genetics</i> , 2020, 52, 1024-1035.	9.4	191
11462	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippelâ€Lindau tumor suppressor. <i>Scientific Reports</i> , 2020, 10, 15850.	1.6	2
11463	Virtual Screening Technique Used to Estimate the Mechanism of Adhatoda vasica Nees for the Treatment of Rheumatoid Arthritis Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	7
11464	Immunoprecipitation and mass spectrometry define TET1 interactome during oligodendrocyte differentiation. <i>Cell and Bioscience</i> , 2020, 10, 110.	2.1	7
11465	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	1.6	2
11466	MicroRNA-203 inhibits epithelial-mesenchymal transition, migration, and invasion of renal cell carcinoma cells via the inactivation of the PI3K/AKT signaling pathway by inhibiting CAV1. <i>Cell Adhesion and Migration</i> , 2020, 14, 227-241.	1.1	13
11467	Identification of osteoporosis markers through bioinformatic functional analysis of serum proteome. <i>Medicine (United States)</i> , 2020, 99, e22172.	0.4	5
11468	Integrated metabolic profiling and transcriptome analysis of pigment accumulation in diverse petal tissues in the lily cultivar â€Vivianâ€™. <i>BMC Plant Biology</i> , 2020, 20, 446.	1.6	13
11469	Both Wnt signaling and epidermal stem cell-derived extracellular vesicles are involved in epidermal cell growth. <i>Stem Cell Research and Therapy</i> , 2020, 11, 415.	2.4	6
11470	Identification of the significant pathways of Banxia Houpu decoction in the treatment of depression based on network pharmacology. <i>PLoS ONE</i> , 2020, 15, e0239843.	1.1	7
11471	Defining the proteolytic landscape during enterovirus infection. <i>PLoS Pathogens</i> , 2020, 16, e1008927.	2.1	36
11472	Single-step genome-wide association studies (GWAS) and post-GWAS analyses to identify genomic regions and candidate genes for milk yield in Brazilian Girolando cattle. <i>Journal of Dairy Science</i> , 2020, 103, 10347-10360.	1.4	15
11473	Controls on Soil Organic Matter Degradation and Subsequent Greenhouse Gas Emissions Across a Permafrost Thaw Gradient in Northern Sweden. <i>Frontiers in Earth Science</i> , 2020, 8, .	0.8	29

#	ARTICLE	IF	CITATIONS
11474	Transcriptomic Changes in Young Japanese Males After Exposure to Acute Hypobaric Hypoxia. <i>Frontiers in Genetics</i> , 2020, 11, 559074.	1.1	8
11475	Lineage-Specific Proteomic Signatures in the <i>Mycobacterium tuberculosis</i> Complex Reveal Differential Abundance of Proteins Involved in Virulence, DNA Repair, CRISPR-Cas, Bioenergetics and Lipid Metabolism. <i>Frontiers in Microbiology</i> , 2020, 11, 550760.	1.5	20
11476	Decrease of the pro-inflammatory M1-like response by inhibition of dipeptidyl peptidases 8/9 in THP-1 macrophages – quantitative proteomics of the proteome and secretome. <i>Molecular Immunology</i> , 2020, 127, 193-202.	1.0	6
11477	A novel DNA methylation 10-CpG prognostic signature of disease-free survival reveal that MYBL2 is associated with high risk in prostate cancer. <i>Expert Review of Anticancer Therapy</i> , 2020, 20, 1107-1119.	1.1	4
11478	Genome-wide analysis of differentially expressed mRNAs, lncRNAs, and circRNAs in chicken bursae of <i>Fabricsius</i> during infection with very virulent infectious bursal disease virus. <i>BMC Genomics</i> , 2020, 21, 724.	1.2	8
11479	Discovering the molecular differences between right- and left-sided colon cancer using machine learning methods. <i>BMC Cancer</i> , 2020, 20, 1012.	1.1	9
11480	Theoretical and in silico Analyses Reveal MYC as a Dynamic Network Biomarker in Colon and Rectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 555540.	1.1	3
11481	Integrative transcriptomic analysis for linking acute stress responses to squamous cell carcinoma development. <i>Scientific Reports</i> , 2020, 10, 17209.	1.6	4
11482	Coexpression Module Construction by Weighted Gene Coexpression Network Analysis and Identify Potential Prognostic Markers of Breast Cancer. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2020, , .	0.7	1
11483	Galectin-9-based immune risk score model helps to predict relapse in stage III small cell lung cancer. , 2020, 8, e001391.		20
11484	Predicted functional interactome of <i>Caenorhabditis elegans</i> and a web tool for the functional interpretation of differentially expressed genes. <i>Biology Direct</i> , 2020, 15, 20.	1.9	3
11485	The Endometrial Transcription Landscape of MRKH Syndrome. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 572281.	1.8	17
11486	Transcriptome Profiling of Human Monocyte-Derived Macrophages Upon CCL2 Neutralization Reveals an Association Between Activation of Innate Immune Pathways and Restriction of HIV-1 Gene Expression. <i>Frontiers in Immunology</i> , 2020, 11, 2129.	2.2	7
11487	Dendritic Cells and Microglia Have Non-redundant Functions in the Inflamed Brain with Protective Effects of Type 1 cDCs. <i>Cell Reports</i> , 2020, 33, 108291.	2.9	39
11488	Social network analysis of COVID-19 transmission in Karnataka, India. <i>Epidemiology and Infection</i> , 2020, 148, e230.	1.0	23
11489	Nebulosins: Trisubstituted Thiolane Natural Products from the Northeastern Atlantic Annelid <i>Eupolymnia nebulosa</i> . <i>Journal of Organic Chemistry</i> , 2020, 85, 14026-14041.	1.7	8
11490	Keap1 inhibition sensitizes head and neck squamous cell carcinoma cells to ionizing radiation via impaired non-homologous end joining and induced autophagy. <i>Cell Death and Disease</i> , 2020, 11, 887.	2.7	12
11491	Effects of Antibiotics on the Dynamic Balance of Bacteria and Fungi in the Gut of the German Cockroach. <i>Journal of Economic Entomology</i> , 2020, 113, 2666-2678.	0.8	14

#	ARTICLE	IF	CITATIONS
11492	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. <i>Molecular Ecology</i> , 2020, 29, 5019-5034.	2.0	57
11493	Network-Based Coexpression Analysis Identifies Functional and Prognostic Long Noncoding RNAs in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	1
11494	Identification of Potential Hub Genes and Therapeutic Drugs in Malignant Pleural Mesothelioma by Integrated Bioinformatics Analysis. <i>Oncology Research and Treatment</i> , 2020, 43, 656-671.	0.8	8
11495	Expression of mitochondrial protein genes encoded by nuclear and mitochondrial genomes correlate with energy metabolism in dairy cattle. <i>BMC Genomics</i> , 2020, 21, 720.	1.2	15
11496	Dynamics of food sources, ecotypic distribution and <i>Trypanosoma cruzi</i> infection in <i>Triatoma brasiliensis</i> from the northeast of Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008735.	1.3	18
11497	Transcriptome data reveal conserved patterns of fruiting body development and response to heat stress in the mushroom-forming fungus <i>Flammulina filiformis</i> . <i>PLoS ONE</i> , 2020, 15, e0239890.	1.1	20
11498	Chemical-Genetic Interactions with the Proline Analog L-Azetidine-2-Carboxylic Acid in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4335-4345.	0.8	8
11499	Identifying Pathways and Networks Associated With the SARS-CoV-2 Cell Receptor ACE2 Based on Gene Expression Profiles in Normal and SARS-CoV-2-Infected Human Tissues. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 568954.	1.6	18
11500	KIR+ CD8+ T Lymphocytes in Cancer Immunosurveillance and Patient Survival: Gene Expression Profiling. <i>Cancers</i> , 2020, 12, 2991.	1.7	9
11501	Systems Level Analysis and Identification of Pathways and Key Genes Associated with Delirium. <i>Genes</i> , 2020, 11, 1225.	1.0	7
11502	Slow-Freezing Cryopreservation Ensures High Ovarian Tissue Quality Followed by In Vivo and In Vitro Methods and Is Safe for Fertility Preservation. <i>Medicina (Lithuania)</i> , 2020, 56, 547.	0.8	5
11503	Feature-Based Molecular Networking to Target the Isolation of New Caffeic Acid Esters from Yacon ( <i>Smallanthus sonchifolius</i> , Asteraceae). <i>Metabolites</i> , 2020, 10, 407.	1.3	8
11504	Beneficial Effects of Naringenin in Cigarette Smoke-Induced Damage to the Lung Based on Bioinformatic Prediction and In Vitro Analysis. <i>Molecules</i> , 2020, 25, 4704.	1.7	3
11505	LPCAT1 functions as a novel prognostic molecular marker in hepatocellular carcinoma. <i>Genes and Diseases</i> , 2022, 9, 151-164.	1.5	8
11506	Network-based approach to identify molecular signatures in the brains of depressed suicides. <i>Psychiatry Research</i> , 2020, 294, 113513.	1.7	20
11507	Proximal colon-derived O-glycosylated mucus encapsulates and modulates the microbiota. <i>Science</i> , 2020, 370, 467-472.	6.0	122
11508	Transcriptional landscape of the embryonic chicken Müllerian duct. <i>BMC Genomics</i> , 2020, 21, 688.	1.2	10
11509	Development of an immunogenomic landscape for the competing endogenous RNAs network of peri-implantitis. <i>BMC Medical Genetics</i> , 2020, 21, 208.	2.1	8

#	ARTICLE	IF	CITATIONS
11510	Evaluation of the potential role of long non-coding RNA LINC00961 in luminal breast cancer: a caseâ€“control and systems biology study. <i>Cancer Cell International</i> , 2020, 20, 478.	1.8	4
11511	Altered Regulation of adipomiR Editing with Aging. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6899.	1.8	4
11512	Differences in bacterial N, P, and COD removal in pilot-scale constructed wetlands with varying flow types. <i>Bioresource Technology</i> , 2020, 318, 124061.	4.8	15
11513	Bone Morphogenic Proteins Are Immunoregulatory Cytokines Controlling FOXP3+ Treg Cells. <i>Cell Reports</i> , 2020, 33, 108219.	2.9	13
11514	Mesenchymal stem cells alleviate LPS-induced acute lung injury by inhibiting the proinflammatory function of Ly6C+ CD8+ T cells. <i>Cell Death and Disease</i> , 2020, 11, 829.	2.7	26
11515	Transcriptomic profile analysis of the halophyte <i>Suaeda rigida</i> response and tolerance under NaCl stress. <i>Scientific Reports</i> , 2020, 10, 15148.	1.6	10
11516	Neutrophilic inflammation in the respiratory mucosa predisposes to RSV infection. <i>Science</i> , 2020, 370, .	6.0	100
11517	Identification of Candidate Genes Associated with Charcot-Marie-Tooth Disease by Network and Pathway Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	2
11518	Prognosis prediction model based on competing endogenous RNAs for recurrence of colon adenocarcinoma. <i>BMC Cancer</i> , 2020, 20, 968.	1.1	10
11519	Tn Antigen Expression Contributes to an Immune Suppressive Microenvironment and Drives Tumor Growth in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1622.	1.3	41
11520	c-Abl Tyrosine Kinase Is Regulated Downstream of the Cytoskeletal Protein Synemin in Head and Neck Squamous Cell Carcinoma Radioresistance and DNA Repair. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7277.	1.8	5
11521	Investigating the Role of Telomere and Telomerase Associated Genes and Proteins in Endometrial Cancer. <i>Methods and Protocols</i> , 2020, 3, 63.	0.9	8
11522	Network Pharmacology Approach to Investigate the Preventive Mechanism of Hunan Expert Group Recommended Chinese Medicine Prevention No. 2 Prescription Against COVID-19. <i>Digital Chinese Medicine</i> , 2020, 3, 116-132.	0.5	1
11523	The CRISPR-Cas9 crATIC HeLa transcriptome: Characterization of a novel cellular model of ATIC deficiency and ZMP accumulation. <i>Molecular Genetics and Metabolism Reports</i> , 2020, 25, 100642.	0.4	7
11524	A combination of metabolite profiling and network pharmacology to explore the potential pharmacological changes of secoisolariciresinol-diglycoside. <i>RSC Advances</i> , 2020, 10, 34847-34858.	1.7	10
11525	RNA sequence analysis of dermal papilla cellsâ€™ regeneration in 3D culture. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13421-13430.	1.6	6
11526	Reconstruction of lncRNA-miRNA-mRNA network based on competitive endogenous RNA reveals functional lncRNAs in skin cutaneous melanoma. <i>BMC Cancer</i> , 2020, 20, 927.	1.1	14
11527	Profiling pro-neural to mesenchymal transition identifies a lncRNA signature in glioma. <i>Journal of Translational Medicine</i> , 2020, 18, 378.	1.8	20

#	ARTICLE	IF	CITATIONS
11528	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , 2020, 8, 145.	4.9	77
11529	Genome Complexity Browser: Visualization and quantification of genome variability. <i>PLoS Computational Biology</i> , 2020, 16, e1008222.	1.5	1
11530	Whole Genome DNA Methylation and Gene Expression Profiling of Oropharyngeal Cancer Patients in North-Eastern India: Identification of Epigenetically Altered Gene Expression Reveals Potential Biomarkers. <i>Frontiers in Genetics</i> , 2020, 11, 986.	1.1	4
11531	Genome Mining of the Genus <i>Streptacidiphilus</i> for Biosynthetic and Biodegradation Potential. <i>Genes</i> , 2020, 11, 1166.	1.0	14
11532	Identifying Differentially Expressed MicroRNAs, Target Genes, and Key Pathways Deregulated in Patients with Liver Diseases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7368.	1.8	7
11533	Investigating the mechanism of ShuFeng JieDu capsule for the treatment of novel Coronavirus pneumonia (COVID-19) based on network pharmacology. <i>International Journal of Medical Sciences</i> , 2020, 17, 2511-2530.	1.1	22
11534	Transcriptomic analysis of bisphenol AF on early growth and development of zebrafish ( <i>Danio rerio</i> ) larvae. <i>Environmental Science and Ecotechnology</i> , 2020, 4, 100054.	6.7	9
11535	Identification of differentially expressed genes present in the whole blood of Pulmonary Arterial Hypertension patients and control patients: An integrated bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100380.	1.9	2
11536	Integrated querying and version control of context-specific biological networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	4
11537	Proteomic Evaluation of the Comorbidity-Inflammation Paradigm in Heart Failure With Preserved Ejection Fraction. <i>Circulation</i> , 2020, 142, 2029-2044.	1.6	117
11538	Characterization of soil microbes associated with a grazing-tolerant grass species, <i>Stipa breviflora</i> , in the Inner Mongolian desert steppe. <i>Ecology and Evolution</i> , 2020, 10, 10607-10618.	0.8	17
11539	The Proteome of Community Living <i>Candida albicans</i> Is Differentially Modulated by the Morphologic and Structural Features of the Bacterial Cohabitants. <i>Microorganisms</i> , 2020, 8, 1541.	1.6	1
11540	Extensive SUMO Modification of Repressive Chromatin Factors Distinguishes Pluripotent from Somatic Cells. <i>Cell Reports</i> , 2020, 32, 108146.	2.9	33
11541	CTNNB1 mutation suppresses infiltration of immune cells in hepatocellular carcinoma through miRNA-mediated regulation of chemokine expression. <i>International Immunopharmacology</i> , 2020, 89, 107043.	1.7	18
11542	Impact of a resistance gene against a fungal pathogen on the plant host residue microbiome: The case of the <i>Leptosphaeria maculans</i> - <i>Brassica napus</i> pathosystem. <i>Molecular Plant Pathology</i> , 2020, 21, 1545-1558.	2.0	9
11543	Survival Strategies of Pathogenic <i>Candida</i> Species in Human Blood Show Independent and Specific Adaptations. <i>MBio</i> , 2020, 11, .	1.8	29
11544	Identification of the Key Genes Involved in the Effect of Folic Acid on Endothelial Progenitor Cell Transcriptome of Patients with Type 1 Diabetes. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-7.	0.7	1
11545	SWATH-MS based proteomic profiling of pancreatic ductal adenocarcinoma tumours reveals the interplay between the extracellular matrix and related intracellular pathways. <i>PLoS ONE</i> , 2020, 15, e0240453.	1.1	9

#	ARTICLE	IF	CITATIONS
11546	ASDmiR: A Stepwise Method to Uncover miRNA Regulation Related to Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2020, 11, 562971.	1.1	5
11547	Exploring the Interactions of Physical, Chemical and Biological Variables of an Urban River Using Network Analysis. <i>Water (Switzerland)</i> , 2020, 12, 2578.	1.2	0
11548	Analysis of mesenchymal stem cell proteomes in situ in the ischemic heart. <i>Theranostics</i> , 2020, 10, 11324-11338.	4.6	11
11549	Transcriptomic profiling of long non-coding RNAs in non-virus associated hepatocellular carcinoma. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 465-474.	0.9	3
11550	lncRNA-miRNA-mRNA interaction network for colorectal cancer; An in silico analysis. <i>Computational Biology and Chemistry</i> , 2020, 89, 107370.	1.1	24
11551	Multi- and transgenerational effects following early-life exposure of zebrafish to permethrin and coumarin 47: Impact on growth, fertility, behavior and lipid metabolism. <i>Ecotoxicology and Environmental Safety</i> , 2020, 205, 111348.	2.9	16
11552	Machine learning approach to integrated endometrial transcriptomic datasets reveals biomarkers predicting uterine receptivity in cattle at seven days after estrous. <i>Scientific Reports</i> , 2020, 10, 16981.	1.6	11
11553	Inorganic arsenic promotes luminal to basal transition and metastasis of breast cancer. <i>FASEB Journal</i> , 2020, 34, 16034-16048.	0.2	7
11554	Cell Development Deficiency and Gene Expression Dysregulation of Trisomy 21 Retina Revealed by Single-Nucleus RNA Sequencing. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 564057.	2.0	2
11555	An Integrative miRNA-mRNA Expression Analysis Reveals Striking Transcriptomic Similarities between Severe Equine Asthma and Specific Asthma Endotypes in Humans. <i>Genes</i> , 2020, 11, 1143.	1.0	11
11556	Delayed microglial depletion after spinal cord injury reduces chronic inflammation and neurodegeneration in the brain and improves neurological recovery in male mice. <i>Theranostics</i> , 2020, 10, 11376-11403.	4.6	88
11557	Machine learning techniques for sequence-based prediction of viral-host interactions between SARS-CoV-2 and human proteins. <i>Biomedical Journal</i> , 2020, 43, 438-450.	1.4	73
11558	Comprehensive analysis of genomic alterations, clinical outcomes, putative functions and potential therapeutic value of MMP11 in human breast cancer. <i>Gene Reports</i> , 2020, 21, 100852.	0.4	2
11559	Systematic analyses on the potential immune and anti-inflammatory mechanisms of Shufeng Jiedu Capsule against Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)-caused pneumonia. <i>Journal of Functional Foods</i> , 2020, 75, 104243.	1.6	22
11560	1H-NMR-based metabolomics for cancer targeting and metabolic engineering – A review. <i>Process Biochemistry</i> , 2020, 99, 112-122.	1.8	27
11561	Dynamics in Secondary Metabolite Gene Clusters in Otherwise Highly Syntenic and Stable Genomes in the Fungal Genus <i>Botrytis</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2491-2507.	1.1	22
11562	Use of Flavin-Containing Monooxygenases for Conversion of Trimethylamine in Salmon Protein Hydrolysates. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	5
11563	Network Pharmacology Analysis to Uncover the Potential Mechanisms of <i>Lycium barbarum</i> on Colorectal Cancer. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 515-525.	2.2	8



#	ARTICLE	IF	CITATIONS
11564	In silico drug discovery of major metabolites from spices as SARS-CoV-2 main protease inhibitors. <i>Computers in Biology and Medicine</i> , 2020, 126, 104046.	3.9	98
11565	Comparative bioinformatics analysis of prognostic and differentially expressed genes in non-muscle and muscle invasive bladder cancer. <i>Journal of Proteomics</i> , 2020, 229, 103951.	1.2	4
11566	Characterization of Metabolic Patterns in Mouse Oocytes during Meiotic Maturation. <i>Molecular Cell</i> , 2020, 80, 525-540.e9.	4.5	74
11567	Association of the Sp1 binding site and -1997 promoter variations in COL1A1 with osteoporosis risk: The application of meta-analysis and bioinformatics approaches offers a new perspective for future research. <i>Mutation Research - Reviews in Mutation Research</i> , 2020, 786, 108339.	2.4	12
11568	Streamlined targeting of Amaryllidaceae alkaloids from the bulbs of <i>Crinum scillifolium</i> using spectrometric and taxonomically-informed scoring metabolite annotations. <i>Phytochemistry</i> , 2020, 179, 112485.	1.4	6
11569	Elucidating potential molecular signatures through host-microbe interactions for reactive arthritis and inflammatory bowel disease using combinatorial approach. <i>Scientific Reports</i> , 2020, 10, 15131.	1.6	9
11570	The GATOR <sup>1</sup> Rag GTPase pathway inhibits mTORC1 activation by lysosome-derived amino acids. <i>Science</i> , 2020, 370, 351-356.	6.0	53
11571	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
11572	LRRK2 mediates microglial neurotoxicity via NFATc2 in rodent models of synucleinopathies. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	49
11573	Multiplex enCas12a screens detect functional buffering among paralogs otherwise masked in monogenic Cas9 knockout screens. <i>Genome Biology</i> , 2020, 21, 262.	3.8	62
11574	A Systems Biology Workflow for Drug and Vaccine Repurposing: Identifying Small-Molecule BCG Mimics to Reduce or Prevent COVID-19 Mortality. <i>Pharmaceutical Research</i> , 2020, 37, 212.	1.7	14
11575	Gene set enrichment analysis, network pharmacology and in silico docking approach to understand the molecular mechanism of traditional medicines for the treatment of diabetes mellitus. <i>Journal of Proteins and Proteomics</i> , 2020, 11, 297-310.	1.0	12
11576	Effects of pharmacological calcimimetics on colorectal cancer cells over-expressing the human calcium-sensing receptor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118836.	1.9	12
11577	Heterotrimeric G-proteins mediated hormonal responses in plants. <i>Cellular Signalling</i> , 2020, 76, 109799.	1.7	17
11578	Chronic methylmercury exposure causes spinal cord impairment: Proteomic modulation and oxidative stress. <i>Food and Chemical Toxicology</i> , 2020, 146, 111772.	1.8	9
11579	Multi-omics analysis revealed crucial genes and pathways associated with black carp antiviral innate immunity. <i>Fish and Shellfish Immunology</i> , 2020, 106, 724-732.	1.6	6
11580	Genomic and functional characterization of the lect2 gene from <i>Siniperca chuatsi</i> . <i>Fish and Shellfish Immunology</i> , 2020, 107, 146-155.	1.6	5
11581	Unravelling host-pathogen interactions: ceRNA network in SARS-CoV-2 infection (COVID-19). <i>Gene</i> , 2020, 762, 145057.	1.0	50



#	ARTICLE	IF	CITATIONS
11582	DSS1 allosterically regulates the conformation of the tower domain of BRCA2 that has dsDNA binding specificity for homologous recombination. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 918-929.	3.6	2
11583	Scientific research and information flow in the small-scale fisheries of the central Mexican Pacific coast. <i>Ocean and Coastal Management</i> , 2020, 198, 105324.	2.0	5
11584	Maternal oxycodone treatment causes pathophysiological changes in the mouse placenta. <i>Placenta</i> , 2020, 100, 96-110.	0.7	16
11585	Isolation of Picrotoxanes from <i>Austroboxus carunculatus</i> Using Taxonomy-Based Molecular Networking. <i>Journal of Natural Products</i> , 2020, 83, 3069-3079.	1.5	12
11586	Molecular Simulations and Network Modeling Reveal an Allosteric Signaling in the SARS-CoV-2 Spike Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 4587-4608.	1.8	72
11587	Coexpression network analysis reveals an MYB transcriptional activator involved in capsaicinoid biosynthesis in hot peppers. <i>Horticulture Research</i> , 2020, 7, 162.	2.9	49
11588	SARS-CoV2-mediated suppression of NRF2-signaling reveals potent antiviral and anti-inflammatory activity of 4-octyl-itaconate and dimethyl fumarate. <i>Nature Communications</i> , 2020, 11, 4938.	5.8	272
11589	Consensus transcriptional regulatory networks of coronavirus-infected human cells. <i>Scientific Data</i> , 2020, 7, 314.	2.4	24
11590	Part 1: profiling extra cellular matrix core proteome of human fetal nucleus pulposus in search for regenerative targets. <i>Scientific Reports</i> , 2020, 10, 15684.	1.6	5
11591	Insights Into the Mechanism of Anticancer Drug Imatinib Revealed Through Multi-Omic Analyses in Yeast. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 667-678.	1.0	6
11592	Identification of the collagen family as prognostic biomarkers and immune-associated targets in gastric cancer. <i>International Immunopharmacology</i> , 2020, 87, 106798.	1.7	17
11593	Comprehensive analysis of protein expression levels and phosphorylation levels in host skin in response to tick ( <i>Haemaphysalis longicornis</i> ) bite. <i>Journal of Proteomics</i> , 2020, 226, 103898.	1.2	3
11594	Translocation of PpNPR1 is required for Î²-aminobutyric acid-triggered resistance against <i>Rhizopus stolonifer</i> in peach fruit. <i>Scientia Horticulturae</i> , 2020, 272, 109556.	1.7	5
11595	Identifying potential functional lncRNAs in metabolic syndrome by constructing a lncRNA-miRNA-mRNA network. <i>Journal of Human Genetics</i> , 2020, 65, 927-938.	1.1	4
11596	An OTX2-PAX3 signaling axis regulates Group 3 medulloblastoma cell fate. <i>Nature Communications</i> , 2020, 11, 3627.	5.8	21
11597	A mass spectrometry-based proteome map of drug action in lung cancer cell lines. <i>Nature Chemical Biology</i> , 2020, 16, 1111-1119.	3.9	31
11598	Integrative analyses of biomarkers and pathways for adipose tissue after bariatric surgery. <i>Adipocyte</i> , 2020, 9, 384-400.	1.3	19
11599	Transcriptional reprogramming and enhanced photosynthesis drive inducible salt tolerance in sugarcane mutant line M4209. <i>Journal of Experimental Botany</i> , 2020, 71, 6159-6173.	2.4	9

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11600	Intra-Protein Coevolution Is Increasingly Functional with Greater Proximity to Fertilization. <i>Cytogenetic and Genome Research</i> , 2020, 160, 295-308.	0.6	1
11601	Identification of biomarkers correlated with diagnosis and prognosis of endometrial cancer using bioinformatics analysis. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4908-4921.	1.2	7
11602	Degradome, small RNAs and transcriptome sequencing of a high-nicotine cultivated tobacco uncovers miRNA's function in nicotine biosynthesis. <i>Scientific Reports</i> , 2020, 10, 11751.	1.6	8
11603	Prefoldins contribute to maintaining the levels of the spliceosome LSM2-8 complex through Hsp90 in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2020, 48, 6280-6293.	6.5	20
11604	Effect of BRCA1 on the Concurrent Chemoradiotherapy Resistance of Cervical Squamous Cell Carcinoma Based on Transcriptome Sequencing Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	17
11605	Systems Pharmacology-Based Research on the Mechanism of Tusizi-Sangjisheng Herb Pair in the Treatment of Threatened Abortion. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	6
11606	A Network-Based Approach to Explore the Mechanism and Bioactive Compounds of Erzhi Pill against Metabolic Dysfunction-Associated Fatty Liver Disease. <i>Journal of Diabetes Research</i> , 2020, 2020, 1-15.	1.0	5
11607	Mechanisms of Spica Prunellae against thyroid-associated Ophthalmopathy based on network pharmacology and molecular docking. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 229.	1.2	11
11608	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments. <i>PLoS Computational Biology</i> , 2020, 16, e1007980.	1.5	17
11609	PLD2-PI(4,5)P2 interactions in fluid phase membranes: Structural modeling and molecular dynamics simulations. <i>PLoS ONE</i> , 2020, 15, e0236201.	1.1	5
11610	Identification of DGUOK-AS1 as a Prognostic Factor in Breast Cancer by Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 1092.	1.3	12
11611	Selectively-Packaged Proteins in Breast Cancer Extracellular Vesicles Involved in Metastasis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4990.	1.8	13
11612	Parallel bimodal single-cell sequencing of transcriptome and chromatin accessibility. <i>Genome Research</i> , 2020, 30, 1027-1039.	2.4	52
11613	MYB30 Orchestrates Systemic Reactive Oxygen Signaling and Plant Acclimation. <i>Plant Physiology</i> , 2020, 184, 666-675.	2.3	54
11614	DNA demethylases are required for myo-inositol-mediated mutualism between plants and beneficial rhizobacteria. <i>Nature Plants</i> , 2020, 6, 983-995.	4.7	48
11615	Adenovirus-mediated ubiquitination alters protein-RNA binding and aids viral RNA processing. <i>Nature Microbiology</i> , 2020, 5, 1217-1231.	5.9	22
11616	A quantitative method for proteome reallocation using minimal regulatory interventions. <i>Nature Chemical Biology</i> , 2020, 16, 1026-1033.	3.9	26
11617	Gene Loss Predictably Drives Evolutionary Adaptation. <i>Molecular Biology and Evolution</i> , 2020, 37, 2989-3002.	3.5	55

#	ARTICLE	IF	CITATIONS
11618	Community assembly of the native <i>C. elegans</i> microbiome is influenced by time, substrate and individual bacterial taxa. <i>Environmental Microbiology</i> , 2020, 22, 1265-1279.	1.8	39
11619	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. <i>New Phytologist</i> , 2020, 226, 1738-1752.	3.5	74
11620	Mitochondrial signalling is critical for acclimation and adaptation to flooding in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2020, 103, 227-247.	2.8	51
11621	Understanding the evolution of a scientific field by clustering and visualizing knowledge graphs. <i>Journal of Information Science</i> , 2022, 48, 71-89.	2.0	9
11622	Comparative transcriptomic analysis identifies distinct molecular signatures and regulatory networks of chondroclasts and osteoclasts. <i>Arthritis Research and Therapy</i> , 2020, 22, 168.	1.6	14
11623	Identification of functionally connected multi-omic biomarkers for Alzheimer's disease using modularity-constrained Lasso. <i>PLoS ONE</i> , 2020, 15, e0234748.	1.1	6
11624	Mechanisms of site-specific dephosphorylation and kinase opposition imposed by PP2A regulatory subunits. <i>EMBO Journal</i> , 2020, 39, e103695.	3.5	79
11625	CircRNA ZNF609 in peripheral blood leukocytes acts as a protective factor and a potential biomarker for coronary artery disease. <i>Annals of Translational Medicine</i> , 2020, 8, 741-741.	0.7	27
11626	Bulk and Active Sediment Prokaryotic Communities in the Mariana and Mussau Trenches. <i>Frontiers in Microbiology</i> , 2020, 11, 1521.	1.5	19
11627	Voltage-Dependent Anion Channels Influence Cytotoxicity of ME-344, a Therapeutic Isoflavone. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2020, 374, 308-318.	1.3	6
11628	A circRNA-miRNA-mRNA network plays a role in the protective effect of diosgenin on alveolar bone loss in ovariectomized rats. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 220.	1.2	10
11629	Characteristics of three microbial colonization states in the duodenum of the cirrhotic patients. <i>Future Microbiology</i> , 2020, 15, 855-868.	1.0	7
11630	Transcriptional Profiling of Normal, Stenotic, and Regurgitant Human Aortic Valves. <i>Genes</i> , 2020, 11, 789.	1.0	14
11631	Fungal Diversity Analysis of Grape Musts from Central Valley-Chile and Characterization of Potential New Starter Cultures. <i>Microorganisms</i> , 2020, 8, 956.	1.6	7
11632	Analyzing Functional Pathways and constructing gene-gene network for Narcolepsy based on candidate genes. <i>International Journal of Medical Sciences</i> , 2020, 17, 1508-1514.	1.1	2
11633	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	2.9	42
11634	PRL3-DDX21 Transcriptional Control of Endolysosomal Genes Restricts Melanocyte Stem Cell Differentiation. <i>Developmental Cell</i> , 2020, 54, 317-332.e9.	3.1	30
11635	Nest microbiota and pathogen abundance in sea turtle hatcheries. <i>Fungal Ecology</i> , 2020, 47, 100964.	0.7	21

#	ARTICLE	IF	CITATIONS
11636	Understanding the impact of DIS3 cancer-associated mutations by in silico structure modeling. <i>Gene Reports</i> , 2020, 20, 100779.	0.4	0
11637	Prediction of biomarker signatures and therapeutic agents from blood sample against Pancreatic Ductal Adenocarcinoma (PDAC): A network-based study. <i>Informatics in Medicine Unlocked</i> , 2020, 19, 100346.	1.9	4
11638	SARS-CoV and SARS-CoV-2 main protease residue interaction networks change when bound to inhibitor N3. <i>Journal of Structural Biology</i> , 2020, 211, 107575.	1.3	18
11639	Evaluating the Potential of T Cell Receptor Repertoires in Predicting the Prognosis of Resectable Non-Small Cell Lung Cancers. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 18, 73-83.	1.8	24
11640	Sindbis Virus with Anti-OX40 Overcomes the Immunosuppressive Tumor Microenvironment of Low-Immunogenic Tumors. <i>Molecular Therapy - Oncolytics</i> , 2020, 17, 431-447.	2.0	13
11641	Technological Heterogeneity and Path Diversity in Smart Home Resilience: A Simulation Approach. <i>Procedia Computer Science</i> , 2020, 170, 177-186.	1.2	5
11642	Small-world networks of prognostic genes associated with lung adenocarcinoma development. <i>Genomics</i> , 2020, 112, 4078-4088.	1.3	7
11643	Systems Toxicology Approach for Testing Chemical Cardiotoxicity in Larval Zebrafish. <i>Chemical Research in Toxicology</i> , 2020, 33, 2550-2564.	1.7	13
11644	Screening and identification of biomarkers associated with the diagnosis and prognosis of lung adenocarcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2020, 34, e23450.	0.9	12
11645	XPA deficiency affects the ubiquitin-proteasome system function. <i>DNA Repair</i> , 2020, 94, 102937.	1.3	6
11646	Conventional seed coating reduces prevalence of proteobacterial endophytes in <i>Nicotiana tabacum</i> . <i>Industrial Crops and Products</i> , 2020, 155, 112784.	2.5	16
11647	Study on Mechanism of Iridoid Glycosides Derivatives from <i>Fructus Gardeniae</i> in Jiangxi Province by Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	6
11648	Systematic Identification of lncRNA-Associated ceRNA Networks in Immune Thrombocytopenia. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-8.	0.7	5
11649	Identification of candidate biomarkers and pathways associated with psoriasis using bioinformatics analysis. <i>Hereditas</i> , 2020, 157, 30.	0.5	14
11650	Identification and Functional Annotation of Genes Related to Horses' Performance: From GWAS to Post-GWAS. <i>Animals</i> , 2020, 10, 1173.	1.0	9
11651	Mapping the Interactome of the Nuclear Heparan Sulfate Proteoglycan Syndecan-1 in Mesothelioma Cells. <i>Biomolecules</i> , 2020, 10, 1034.	1.8	12
11652	Network Analysis Identifies Gene Regulatory Network Indicating the Role of RUNX1 in Human Intervertebral Disc Degeneration. <i>Genes</i> , 2020, 11, 771.	1.0	9
11653	Co-Expression Networks for Causal Gene Identification Based on RNA-Seq Data of <i>Corynebacterium pseudotuberculosis</i> . <i>Genes</i> , 2020, 11, 794.	1.0	3

#	ARTICLE	IF	CITATIONS
11654	Integrating Molecular Networking and 1H NMR Spectroscopy for Isolation of Bioactive Metabolites from the Persian Gulf Sponge <i>Axinella sinoxea</i> . <i>Marine Drugs</i> , 2020, 18, 366.	2.2	8
11655	Association of CXCL13 and Immune Cell Infiltration Signature in Clear Cell Renal Cell Carcinoma. <i>International Journal of Medical Sciences</i> , 2020, 17, 1610-1624.	1.1	16
11656	Elevated Glucose Levels Favor SARS-CoV-2 Infection and Monocyte Response through a HIF-1 $\alpha$ /Glycolysis-Dependent Axis. <i>Cell Metabolism</i> , 2020, 32, 437-446.e5.	7.2	578
11657	Matrix metalloproteinase 9 as a host protein target of chloroquine and melatonin for immunoregulation in COVID-19: A network-based meta-analysis. <i>Life Sciences</i> , 2020, 257, 118096.	2.0	45
11658	Gene expression profiling by targeted RNA sequencing in pathological stage I lung adenocarcinoma with a solid component. <i>Lung Cancer</i> , 2020, 147, 56-63.	0.9	9
11659	<i>Bordetella pertussis</i> Acetylome is Shaped by Lysine Deacetylase Bkd1. <i>Journal of Proteome Research</i> , 2020, 19, 3680-3696.	1.8	8
11660	AXL confers cell migration and invasion by hijacking a PEAK1-regulated focal adhesion protein network. <i>Nature Communications</i> , 2020, 11, 3586.	5.8	37
11661	Transcriptome analysis of the zebrafish <i>atoh7</i> mutant, <i>lakritz</i> , highlights <i>Atoh7</i> -dependent genetic networks with potential implications for human eye diseases. <i>FASEB BioAdvances</i> , 2020, 2, 434-448.	1.3	2
11662	Metabolite AutoPlotter - an application to process and visualise metabolite data in the web browser. <i>Cancer &amp; Metabolism</i> , 2020, 8, 15.	2.4	22
11663	Psychrophilic <i>Pseudomonas helmanticensis</i> proteome under simulated cold stress. <i>Cell Stress and Chaperones</i> , 2020, 25, 1025-1032.	1.2	28
11664	Long non-coding RNA366.2 controls endometrial epithelial cell proliferation and migration by upregulating WNT6 as a ceRNA of miR-1576 in sheep uterus. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194606.	0.9	11
11665	Mammary tissue transcriptomic analysis for construction of integrated regulatory networks involved in lactogenesis of <i>Ovis aries</i> . <i>Genomics</i> , 2020, 112, 4277-4287.	1.3	5
11666	Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070.	1.0	9
11667	ExoRNA atlas: A database of cancer ceRNAs in human blood exosomes. <i>Life Sciences</i> , 2020, 257, 118092.	2.0	6
11668	Integrated Value of Influence: An Integrative Method for the Identification of the Most Influential Nodes within Networks. <i>Patterns</i> , 2020, 1, 100052.	3.1	49
11669	OCSANA+: optimal control and simulation of signaling networks from network analysis. <i>Bioinformatics</i> , 2020, 36, 4960-4962.	1.8	4
11670	TfR1 Extensively Regulates the Expression of Genes Associated with Ion Transport and Immunity. <i>Current Medical Science</i> , 2020, 40, 493-501.	0.7	6
11671	Identification of vital regulatory genes with network pathways among Huntington's, Parkinson's, and Alzheimer's diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	3

#	ARTICLE	IF	CITATIONS
11672	A Patient-Derived Cell Atlas Informs Precision Targeting of Glioblastoma. <i>Cell Reports</i> , 2020, 32, 107897.	2.9	41
11673	Nested structure of intraspecific competition network in <i>Carnobacterium maltaromaticum</i> . <i>Scientific Reports</i> , 2020, 10, 7335.	1.6	10
11674	Effects of repetitive Iodine thyroid blocking on the foetal brain and thyroid in rats: a systems biology approach. <i>Scientific Reports</i> , 2020, 10, 10839.	1.6	2
11675	Glomerular endothelial cell heterogeneity in Alport syndrome. <i>Scientific Reports</i> , 2020, 10, 11414.	1.6	9
11676	Flexible use of allocentric and egocentric spatial memories activates differential neural networks in mice. <i>Scientific Reports</i> , 2020, 10, 11338.	1.6	19
11677	AChR antibodies show a complex interaction with human skeletal muscle cells in a transcriptomic study. <i>Scientific Reports</i> , 2020, 10, 11230.	1.6	5
11678	Viral control of biomass and diversity of bacterioplankton in the deep sea. <i>Communications Biology</i> , 2020, 3, 256.	2.0	18
11679	Identification of long non-coding RNAs in the early growth stage of Holstein mammary gland. , 2020, 87, 214-222.		1
11680	Exploring the Molecular Mechanisms of Pterygium by Constructing lncRNAâ€“miRNAâ€“mRNA Regulatory Network. , 2020, 61, 12.		13
11681	Microbiomeâ€“host co-oscillation patterns in remodeling of colonic homeostasis during adaptation to a high-grain diet in a sheep model. <i>Animal Microbiome</i> , 2020, 2, 22.	1.5	11
11682	Quickly evaluating the synergistic effects of top anti-cancer drugs by the computer high performance computing power and complex network visualization. <i>Journal of Intelligent and Fuzzy Systems</i> , 2020, 38, 277-281.	0.8	2
11683	Distribution of Dimethylsulfonylpropionate Degradation Genes Reflects Strong Water Current Dependencies in the Sanriku Coastal Region in Japan: From Mesocosm to Field Study. <i>Frontiers in Microbiology</i> , 2020, 11, 1372.	1.5	8
11684	Schwann cell p75 neurotrophin receptor modulates small fiber degeneration in diabetic neuropathy. <i>Glia</i> , 2020, 68, 2725-2743.	2.5	15
11685	Overexpression of <i>SNTG2</i> , <i>TRAF3IP2</i> , and <i>ITGA6</i> transcripts is associated with osteoporotic vertebral fracture in elderly women from community. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1391.	0.6	10
11686	Networks of transcription factors. , 2020, , 137-155.		3
11687	Ensemble-Based Analysis of the Dynamic Allostery in the PSD-95 PDZ3 Domain in Relation to the General Variability of PDZ Structures. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8348.	1.8	4
11688	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020, 32, 108050.	2.9	64
11689	Biogeography and Diversity of Multi-Trophic Root Zone Microbiomes in Michigan Apple Orchards: Analysis of Rootstock, Scion, and Local Growing Region. <i>Phytobiomes Journal</i> , 2020, 4, 122-132.	1.4	8



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11690	Virtual screening and network pharmacology-based synergistic mechanism identification of multiple components contained in Guanxin V against coronary artery disease. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 345.	1.2	24
11691	Next Generation Sequencing Identify Rare Copy Number Variants in Non-syndromic Patent Ductus Arteriosus. <i>Frontiers in Genetics</i> , 2020, 11, 600787.	1.1	5
11692	Comparative Ubiquitome Analysis under Heat Stress Reveals Diverse Functions of Ubiquitination in <i>Saccharina japonica</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 8210.	1.8	8
11693	Proteomic Profiling of the Human Fetal Multipotent Mesenchymal Stromal Cells Secretome. <i>Molecules</i> , 2020, 25, 5283.	1.7	4
11694	Identification of immune-related gene signature predicting survival in the tumor microenvironment of lung adenocarcinoma. <i>Immunogenetics</i> , 2020, 72, 455-465.	1.2	17
11695	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , 2020, 183, 1185-1201.e20.	13.5	161
11696	LncRNA MIAT correlates with immune infiltrates and drug reactions in hepatocellular carcinoma. <i>International Immunopharmacology</i> , 2020, 89, 107071.	1.7	47
11697	Understanding complex dynamics of behavioral, neurochemical and transcriptomic changes induced by prolonged chronic unpredictable stress in zebrafish. <i>Scientific Reports</i> , 2020, 10, 19981.	1.6	24
11698	New insights into quetiapine metabolism using molecular networking. <i>Scientific Reports</i> , 2020, 10, 19921.	1.6	32
11699	Tracing the footsteps of autophagy in computational biology. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
11700	<p></p>Analyses of Potential Driver and Passenger Bacteria in Human Colorectal Cancer<p></p>. <i>Cancer Management and Research</i> , 2020, Volume 12, 11553-11561.	0.9	29
11701	In silico Analysis Excavates A Novel Competing Endogenous RNA Subnetwork in Adolescent Idiopathic Scoliosis. <i>Frontiers in Medicine</i> , 2020, 7, 583243.	1.2	5
11702	Exploring the Microbiota of East African Indigenous Leafy Greens for Plant Growth, Health, and Resilience. <i>Frontiers in Microbiology</i> , 2020, 11, 585690.	1.5	5
11703	Large-Scale Phosphoproteomic Study of Arabidopsis Membrane Proteins Reveals Early Signaling Events in Response to Cold. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8631.	1.8	19
11704	Demyelination Regulates the Circadian Transcription Factor BMAL1 to Signal Adult Neural Stem Cells to Initiate Oligodendrogenesis. <i>Cell Reports</i> , 2020, 33, 108394.	2.9	19
11705	Identification and dereplication of endophytic <i>Colletotrichum</i> strains by MALDI TOF mass spectrometry and molecular networking. <i>Scientific Reports</i> , 2020, 10, 19788.	1.6	13
11706	Draft genome and transcriptome analyses of halophyte rice <i>Oryza coarctata</i> provide resources for salinity and submergence stress response factors. <i>Physiologia Plantarum</i> , 2021, 173, 1309-1322.	2.6	13
11707	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020, 5, .	5.6	132



#	ARTICLE	IF	CITATIONS
11708	Identification and Characterization of circRNAs in the Developing Stem Cambium of Poplar Seedlings. <i>Molecular Biology</i> , 2020, 54, 708-718.	0.4	2
11709	Potential Diagnostic and Prognostic Utility of miR-141, miR-181b1, and miR-23b in Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8589.	1.8	19
11710	The Intersection between Oral Microbiota, Host Gene Methylation and Patient Outcomes in Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2020, 12, 3425.	1.7	33
11711	Gene expression changes occurring at bolting time are associated with leaf senescence in Arabidopsis. <i>Plant Direct</i> , 2020, 4, e00279.	0.8	15
11712	Proteomics dataset of adult Anopheles Stephensi female brain. <i>Data in Brief</i> , 2020, 32, 106243.	0.5	1
11713	Bioinformatics analyses of significant genes, related pathways, and candidate diagnostic biomarkers and molecular targets in SARS-CoV-2/COVID-19. <i>Gene Reports</i> , 2020, 21, 100956.	0.4	29
11714	Potential Regulatory Role of Human-Carboxylesterase-1 Glycosylation in Liver Cancer Cell Growth. <i>Journal of Proteome Research</i> , 2020, 19, 4867-4883.	1.8	19
11715	Obesity and metabolic syndrome related macrophage promotes PD-L1 expression in TNBC through IL6/JAK/STAT pathway and can be reversed by telmisartan. <i>Cancer Biology and Therapy</i> , 2020, 21, 1179-1190.	1.5	10
11716	Network Pharmacology-Based Strategy to Investigate Pharmacological Mechanisms of Qiaoshao Formula for Treatment of Premature Ejaculation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	3
11717	Investigation of the miRNA and mRNA Coexpression Network and Their Prognostic Value in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-19.	0.9	7
11718	Systematic Investigation of mRNA N6-Methyladenosine Machinery in Primary Prostate Cancer. <i>Disease Markers</i> , 2020, 2020, 1-21.	0.6	9
11719	Impact of Long Non-coding RNAs Associated With Microenvironment on Survival for Bladder Cancer Patients. <i>Frontiers in Genetics</i> , 2020, 11, 567200.	1.1	6
11720	Integrative Computational Approach Revealed Crucial Genes Associated With Different Stages of Diabetic Retinopathy. <i>Frontiers in Genetics</i> , 2020, 11, 576442.	1.1	4
11721	SPOCK2 Serves as a Potential Prognostic Marker and Correlates With Immune Infiltration in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 588499.	1.1	23
11722	Whole-Genome Sequencing and Bioinformatic Analysis of Environmental, Agricultural, and Human <i>Campylobacter jejuni</i> Isolates From East Tennessee. <i>Frontiers in Microbiology</i> , 2020, 11, 571064.	1.5	7
11723	Tumor Derived SIGLEC Family Genes May Play Roles in Tumor Genesis, Progression, and Immune Microenvironment Regulation. <i>Frontiers in Oncology</i> , 2020, 10, 586820.	1.3	17
11724	Label-Free Mass Spectrometry-Based Quantitative Proteomics Analysis of Serum Proteins During Early Pregnancy in Jennies ( <i>Equus asinus</i> ). <i>Frontiers in Veterinary Science</i> , 2020, 7, 569587.	0.9	4
11725	Integrative omics analysis reveals relationships of genes with synthetic lethal interactions through a pan-cancer analysis. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3243-3254.	1.9	4

#	ARTICLE	IF	CITATIONS
11726	Chemocentric Informatics Analysis: Dexamethasone <i>Versus</i> Combination Therapy for COVID-19. ACS Omega, 2020, 5, 29765-29779.	1.6	11
11727	Genome-Wide Analysis of the Expression of Circular RNA Full-Length Transcripts and Construction of the circRNA-miRNA-mRNA Network in Cervical Cancer. Frontiers in Cell and Developmental Biology, 2020, 8, 603516.	1.8	16
11728	Integrated Co-functional Network Analysis on the Resistance and Virulence Features in Acinetobacter baumannii. Frontiers in Microbiology, 2020, 11, 598380.	1.5	8
11729	Identification and Characterization of the Heat-Induced Plastidial Stress Granules Reveal New Insight Into Arabidopsis Stress Response. Frontiers in Plant Science, 2020, 11, 595792.	1.7	24
11730	Teratoma Growth Retardation by HDACi Treatment of the Tumor Embryonal Source. Cancers, 2020, 12, 3416.	1.7	5
11731	Quantitative comparison of the biomass-degrading enzyme repertoires of five filamentous fungi. Scientific Reports, 2020, 10, 20267.	1.6	51
11732	Exploring the Possible Mechanism and Drug Targets of Huang-Qi-Gui-Zhi-Wu-Wu Decoction for the Treatment of Chemotherapy-Induced Peripheral Neuropathy on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-12.	0.5	10
11733	Comprehensive proteomic atlas of skin biomatrix scaffolds reveals a supportive microenvironment for epidermal development. Journal of Tissue Engineering, 2020, 11, 204173142097231.	2.3	17
11734	Genomics and prognosis analysis of epithelial-mesenchymal transition in colorectal cancer patients. BMC Cancer, 2020, 20, 1135.	1.1	19
11735	Phenotyping of Adaptive Immune Responses in Inflammatory Diseases. Frontiers in Immunology, 2020, 11, 604464.	2.2	6
11736	&lt;p&gt;Identification and Validation of MSX1 as a Key Candidate for Progesterin Resistance in Endometrial Cancer&lt;/p&gt;. OncoTargets and Therapy, 2020, Volume 13, 11669-11688.	1.0	15
11737	Integrated Multichip Analysis Identifies Potential Key Genes in the Pathogenesis of Nonalcoholic Steatohepatitis. Frontiers in Endocrinology, 2020, 11, 601745.	1.5	6
11738	Gene Co-expression Networks Identifies Common Hub Genes Between Cutaneous Sarcoidosis and Discoid Lupus Erythematosus. Frontiers in Medicine, 2020, 7, 606461.	1.2	3
11739	Gene Mapping, Genome-Wide Transcriptome Analysis, and WGCNA Reveals the Molecular Mechanism for Triggering Programmed Cell Death in Rice Mutant pir1. Plants, 2020, 9, 1607.	1.6	10
11740	Diurnal metabolic regulation of isoflavones and soyasaponins in soybean roots. Plant Direct, 2020, 4, e00286.	0.8	19
11741	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
11742	Hsa_circ_0004831 serves as a blood-based prognostic biomarker for colorectal cancer and its potentially circRNA-miRNA-mRNA regulatory network construction. Cancer Cell International, 2020, 20, 557.	1.8	14
11743	<p>Identifying a Potential Key Gene, TIMP1, Associated with Liver Metastases of Uveal Melanoma by Weight Gene Co-Expression Network Analysis</p>. OncoTargets and Therapy, 2020, Volume 13, 11923-11934.	1.0	2

#	ARTICLE	IF	CITATIONS
11744	Identification of Interleukin-9 Producing Immune Cells in Endometrial Carcinoma and Establishment of a Prognostic Nomogram. <i>Frontiers in Immunology</i> , 2020, 11, 544248.	2.2	11
11745	The Underlying Mechanism of <i>Paeonia lactiflora</i> Pall. in Parkinson's Disease Based on a Network Pharmacology Approach. <i>Frontiers in Pharmacology</i> , 2020, 11, 581984.	1.6	29
11746	ACE2 Interaction Networks in COVID-19: A Physiological Framework for Prediction of Outcome in Patients with Cardiovascular Risk Factors. <i>Journal of Clinical Medicine</i> , 2020, 9, 3743.	1.0	74
11747	The Urine Metabolome of Young Autistic Children Correlates with Their Clinical Profile Severity. <i>Metabolites</i> , 2020, 10, 476.	1.3	20
11748	Experimental validation and network pharmacology evaluation to decipher the mechanism of action of <i>Erythrina variegata</i> L. bark against scopolamine-induced memory impairment in rats. <i>Advances in Traditional Medicine</i> , 2022, 22, 193-206.	1.0	4
11749	LINC01018 and SMIM25 sponged miR-182-5p in endometriosis revealed by the ceRNA network construction. <i>International Journal of Immunopathology and Pharmacology</i> , 2020, 34, 205873842097630.	1.0	13
11750	Liver Immune Profiling Reveals Pathogenesis and Therapeutics for Biliary Atresia. <i>Cell</i> , 2020, 183, 1867-1883.e26.	13.5	70
11751	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448.	2.9	35
11752	UBC9 coordinates inflammation affecting development of bladder cancer. <i>Scientific Reports</i> , 2020, 10, 20670.	1.6	15
11753	Combined the SMAC mimetic and BCL2 inhibitor sensitizes neoadjuvant chemotherapy by targeting necrosome complexes in tyrosine aminoacyl-tRNA synthase-positive breast cancer. <i>Breast Cancer Research</i> , 2020, 22, 130.	2.2	7
11754	Increased NFATC4 Correlates With Poor Prognosis of AML Through Recruiting Regulatory T Cells. <i>Frontiers in Genetics</i> , 2020, 11, 573124.	1.1	6
11755	Full-Length Transcriptome from <i>Camellia oleifera</i> Seed Provides Insight into the Transcript Variants Involved in Oil Biosynthesis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 14670-14683.	2.4	33
11756	Integrated computational approach toward discovery of multi-targeted natural products from <i>Thumbai (Leucas aspera)</i> for attuning NKT cells. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2893-2907.	2.0	5
11757	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	1.7	9
11758	Weighted gene co-expression network analysis identified underlying hub genes and mechanisms in the occurrence and development of viral myocarditis. <i>Annals of Translational Medicine</i> , 2020, 8, 1348-1348.	0.7	7
11759	ATP-Dependent Chromatin Remodeler CHD9 Controls the Proliferation of Embryonic Stem Cells in a Cell Culture Condition-Dependent Manner. <i>Biology</i> , 2020, 9, 428.	1.3	4
11760	Global Assessment of Substituents on the Basis of Analogue Series. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 15013-15020.	2.9	7
11761	The structural basis of promiscuity in small multidrug resistance transporters. <i>Nature Communications</i> , 2020, 11, 6064.	5.8	35

#	ARTICLE	IF	CITATIONS
11762	Transcriptome divergence between developmental senescence and premature senescence in <i>Nicotiana tabacum</i> L.. <i>Scientific Reports</i> , 2020, 10, 20556.	1.6	6
11763	Identification of the anti-breast cancer targets of triterpenoids in <i>Liquidambaris Fructus</i> and the hints for its traditional applications. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 369.	1.2	7
11764	Frameshift Variant in Novel Adenosine-A1-Receptor Homolog Associated With Bovine Spastic Syndrome/Late-Onset Bovine Spastic Paresis in Holstein Sires. <i>Frontiers in Genetics</i> , 2020, 11, 591794.	1.1	3
11765	Molecular Genetic Architecture of Monogenic Pediatric IBD Differs from Complex Pediatric and Adult IBD. <i>Journal of Personalized Medicine</i> , 2020, 10, 243.	1.1	4
11766	Diversity and connectivity of microeukaryote communities across multiple habitats from intertidal zone to deep-sea floor in the Western Pacific Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 165, 103395.	0.6	4
11767	Impact of Terrestrial Input on Deep-Sea Benthic Archaeal Community Structure in South China Sea Sediments. <i>Frontiers in Microbiology</i> , 2020, 11, 572017.	1.5	4
11768	Differential Gene Expression in Longissimus Dorsi Muscle of Hanwoo Steers—New Insight in Genes Involved in Marbling Development at Younger Ages. <i>Genes</i> , 2020, 11, 1381.	1.0	10
11769	Structural and conformational changes induced by missense variants in the zinc finger domains of GATA3 involved in breast cancer. <i>RSC Advances</i> , 2020, 10, 39640-39653.	1.7	8
11770	PhaeoNet: A Holistic RNAseq-Based Portrait of Transcriptional Coordination in the Model Diatom <i>Phaeodactylum tricornutum</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 590949.	1.7	26
11771	Systematic Analysis of Protein-Protein and Gene-Environment Interactions to Decipher the Cognitive Mechanisms of Autism Spectrum Disorder. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 1091-1103.	1.7	5
11772	Molecular insight into regulation of miRNAs in the spleen of zebrafish ( <i>Danio rerio</i> ) upon pathogenic <i>Streptococcus parauberis</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 106, 898-909.	1.6	17
11773	Unravelling the importance of the eukaryotic and bacterial communities and their relationship with <i>Legionella</i> spp. ecology in cooling towers: a complex network. <i>Microbiome</i> , 2020, 8, 157.	4.9	19
11774	Flux variability analysis reveals a tragedy of commons in cancer cells. <i>SN Applied Sciences</i> , 2020, 2, 1.	1.5	2
11775	On the correlation between material-induced cell shape and phenotypical response of human mesenchymal stem cells. <i>Scientific Reports</i> , 2020, 10, 18988.	1.6	19
11776	Real-Time Investigation of a Large Nosocomial Influenza A Outbreak Informed by Genomic Epidemiology. <i>Clinical Infectious Diseases</i> , 2021, 73, e4375-e4383.	2.9	13
11777	Neuroretinal-Derived Caveolin-1 Promotes Endotoxin-Induced Inflammation in the Murine Retina. , 2020, 61, 19.		4
11778	Genome-wide identification and characterization of long non-coding RNAs related to grain yield in foxtail millet [ <i>Setaria italica</i> (L.) P. Beauv.]. <i>BMC Genomics</i> , 2020, 21, 853.	1.2	6
11779	Tandem Mass Tag-based quantitative proteomics analysis of metabolic associated fatty liver disease induced by high fat diet in mice. <i>Nutrition and Metabolism</i> , 2020, 17, 97.	1.3	7

#	ARTICLE	IF	CITATIONS
11780	RNA sequencing analysis of altered expression of long noncoding RNAs associated with <i>Schistosoma japonicum</i> infection in the murine liver and spleen. <i>Parasites and Vectors</i> , 2020, 13, 601.	1.0	11
11781	&lt;p&gt;Research on the Potential Mechanism of Gentiopicroside Against Gastric Cancer Based on Network Pharmacology&lt;/p&gt;. <i>Drug Design, Development and Therapy</i> , 2020, Volume 14, 5109-5118.	2.0	21
11782	Initial response of ovarian tissue transcriptome to vitrification or microwave-assisted dehydration in the domestic cat model. <i>BMC Genomics</i> , 2020, 21, 828.	1.2	6
11783	Identification of biomarkers in colon cancer based on bioinformatic analysis. <i>Translational Cancer Research</i> , 2020, 9, 4879-4895.	0.4	5
11784	Soil Microbial Community Profiling and Bacterial Metabolic Activity of Technosols as an Effect of Soil Properties following Land Reclamation: A Case Study from the Abandoned Iron Sulphide and Uranium Mine in Rudki (South-Central Poland). <i>Agronomy</i> , 2020, 10, 1795.	1.3	13
11785	Possible A2E Mutagenic Effects on RPE Mitochondrial DNA from Innovative RNA-Seq Bioinformatics Pipeline. <i>Antioxidants</i> , 2020, 9, 1158.	2.2	42
11786	An Investigation into Proteomic Constituents of Cerebrospinal Fluid in Patients with Chronic Peripheral Neuropathic Pain Medicated with Opioids- a Pilot Study. <i>Journal of NeuroImmune Pharmacology</i> , 2020, 16, 634-650.	2.1	2
11787	The Microfluidic Environment Reveals a Hidden Role of Self-Organizing Extracellular Matrix in Hepatic Commitment and Organoid Formation of hiPSCs. <i>Cell Reports</i> , 2020, 33, 108453.	2.9	26
11788	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimerâ€™s Disease. <i>Cell Reports Medicine</i> , 2020, 1, 100138.	3.3	102
11789	Grazing pressure-induced shift in planktonic bacterial communities with the dominance of acIII-A1 actinobacterial lineage in soda pans. <i>Scientific Reports</i> , 2020, 10, 19871.	1.6	12
11790	Comparative transcriptome analysis in three sorghum ( <i>Sorghum bicolor</i> ) cultivars reveal genomic basis of differential seed quality. <i>Plant Biosystems</i> , 2022, 156, 232-241.	0.8	3
11791	The landscape of long noncoding RNA-involved and tumor-specific fusions across various cancers. <i>Nucleic Acids Research</i> , 2020, 48, 12618-12631.	6.5	24
11792	An Investigation of the Molecular Mechanisms Underlying the Analgesic Effect of Jakyak-Gamcho Decoction: A Network Pharmacology Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-20.	0.5	8
11793	Computational identification of biomarker genes for lung cancer considering treatment and non-treatment studies. <i>BMC Bioinformatics</i> , 2020, 21, 218.	1.2	7
11794	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	17
11795	&lt;p&gt;Bioinformatics Analysis and Validation Identify CDK1 and MAD2L1 as Prognostic Markers of Rhabdomyosarcoma&lt;/p&gt;. <i>Cancer Management and Research</i> , 2020, Volume 12, 12123-12136.	0.9	10
11796	Slow Adaptive Response of Budding Yeast Cells to Stable Conditions of Continuous Culture Can Occur without Genome Modifications. <i>Genes</i> , 2020, 11, 1419.	1.0	1
11797	Exploring the Interaction between the SWI/SNF Chromatin Remodeling Complex and the Zinc Finger Factor CTCF. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8950.	1.8	14

#	ARTICLE	IF	CITATIONS
11798	Amino Acid and Carbohydrate Metabolism Are Coordinated to Maintain Energetic Balance during Drought in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9124.	1.8	25
11799	<i>Saccharomyces paradoxus</i> Transcriptional Alterations in Cells of Distinct Phenotype and Viral dsRNA Content. <i>Microorganisms</i> , 2020, 8, 1902.	1.6	4
11800	Satellite Cell Depletion Disrupts Transcriptional Coordination and Muscle Adaptation to Exercise. <i>Function</i> , 2020, 2, zqaa033.	1.1	43
11801	miRNA signature associated with R $\infty$ CHOP refractoriness in patients diagnosed with diffuse large B cell lymphoma. <i>Non-coding RNA Research</i> , 2020, 5, 185-190.	2.4	4
11802	Genome-wide DNA methylation analysis of peripheral blood cells derived from patients with first-episode schizophrenia in the Chinese Han population. <i>Molecular Psychiatry</i> , 2021, 26, 4475-4485.	4.1	24
11803	Integrated Analysis of Gene Expression and Metabolite Data Reveals Candidate Molecular Markers in Colorectal Carcinoma. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2020, , .	0.7	5
11804	Zika virus depletes neural stem cells and evades selective autophagy by suppressing the Fanconi anemia protein <scp>FANCC</scp>. <i>EMBO Reports</i> , 2020, 21, e49183.	2.0	17
11805	Network Pharmacology-Based Strategy for the Investigation of the Anti-Obesity Effects of an Ethanolic Extract of <i>Zanthoxylum bungeanum</i> Maxim. <i>Frontiers in Pharmacology</i> , 2020, 11, 572387.	1.6	22
11806	Improvement of Disease Resistance in Livestock: Application of Immunogenomics and CRISPR/Cas9 Technology. <i>Animals</i> , 2020, 10, 2236.	1.0	15
11807	Muscle progenitor specification and myogenic differentiation are associated with changes in chromatin topology. <i>Nature Communications</i> , 2020, 11, 6222.	5.8	28
11808	Mechanism of Action of Bu-Fei-Yi-Shen Formula in Treating Chronic Obstructive Pulmonary Disease Based on Network Pharmacology Analysis and Molecular Docking Validation. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
11809	m5C RNA Methylation Primarily Affects the ErbB and PI3K $\infty$ Akt Signaling Pathways in Gastrointestinal Cancer. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 599340.	1.6	17
11810	Quantitative Changes in the Mitochondrial Proteome of Cerebellar Synaptosomes From Preclinical Cystatin B-Deficient Mice. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 570640.	1.4	11
11811	CXCL12 and IL7R as Novel Therapeutic Targets for Liver Hepatocellular Carcinoma Are Correlated With Somatic Mutations and the Tumor Immunological Microenvironment. <i>Frontiers in Oncology</i> , 2020, 10, 574853.	1.3	4
11812	Tackling <i>Pseudomonas aeruginosa</i> Virulence by Mulinane-Like Diterpenoids from <i>Azorella atacamensis</i> . <i>Biomolecules</i> , 2020, 10, 1626.	1.8	11
11813	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	2.9	26
11814	TTK, CDC25A, and ESPL1 as Prognostic Biomarkers for Endometrial Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	12
11815	Systematic Identification of Key Functional Modules and Genes in Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	2



#	ARTICLE	IF	CITATIONS
11816	Network Pharmacology-Based Study on the Mechanism of Gegen Qinlian Decoction against Colorectal Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	6
11817	Translational changes induced by acute sleep deprivation uncovered by TRAP-Seq. <i>Molecular Brain</i> , 2020, 13, 165.	1.3	23
11818	Transcriptome Remodeling in Gradual Development of Inverse Resistance between Paclitaxel and Cisplatin in Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9218.	1.8	9
11819	Bioinformatic and Reactivity-Based Discovery of Linaridins. <i>ACS Chemical Biology</i> , 2020, 15, 2976-2985.	1.6	25
11820	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	13.7	230
11821	Bovine hepatic miRNAome profiling and differential miRNA expression analyses between beef steers with divergent feed efficiency phenotypes. <i>Scientific Reports</i> , 2020, 10, 19309.	1.6	10
11822	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimer's disease created by integrative analysis of multi-omics data. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 145.	3.0	33
11823	Metabolic Profiling of Cognitive Aging in Midlife. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 555850.	1.7	8
11824	Culture-Dependent Microbiome of the <i>Ciona intestinalis</i> Tunic: Isolation, Bioactivity Profiling and Untargeted Metabolomics. <i>Microorganisms</i> , 2020, 8, 1732.	1.6	11
11825	Network Pharmacology Strategy to Investigate the Pharmacological Mechanism of HuangQiXiXin Decoction on Cough Variant Asthma and Evidence-Based Medicine Approach Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	7
11826	A Study on the Mechanism of Milkvetch Root in the Treatment of Diabetic Nephropathy Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-18.	0.5	7
11827	Transcriptome analysis reveals mechanism of early ripening in Kyoho grape with hydrogen peroxide treatment. <i>BMC Genomics</i> , 2020, 21, 784.	1.2	29
11828	Small RNA sequencing of extracellular vesicles identifies circulating miRNAs related to inflammation and oxidative stress in HIV patients. <i>BMC Immunology</i> , 2020, 21, 57.	0.9	40
11829	Unraveling <i>Pseudomonas aeruginosa</i> and <i>Candida albicans</i> Communication in Coinfection Scenarios: Insights Through Network Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 550505.	1.8	35
11830	Clinical HDAC Inhibitors Are Effective Drugs to Prevent the Entry of SARS-CoV2. <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 1361-1370.	2.5	25
11831	Digital microfluidic isolation of single cells for -Omics. <i>Nature Communications</i> , 2020, 11, 5632.	5.8	85
11832	Lung transcriptome of a COVID-19 patient and systems biology predictions suggest impaired surfactant production which may be druggable by surfactant therapy. <i>Scientific Reports</i> , 2020, 10, 19395.	1.6	75
11833	DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. <i>Science Advances</i> , 2020, 6, .	4.7	34



#	ARTICLE	IF	CITATIONS
11834	Measuring the contribution of human mobility to malaria persistence. <i>Malaria Journal</i> , 2020, 19, 404.	0.8	11
11835	Identification of biomarkers and pathways in hypertensive nephropathy based on the ceRNA regulatory network. <i>BMC Nephrology</i> , 2020, 21, 476.	0.8	8
11836	An integrated approach to unravel a putative crosstalk network in Alzheimer's disease and Parkinson's disease. <i>Neuropeptides</i> , 2020, 83, 102078.	0.9	12
11837	Can Statistical Evaluation Tools for Chromatographic Method Development Assist in the Natural Products Workflow? A Case Study on Selected Species of the Plant Family Malpighiaceae. <i>Journal of Natural Products</i> , 2020, 83, 3239-3249.	1.5	13
11838	Screening of T Cell-Related Long Noncoding RNA-MicroRNA-mRNA Regulatory Networks in Non-Small-Cell Lung Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	6
11839	Mechanisms of Core Chinese Herbs against Colorectal Cancer: A Study Based on Data Mining and Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	5
11840	A comprehensive analysis of cotton VQ gene superfamily reveals their potential and extensive roles in regulating cotton abiotic stress. <i>BMC Genomics</i> , 2020, 21, 795.	1.2	17
11841	Putative positive role of inflammatory genes in fat deposition supported by altered gene expression in purified human adipocytes and preadipocytes from lean and obese adipose tissues. <i>Journal of Translational Medicine</i> , 2020, 18, 433.	1.8	5
11842	Exploring active ingredients and function mechanisms of Ephedra-bitter almond for prevention and treatment of Corona virus disease 2019 (COVID-19) based on network pharmacology. <i>BioData Mining</i> , 2020, 13, 19.	2.2	30
11843	Transcriptomic Data Analyses Reveal a Reprogrammed Lipid Metabolism in HCV-Derived Hepatocellular Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 581863.	1.8	6
11844	Microbiome Profiling Reveals Gut Dysbiosis in the Metabotropic Glutamate Receptor 5 Knockout Mouse Model of Schizophrenia. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 582320.	1.8	16
11845	Proteomic Analysis of Exosome-Like Vesicles Isolated From Saliva of the Tick <i>Haemaphysalis longicornis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 542319.	1.8	21
11846	A Comprehensive Analysis of MicroRNAs in Human Osteoporosis. <i>Frontiers in Endocrinology</i> , 2020, 11, 516213.	1.5	16
11847	Identification of Potential Core Genes Associated With the Progression of Stomach Adenocarcinoma Using Bioinformatic Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 517362.	1.1	11
11848	Screening and Identification of Potential Biomarkers in Hepatitis B Virus-Related Hepatocellular Carcinoma by Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 555537.	1.1	11
11849	Novel Gene Signature Reveals Prognostic Model in Acute Myeloid Leukemia. <i>Frontiers in Genetics</i> , 2020, 11, 566024.	1.1	9
11850	Genome- and Proteome-Wide Analysis of Lysine Acetylation in <i>Vibrio vulnificus</i> Vv180806 Reveals Its Regulatory Roles in Virulence and Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 591287.	1.5	11
11851	Electroacupuncture Alleviates Mechanical Allodynia of a Rat Model of CRPS-I and Modulates Gene Expression Profiles in Dorsal Root Ganglia. <i>Frontiers in Neurology</i> , 2020, 11, 580997.	1.1	8

#	ARTICLE	IF	CITATIONS
11852	Sex-Dependent Molecular Mechanisms of Lipotoxic Injury in Brain Microvasculature: Implications for Dementia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8146.	1.8	7
11853	Genome-Wide Dynamic Evaluation of the UV-Induced DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2981-2988.	0.8	1
11854	Transcriptomic Analysis Revealed the Common and Divergent Responses of Maize Seedling Leaves to Cold and Heat Stresses. <i>Genes</i> , 2020, 11, 881.	1.0	26
11855	Removal of antibiotic resistance genes in pig manure composting influenced by inoculation of compound microbial agents. <i>Bioresource Technology</i> , 2020, 317, 123966.	4.8	33
11856	Prediction of the differentially expressed circRNAs to decipher their roles in the onset of human colorectal cancers. <i>Gene</i> , 2020, 762, 145035.	1.0	10
11857	ceRNA network development and tumour-infiltrating immune cell analysis of metastatic breast cancer to bone. <i>Journal of Bone Oncology</i> , 2020, 24, 100304.	1.0	17
11858	A biochemical network modeling of a whole-cell. <i>Scientific Reports</i> , 2020, 10, 13303.	1.6	9
11859	Bioinformatics analysis of microRNA profiles and identification of microRNA-mRNA network and biological markers in intracranial aneurysm. <i>Medicine (United States)</i> , 2020, 99, e21186.	0.4	9
11860	Comparative Genomic Analysis of Rapidly Evolving SARS-CoV-2 Reveals Mosaic Pattern of Phylogeographical Distribution. <i>MSystems</i> , 2020, 5, .	1.7	60
11861	KSP: an integrated method for predicting catalyzing kinases of phosphorylation sites in proteins. <i>BMC Genomics</i> , 2020, 21, 537.	1.2	6
11862	Exploring the lncRNAs Related to Skeletal Muscle Fiber Types and Meat Quality Traits in Pigs. <i>Genes</i> , 2020, 11, 883.	1.0	24
11863	Seasonal dynamics of prokaryotes and their associations with diatoms in the Southern Ocean as revealed by an autonomous sampler. <i>Environmental Microbiology</i> , 2020, 22, 3968-3984.	1.8	41
11864	RNA-Seq Analysis Reveals Hub Genes Involved in Chicken Intramuscular Fat and Abdominal Fat Deposition During Development. <i>Frontiers in Genetics</i> , 2020, 11, 1009.	1.1	25
11865	A Molecular Signal Integration Network Underpinning Arabidopsis Seed Germination. <i>Current Biology</i> , 2020, 30, 3703-3712.e4.	1.8	56
11866	A robust signature associated with patient prognosis and tumor immune microenvironment based on immune-related genes in lung squamous cell carcinoma. <i>International Immunopharmacology</i> , 2020, 88, 106856.	1.7	6
11867	An integrated strategy for revealing the pharmacological changes based on metabolites profiling and network pharmacology: Arctiin as an example. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2020, 1157, 122270.	1.2	14
11868	Whole-brain signatures of functional connectivity after bidirectional modulation of the dopaminergic system in mice. <i>Neuropharmacology</i> , 2020, 178, 108246.	2.0	6
11869	MicroRNA Profiling in Paired Left and Right Eyes, Lungs, and Testes of Normal Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 687-695.	2.3	3

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11870	Molecular Signatures and Networks of Cardiomyocyte Differentiation in Humans and Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 696-711.	2.3	11
11871	Tales of 1,008 small molecules: phenomic profiling through live-cell imaging in a panel of reporter cell lines. <i>Scientific Reports</i> , 2020, 10, 13262.	1.6	35
11872	A field-based quantitative analysis of sublethal effects of air pollution on pollinators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20653-20661.	3.3	58
11873	The effect of Jiedu Huoxue decoction on rat model of experimental nonbacterial prostatitis via regulation of miRNAs. <i>Pharmaceutical Biology</i> , 2020, 58, 745-759.	1.3	7
11874	Drug discovery strategies for modulating oxidative stress in gastrointestinal disorders. <i>Expert Opinion on Drug Discovery</i> , 2020, 15, 1309-1341.	2.5	18
11875	Culturable diversity of bacterial endophytes associated with medicinal plants of the Western Ghats, India. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	18
11876	Fto-modulated lipid niche regulates adult neurogenesis through modulating adenosine metabolism. <i>Human Molecular Genetics</i> , 2020, 29, 2775-2787.	1.4	15
11877	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	6.5	410
11878	Screening of significant biomarkers with poor prognosis in hepatocellular carcinoma via bioinformatics analysis. <i>Medicine (United States)</i> , 2020, 99, e21702.	0.4	3
11879	An interspecies translation model implicates integrin signaling in infliximab-resistant inflammatory bowel disease. <i>Science Signaling</i> , 2020, 13, .	1.6	19
11880	Integrated Bioinformatic Analysis Identifies Networks and Promising Biomarkers for Hepatitis B Virus-Related Hepatocellular Carcinoma. <i>International Journal of Genomics</i> , 2020, 2020, 1-18.	0.8	17
11881	Immune Cell Infiltration and Identifying Genes of Prognostic Value in the Papillary Renal Cell Carcinoma Microenvironment by Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
11882	The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.	0.8	21
11883	Multiple Myeloma-Derived Extracellular Vesicles Induce Osteoclastogenesis through the Activation of the XBP1/IRE1 $\beta$ Axis. <i>Cancers</i> , 2020, 12, 2167.	1.7	27
11884	Anthraquinone Derivatives as an Immune Booster and their Therapeutic Option Against COVID-19. <i>Natural Products and Bioprospecting</i> , 2020, 10, 325-335.	2.0	55
11885	Metabolomic signatures of lead exposure in the VA Normative Aging Study. <i>Environmental Research</i> , 2020, 190, 110022.	3.7	24
11886	Identification of Players Controlling Meristem Arrest Downstream of the FRUITFULL-APETALA2 Pathway. <i>Plant Physiology</i> , 2020, 184, 945-959.	2.3	16
11887	Co-expression gene modules involved in cisplatin-induced peripheral neuropathy according to sensitivity, status, and severity. <i>Journal of the Peripheral Nervous System</i> , 2020, 25, 366-376.	1.4	3

#	ARTICLE	IF	CITATIONS
11888	Lasting and Sex-Dependent Impact of Maternal Immune Activation on Molecular Pathways of the Amygdala. <i>Frontiers in Neuroscience</i> , 2020, 14, 774.	1.4	25
11889	Network-based disease gene prioritization based on Protein-Protein Interaction Networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	2
11890	Identification and Characterization of the Copy Number Dosage-Sensitive Genes in Colorectal Cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 18, 501-510.	1.8	9
11891	Generation of Functional Brown Adipocytes from Human Pluripotent Stem Cells via Progression through a Paraxial Mesoderm State. <i>Cell Stem Cell</i> , 2020, 27, 784-797.e11.	5.2	15
11892	Integrated Analysis of Tissue-Specific Promoter Methylation and Gene Expression Profile in Complex Diseases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5056.	1.8	10
11893	Tuft Cells Inhibit Pancreatic Tumorigenesis in Mice by Producing Prostaglandin D2. <i>Gastroenterology</i> , 2020, 159, 1866-1881.e8.	0.6	45
11894	An integrative network-driven pipeline for systematic identification of lncRNA-associated regulatory network motifs in metastatic melanoma. <i>BMC Bioinformatics</i> , 2020, 21, 329.	1.2	6
11895	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	3.8	419
11896	Molecular Signature of Multisystem Cardiometabolic Stress and Its Association With Prognosis. <i>JAMA Cardiology</i> , 2020, 5, 1144.	3.0	15
11897	Elevation rather than season determines the assembly and co-occurrence patterns of soil bacterial communities in forest ecosystems of Mount Gongga. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7589-7602.	1.7	28
11898	Physiological and transcriptomic analyses of brassinosteroid function in moso bamboo ( <i>Phyllostachys edulis</i> ) seedlings. <i>Planta</i> , 2020, 252, 27.	1.6	9
11899	Microbial Diversity and Composition Is Associated with Patient-Reported Toxicity during Chemoradiation Therapy for Cervical Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2020, 107, 163-171.	0.4	46
11900	A Novel Link between the Oxytocin Receptor Gene and Impulsivity. <i>Neuroscience</i> , 2020, 444, 196-208.	1.1	7
11901	Proteinarium: Multi-sample protein-protein interaction analysis and visualization tool. <i>Genomics</i> , 2020, 112, 4288-4296.	1.3	10
11902	The Meningioma Enhancer Landscape Delineates Novel Subgroups and Drives Druggable Dependencies. <i>Cancer Discovery</i> , 2020, 10, 1722-1741.	7.7	30
11903	Gene regulation network analysis reveals core genes associated with survival in glioblastoma multiforme. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 10075-10087.	1.6	24
11904	Identification of a three-long noncoding RNA prognostic model involved competitive endogenous RNA in kidney renal clear cell carcinoma. <i>Cancer Cell International</i> , 2020, 20, 319.	1.8	25
11905	N6-Methyladenosine-Related lncRNAs Are Potential Biomarkers for Predicting the Overall Survival of Lower-Grade Glioma Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 642.	1.8	117

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11906	Phylogenetic Relationships and Potential Functional Attributes of the Genus <i>Parapedobacter</i> : A Member of Family Sphingobacteriaceae. <i>Frontiers in Microbiology</i> , 2020, 11, 1725.	1.5	6
11907	Identification of Tomato Proteins That Interact With Replication Initiator Protein (Rep) of the Geminivirus TYLCV. <i>Frontiers in Plant Science</i> , 2020, 11, 1069.	1.7	19
11908	Soil physicochemical properties and bacterial community composition jointly affect crop yield. <i>Agronomy Journal</i> , 2020, 112, 4358-4372.	0.9	7
11909	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7
11910	New insight into comprehensive analysis of INDETERMINATE DOMAIN (IDD) gene family in rice. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 547-556.	2.8	6
11911	Topological and system-level protein interaction network (PIN) analyses to deduce molecular mechanism of curcumin. <i>Scientific Reports</i> , 2020, 10, 12045.	1.6	16
11912	Mapping of host-parasite-microbiome interactions reveals metabolic determinants of tropism and tolerance in Chagas disease. <i>Science Advances</i> , 2020, 6, eaaz2015.	4.7	39
11913	Weighed Gene Coexpression Network Analysis Screens the Potential Long Noncoding RNAs and Genes Associated with Progression of Coronary Artery Disease. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-14.	0.7	6
11914	Genome-wide analysis and transcript profiling of PSKR gene family members in <i>Oryza sativa</i> . <i>PLoS ONE</i> , 2020, 15, e0236349.	1.1	14
11915	Integrative Bioinformatics Approaches to Screen Potential Prognostic Immune-Related Genes and Drugs in the Cervical Cancer Microenvironment. <i>Frontiers in Genetics</i> , 2020, 11, 727.	1.1	15
11916	Effects of Different Hosts on Bacterial Communities of Parasitic Wasp <i>Nasonia vitripennis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1435.	1.5	11
11917	Extracellular Vesicles Produced by the Probiotic <i>Propionibacterium freudenreichii</i> CIRM-BIA 129 Mitigate Inflammation by Modulating the NF- $\kappa$ B Pathway. <i>Frontiers in Microbiology</i> , 2020, 11, 1544.	1.5	45
11918	Integrated Transcriptome Analysis of Human Visceral Adipocytes Unravels Dysregulated microRNA-Long Non-coding RNA-mRNA Networks in Obesity and Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1089.	1.3	18
11919	A Novel Network Pharmacology Strategy to Decode Metabolic Biomarkers and Targets Interactions for Depression. <i>Frontiers in Psychiatry</i> , 2020, 11, 667.	1.3	10
11920	On the Risks of Phylogeny-Based Strain Prioritization for Drug Discovery: <i>Streptomyces lunaelactis</i> as a Case Study. <i>Biomolecules</i> , 2020, 10, 1027.	1.8	18
11921	Shedding the Light on <i>Litopenaeus vannamei</i> Differential Muscle and Hepatopancreas Immune Responses in White Spot Syndrome Virus (WSSV) Exposure. <i>Genes</i> , 2020, 11, 805.	1.0	12
11922	Interactions of the $\alpha 2$ Nicotinic Acetylcholine Receptor Interfaces with $\alpha$ -Conotoxin LsIA and its Carboxylated C-terminus Analogue: Molecular Dynamics Simulations. <i>Marine Drugs</i> , 2020, 18, 349.	2.2	4
11923	Hair Growth Effect of Emulsion Extracted Brevilin A, a JAK3 Inhibitor, from <i>Centipeda minima</i> . <i>Processes</i> , 2020, 8, 767.	1.3	6

#	ARTICLE	IF	CITATIONS
11924	Decoding the Transcriptional Response to Ischemic Stroke in Young and Aged Mouse Brain. <i>Cell Reports</i> , 2020, 31, 107777.	2.9	66
11925	Argonaute4 Modulates Resistance to <i>Fusarium brachygibbosum</i> Infection by Regulating Jasmonic Acid Signaling. <i>Plant Physiology</i> , 2020, 184, 1128-1152.	2.3	22
11926	Infiltrative tumour growth pattern correlates with poor outcome in oesophageal cancer. <i>BMJ Open Gastroenterology</i> , 2020, 7, e000431.	1.1	2
11927	Transfer of endogenous small RNAs between branches of scions and rootstocks in grafted sweet cherry trees. <i>PLoS ONE</i> , 2020, 15, e0236376.	1.1	11
11928	Analysis of Differentially Expressed Genes and Molecular Pathways in Familial Hypercholesterolemia Involved in Atherosclerosis: A Systematic and Bioinformatics Approach. <i>Frontiers in Genetics</i> , 2020, 11, 734.	1.1	82
11929	Proteomic Profiling of Serum Exosomes From Patients With Metastatic Gastric Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1113.	1.3	47
11930	PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , 2020, 32, 107957.	2.9	28
11931	Transcriptomic comparison reveals modifications in gene expression, photosynthesis, and cell wall in woody plant as responses to external pH changes. <i>Ecotoxicology and Environmental Safety</i> , 2020, 203, 111007.	2.9	9
11932	eNose breath prints as a surrogate biomarker for classifying patients with asthma by atopy. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1045-1055.	1.5	22
11933	Xie2-64, a novel CB2 receptor inverse agonist, reduces cocaine abuse-related behaviors in rodents. <i>Neuropharmacology</i> , 2020, 176, 108241.	2.0	13
11934	Network-based approaches for understanding gene regulation and function in plants. <i>Plant Journal</i> , 2020, 104, 302-317.	2.8	35
11935	Identification of prognosis-related genes and construction of multi-regulatory networks in pancreatic cancer microenvironment by bioinformatics analysis. <i>Cancer Cell International</i> , 2020, 20, 341.	1.8	4
11936	Potential mechanism prediction of Cold-Damp Plague Formula against COVID-19 via network pharmacology analysis and molecular docking. <i>Chinese Medicine</i> , 2020, 15, 78.	1.6	24
11937	Inflammatory Breast Carcinoma: Elevated microRNA miR-181b-5p and Reduced miR-200b-3p, miR-200c-3p, and miR-203a-3p Expression as Potential Biomarkers with Diagnostic Value. <i>Biomolecules</i> , 2020, 10, 1059.	1.8	20
11938	Exploring the Characteristics of an Aroma-Blending Mixture by Investigating the Network of Shared Odors and the Molecular Features of Their Related Odorants. <i>Molecules</i> , 2020, 25, 3032.	1.7	7
11939	Mitochondria and Peroxisome Remodeling across Cytomegalovirus Infection Time Viewed through the Lens of Inter-ViSTA. <i>Cell Reports</i> , 2020, 32, 107943.	2.9	21
11940	Cell-Type Specificity of Genomic Imprinting in Cerebral Cortex. <i>Neuron</i> , 2020, 107, 1160-1179.e9.	3.8	33
11941	Leprosy piRnome: exploring new possibilities for an old disease. <i>Scientific Reports</i> , 2020, 10, 12648.	1.6	11



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11942	Ubiquitinâ€‘proteasome system, lipid metabolism and DNA damage repair are triggered by antipsychotic medication in human oligodendrocytes: implications in schizophrenia. <i>Scientific Reports</i> , 2020, 10, 12655.	1.6	14
11943	Selective Translation of Low Abundance and Upregulated Transcripts in <i>Halobacterium salinarum</i> . <i>MSystems</i> , 2020, 5, .	1.7	10
11944	Circulating miRNA-3552 as a Potential Biomarker for Ischemic Stroke in Rats. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
11945	Integrated Analyses of lncRNA and mRNA Profiles Reveal Characteristic and Functional Changes of Leukocytes in Qi-Deficiency Constitution and Pi-Qi-Deficiency Syndrome of Chronic Superficial Gastritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-16.	0.5	1
11946	Identification of potential hub genes associated with the pathogenesis and prognosis of hepatocellular carcinoma via integrated bioinformatics analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052091001.	0.4	14
11947	Changes in the vaginal microbiota associated with primary ovarian failure. <i>BMC Microbiology</i> , 2020, 20, 230.	1.3	14
11948	scPADGRN: A preconditioned ADMM approach for reconstructing dynamic gene regulatory network using single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1007471.	1.5	9
11949	Comprehensive Construction of a Circular RNA-Associated Competing Endogenous RNA Network Identified Novel Circular RNAs in Hypertrophic Cardiomyopathy by Integrated Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 764.	1.1	16
11950	Systematic Evaluation of the Diagnostic and Prognostic Significance of Competitive Endogenous RNA Networks in Prostate Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 785.	1.1	3
11951	Identification of Immune-Related Prognostic Biomarkers Based on the Tumor Microenvironment in 20 Malignant Tumor Types With Poor Prognosis. <i>Frontiers in Oncology</i> , 2020, 10, 1008.	1.3	11
11952	Lipid Metabolism is the common pathologic mechanism between Type 2 Diabetes Mellitus and Parkinson's disease. <i>International Journal of Medical Sciences</i> , 2020, 17, 1723-1732.	1.1	6
11953	Identification of novel candidate genes in heterotaxy syndrome patients with congenital heart diseases by whole exome sequencing. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165906.	1.8	18
11954	Proteome-wide Prediction of Lysine Methylation Leads to Identification of H2BK43 Methylation and Outlines the Potential Methyllysine Proteome. <i>Cell Reports</i> , 2020, 32, 107896.	2.9	17
11955	Insight into the structures of Interleukin-18 systems. <i>Computational Biology and Chemistry</i> , 2020, 88, 107353.	1.1	5
11956	Developmental GABA polarity switch and neuronal plasticity in Bioengineered Neuronal Organoids. <i>Nature Communications</i> , 2020, 11, 3791.	5.8	77
11957	Gut T cellâ€‘independent IgA responses to commensal bacteria require engagement of the TACI receptor on B cells. <i>Science Immunology</i> , 2020, 5, .	5.6	40
11958	Microbiome and Metabolome Analyses Reveal the Disruption of Lipid Metabolism in Systemic Lupus Erythematosus. <i>Frontiers in Immunology</i> , 2020, 11, 1703.	2.2	56
11959	Seasonal Niche Partitioning of Surface Temperate Open Ocean Prokaryotic Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 1749.	1.5	14



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11960	Integrated PPI- and WGCNA-Retrieval of Hub Gene Signatures Shared Between Barrett's Esophagus and Esophageal Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2020, 11, 881.	1.6	63
11961	Functional Genomics of Epileptogenesis in Animal Models and Humans. <i>Cellular and Molecular Neurobiology</i> , 2020, 41, 1579-1587.	1.7	3
11962	Time-resolved RNA-seq provided a new understanding of intestinal immune response of European eel ( <i>Anguilla anguilla</i> ) following infection with <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2020, 105, 297-309.	1.6	8
11963	Natural Killer cell transcriptome during primary EBV infection and EBV associated Hodgkin Lymphoma in children—A preliminary observation. <i>Immunobiology</i> , 2020, 225, 151907.	0.8	2
11964	Design of an engineered ACE2 as a novel therapeutics against COVID-19. <i>Journal of Theoretical Biology</i> , 2020, 505, 110425.	0.8	13
11965	ZFAT and smart sensor promotes the progression of cervical cancer through mitotic pathway. Measurement: <i>Journal of the International Measurement Confederation</i> , 2020, 164, 108051.	2.5	0
11966	Melatonin Alleviates Neuroinflammation and Metabolic Disorder in DSS-Induced Depression Rats. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-17.	1.9	56
11967	Polyamines and Their Biosynthesis/Catabolism Genes Are Differentially Modulated in Response to Heat Versus Cold Stress in Tomato Leaves ( <i>Solanum lycopersicum</i> L.). <i>Cells</i> , 2020, 9, 1749.	1.8	29
11968	Major role of lactate dehydrogenase D-LDH1 for the synthesis of lactic acid in <i>Fructobacillus tropaeoli</i> CRL 2034. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7409-7426.	1.7	4
11969	Dynamic transcriptome and co-expression network analysis of the cotton ( <i>Gossypium hirsutum</i> ) root response to salinity stress at the seedling stage. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	10
11970	Identification of biomarkers associated with extracellular vesicles based on an integrative pan-cancer bioinformatics analysis. <i>Medical Oncology</i> , 2020, 37, 79.	1.2	5
11971	Biochemical characterization of 2-phosphinomethylmalate synthase from <i>Streptomyces hygrosopicus</i> : A member of the DRE-TIM metallolyase superfamily. <i>Archives of Biochemistry and Biophysics</i> , 2020, 691, 108489.	1.4	2
11972	Comparative investigation of coarse and fine wool sheep skin indicates the early regulators for skin and wool diversity. <i>Gene</i> , 2020, 758, 144968.	1.0	12
11973	Identification of differentially expressed genes profiles in a combined mouse model of Parkinsonism and colitis. <i>Scientific Reports</i> , 2020, 10, 13147.	1.6	7
11974	Neurodegeneration in juvenile Iberian pigs with diet-induced nonalcoholic fatty liver disease. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2020, 319, E592-E606.	1.8	19
11975	Polyvalent therapeutic vaccine for type 2 diabetes mellitus: Immunoinformatics approach to study co-stimulation of cytokines and GLUT1 receptors. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 56.	1.0	1
11976	Survey of rumen microbiota of domestic grazing yak during different growth stages revealed novel maturation patterns of four key microbial groups and their dynamic interactions. <i>Animal Microbiome</i> , 2020, 2, 23.	1.5	33
11977	Comparative Transcriptomic Analysis of the Pituitary Gland between Cattle Breeds Differing in Growth: Yunling Cattle and Leiqiong Cattle. <i>Animals</i> , 2020, 10, 1271.	1.0	10

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11978	Unravelling the Role of miR-20b-5p, CCNB1, HMGA2 and E2F7 in Development and Progression of Non-Small Cell Lung Cancer (NSCLC). <i>Biology</i> , 2020, 9, 201.	1.3	15
11979	Identification of circRNA-lncRNA-miRNA-mRNA Competitive Endogenous RNA Network as Novel Prognostic Markers for Acute Myeloid Leukemia. <i>Genes</i> , 2020, 11, 868.	1.0	65
11980	Effects of Thymol Supplementation on Goat Rumen Fermentation and Rumen Microbiota In Vitro. <i>Microorganisms</i> , 2020, 8, 1160.	1.6	15
11981	Effect of Cathode Material and Its Size on the Abundance of Nitrogen Removal Functional Genes in Microcosms of Integrated Bioelectrochemical-Wetland Systems. <i>Soil Systems</i> , 2020, 4, 47.	1.0	5
11982	Physiological and transcriptional response to heat stress in heat-resistant and heat-sensitive maize ( <i>Zea mays</i> L.) inbred lines at seedling stage. <i>Protoplasma</i> , 2020, 257, 1615-1637.	1.0	19
11983	Tracking of Tumor Cell-Derived Extracellular Vesicles In Vivo Reveals a Specific Distribution Pattern with Consecutive Biological Effects on Target Sites of Metastasis. <i>Molecular Imaging and Biology</i> , 2020, 22, 1501-1510.	1.3	13
11984	A surrogate of Roux-en-Y gastric bypass (the enterogastro anastomosis surgery) regulates multiple beta-cell pathways during resolution of diabetes in ob/ob mice. <i>EBioMedicine</i> , 2020, 58, 102895.	2.7	8
11985	Comparative proteomic analysis of human mesenchymal stromal cell behavior on calcium phosphate ceramics with different osteoinductive potential. <i>Materials Today Bio</i> , 2020, 7, 100066.	2.6	13
11986	Bacterial predation limits microbial sulfate-reduction in a coastal acid sulfate soil (CASS) ecosystem. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107930.	4.2	2
11987	Intermittent electro field regulated mutualistic interspecies electron transfer away from the electrodes for bioenergy recovery from wastewater. <i>Water Research</i> , 2020, 185, 116238.	5.3	52
11988	Myc linked to dysregulation of cholesterol transport and storage in nonsmall cell lung cancer. <i>Journal of Lipid Research</i> , 2020, 61, 1390-1399.	2.0	14
11989	Identifying a Comprehensive ceRNA Network to Reveal Novel Targets for the Pathogenesis of Parkinson's Disease. <i>Frontiers in Neurology</i> , 2020, 11, 810.	1.1	16
11990	Predicted yeast interactome and network-based interpretation of transcriptionally changed genes. <i>Yeast</i> , 2020, 37, 573-583.	0.8	1
11991	Elevated Calprotectin and Abnormal Myeloid Cell Subsets Discriminate Severe from Mild COVID-19. <i>Cell</i> , 2020, 182, 1401-1418.e18.	13.5	663
11992	Integrating metabolomics and network pharmacology to explore the protective effect of gross saponins of <i>Tribulus terrestris</i> L. fruit against ischemic stroke in rat. <i>Journal of Ethnopharmacology</i> , 2020, 263, 113202.	2.0	30
11993	Combined effects of niclosamide and temozolomide against human glioblastoma tumorspheres. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 2817-2828.	1.2	18
11994	Examining the co-expression, transcriptome clustering and variation using fuzzy cluster network of testicular stem cells and pluripotent stem cells compared with other cell types. <i>Computational Biology and Chemistry</i> , 2020, 85, 107227.	1.1	0
11995	Genome-wide characterization, expression profiling, and post-transcriptional study of GASA gene family. <i>Gene Reports</i> , 2020, 20, 100795.	0.4	29

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11996	Myelopoiesis specific gene expression profiling in human CD34+ hematopoietic stem cells. <i>Gene Expression Patterns</i> , 2020, 37, 119128.	0.3	1
11997	New vistas in malignant mesothelioma: MicroRNA architecture and NRF2/MAPK signal transduction. <i>Life Sciences</i> , 2020, 257, 118123.	2.0	12
11998	Partitioning of MLX-Family Transcription Factors to Lipid Droplets Regulates Metabolic Gene Expression. <i>Molecular Cell</i> , 2020, 77, 1251-1264.e9.	4.5	78
11999	Transcriptomic and network analyses reveal distinct nitrate responses in light and dark in rice leaves ( <i>Oryza sativa Indica var. Panvel1</i> ). <i>Scientific Reports</i> , 2020, 10, 12228.	1.6	15
12000	A pooled genome-wide screening strategy to identify and rank influenza host restriction factors in cell-based vaccine production platforms. <i>Scientific Reports</i> , 2020, 10, 12166.	1.6	17
12001	Expression Profiling and Functional Characterization of miR-26a and miR-130a in Regulating Zhongwei Goat Hair Development via the TGF- $\beta$ 2/SMAD Pathway. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5076.	1.8	11
12002	Mapping gene expression in social anxiety reveals the main brain structures involved in this disorder. <i>Behavioural Brain Research</i> , 2020, 394, 112808.	1.2	4
12003	Development of Multiscale Transcriptional Regulatory Network in Esophageal Cancer Based on Integrated Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-17.	0.9	2
12004	ImmunoGlobe: enabling systems immunology with a manually curated intercellular immune interaction network. <i>BMC Bioinformatics</i> , 2020, 21, 346.	1.2	6
12005	Transgelin interacts with PARP1 in human colon cancer cells. <i>Cancer Cell International</i> , 2020, 20, 366.	1.8	11
12006	Anticancer Effects of Fufang Yiliu Yin Formula on Colorectal Cancer Through Modulation of the PI3K/Akt Pathway and BCL-2 Family Proteins. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 704.	1.8	10
12007	P2X7 Receptor-Dependent microRNA Expression Profile in the Brain Following Status Epilepticus in Mice. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 127.	1.4	6
12008	Drug Repositioning for P-Glycoprotein Mediated Co-Expression Networks in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1273.	1.3	15
12009	Network analysis as a tool to understand social development in spider monkeys. <i>American Journal of Primatology</i> , 2020, 82, e23182.	0.8	3
12010	Identification of prognostic biomarkers associated with stromal cell infiltration in muscle-invasive bladder cancer by bioinformatics analyses. <i>Cancer Medicine</i> , 2020, 9, 7253-7267.	1.3	13
12011	Integrative analysis of microRNA and mRNA expression profiles in MARC-145 cells infected with PRRSV. <i>Virus Genes</i> , 2020, 56, 610-620.	0.7	3
12012	<i>Mycoplasma hyopneumoniae</i> J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. <i>Scientific Reports</i> , 2020, 10, 13707.	1.6	6
12013	Construct a circRNA/miRNA/mRNA regulatory network to explore potential pathogenesis and therapy options of clear cell renal cell carcinoma. <i>Scientific Reports</i> , 2020, 10, 13659.	1.6	56

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12014	Deletion of DJ-1 in rats affects protein abundance and mitochondrial function at the synapse. <i>Scientific Reports</i> , 2020, 10, 13719.	1.6	13
12015	Multiple Gene Expression Dataset Analysis Reveals Toll-Like Receptor Signaling Pathway is Strongly Associated With Chronic Obstructive Pulmonary Disease Pathogenesis. <i>COPD: Journal of Chronic Obstructive Pulmonary Disease</i> , 2020, 17, 684-698.	0.7	4
12016	A Systems View of the Genome Guardians: Mapping the Signaling Circuitry Underlying Oligonucleotide/Oligosaccharide-Binding Fold Proteins. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 518-530.	1.0	2
12017	Transcriptomic insights into the roles of HSP70-16 in <i>sepal</i> ™s responses to developmental and mild heat stress signals. <i>Environmental and Experimental Botany</i> , 2020, 179, 104225.	2.0	7
12018	Wall associated kinases (WAKs) gene family in tomato ( <i>Solanum lycopersicum</i> ): Insights into plant immunity. <i>Gene Reports</i> , 2020, 21, 100828.	0.4	4
12019	Computational causal discovery for post-traumatic stress in police officers. <i>Translational Psychiatry</i> , 2020, 10, 233.	2.4	13
12020	Transcriptomic determinants of the response of ST-111 <i>Pseudomonas aeruginosa</i> AG1 to ciprofloxacin identified by a top-down systems biology approach. <i>Scientific Reports</i> , 2020, 10, 13717.	1.6	13
12021	Identification of diagnostic DNA methylation biomarkers specific for early-stage lung adenocarcinoma. <i>Cancer Genetics</i> , 2020, 246-247, 1-11.	0.2	4
12022	Impacts of different sources of animal manures on dissemination of human pathogenic bacteria in agricultural soils. <i>Environmental Pollution</i> , 2020, 266, 115399.	3.7	28
12023	Full-length transcriptome and long non-coding RNA profiling of whiteleg shrimp <i>Penaeus vannamei</i> hemocytes in response to <i>Spiroplasma eriocheiris</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 106, 876-886.	1.6	22
12024	Screening and identification of key regulatory connections and immune cell infiltration characteristics for lung transplant rejection using mucosal biopsies. <i>International Immunopharmacology</i> , 2020, 87, 106827.	1.7	9
12025	The role of land management and elevation in shaping soil microbial communities: Insights from the Central European Alps. <i>Soil Biology and Biochemistry</i> , 2020, 150, 107951.	4.2	37
12026	The protective effect of quercetin on retinal inflammation in mice: the involvement of tumor necrosis factor/nuclear factor- $\kappa$ B signaling pathways. <i>Food and Function</i> , 2020, 11, 8150-8160.	2.1	9
12027	Genomic Evidence for Sensorial Adaptations to a Nocturnal Predatory Lifestyle in Owls. <i>Genome Biology and Evolution</i> , 2020, 12, 1895-1908.	1.1	9
12028	Evaluating the effect of TLR4-overexpressing on the transcriptome profile in ovine peripheral blood mononuclear cells. <i>Journal of Biological Research</i> , 2020, 27, 13.	2.2	3
12029	Transcriptome and Flavonoids Metabolomic Analysis Identifies Regulatory Networks and Hub Genes in Black and White Fruits of <i>Lycium ruthenicum</i> Murray. <i>Frontiers in Plant Science</i> , 2020, 11, 1256.	1.7	18
12030	<i>S</i> -Palmitoylation as a Functional Regulator of Proteins Associated with Cisplatin Resistance in Bladder Cancer. <i>International Journal of Biological Sciences</i> , 2020, 16, 2490-2505.	2.6	26
12031	Transcriptomic and proteomic profiling response of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) to a novel bacteriocin, plantaricin GZ1-27 and its inhibition of biofilm formation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7957-7970.	1.7	21

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12032	Determination of the glycoprotein specificity of lectins on cell membranes through oxidative proteomics. <i>Chemical Science</i> , 2020, 11, 9501-9512.	3.7	22
12033	Biomarker Prioritisation and Power Estimation Using Ensemble Gene Regulatory Network Inference. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7886.	1.8	4
12034	Urban mobility and resilience: exploring Boston's urban mobility network through twitter data. <i>Applied Network Science</i> , 2020, 5, .	0.8	10
12035	Network Pharmacology-Based Study on the Mechanism of <i>Pinellia ternata</i> in Asthma Treatment. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	8
12036	Designing a Network Proximity-Based Drug Repurposing Strategy for COVID-19. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 545089.	1.8	19
12037	Adropin Stimulates Proliferation and Inhibits Adrenocortical Steroidogenesis in the Human Adrenal Carcinoma (HAC15) Cell Line. <i>Frontiers in Endocrinology</i> , 2020, 11, 561370.	1.5	18
12038	Identification of Signatures of Prognosis Prediction for Melanoma Using a Hypoxia Score. <i>Frontiers in Genetics</i> , 2020, 11, 570530.	1.1	21
12039	Genome-Wide Analysis of Prognostic Alternative Splicing Signature and Splicing Factors in Lung Adenocarcinoma. <i>Genes</i> , 2020, 11, 1300.	1.0	13
12040	Bacterial composition and community structure of the oropharynx of adults with asthma are associated with environmental factors. <i>Microbial Pathogenesis</i> , 2020, 149, 104505.	1.3	7
12041	Bio-priming with a hypovirulent phytopathogenic fungus enhances the connection and strength of microbial interaction network in rapeseed. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 45.	2.9	33
12042	Sample-specific perturbation of gene interactions identifies breast cancer subtypes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	20
12043	Global analysis of differentially expressed genes between two Japonica rice varieties induced by low temperature during the booting stage by RNA-Seq. <i>Royal Society Open Science</i> , 2020, 7, 192243.	1.1	12
12044	Genome-wide identification of ATP binding cassette (ABC) transporter and heavy metal associated (HMA) gene families in flax ( <i>Linum usitatissimum</i> L.). <i>BMC Genomics</i> , 2020, 21, 722.	1.2	42
12045	Identification of Prognostic Model and Biomarkers for Cancer Stem Cell Characteristics in Glioblastoma by Network Analysis of Multi-Omics Data and Stemness Indices. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 558961.	1.8	30
12046	Fine-Scale Differentiation in Diet and Metabolomics of Small Mammals Across a Sharp Ecological Transition. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	5
12047	Identification of Prognostic Markers in Cholangiocarcinoma Using Altered DNA Methylation and Gene Expression Profiles. <i>Frontiers in Genetics</i> , 2020, 11, 522125.	1.1	11
12048	A Systems Biology Approach to Identifying a Master Regulator That Can Transform the Fast Growing Cellular State to a Slowly Growing One in Early Colorectal Cancer Development Model. <i>Frontiers in Genetics</i> , 2020, 11, 570546.	1.1	12
12049	VISTA Re-programs Macrophage Biology Through the Combined Regulation of Tolerance and Anti-inflammatory Pathways. <i>Frontiers in Immunology</i> , 2020, 11, 580187.	2.2	24

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12050	Transcriptomic Profiling of Mouse Brain During Acute and Chronic Infections by <i>Toxoplasma gondii</i> Oocysts. <i>Frontiers in Microbiology</i> , 2020, 11, 570903.	1.5	10
12051	Niche differentiation of comammox <i>Nitrospira</i> and canonical ammonia oxidizers in soil aggregate fractions following 27-year fertilizations. <i>Agriculture, Ecosystems and Environment</i> , 2020, 304, 107147.	2.5	46
12052	A complex metabolic rearrangement towards the accumulation of glycerol and sugars consequence of a proteome remodeling is required for the survival of <i>Chlamydomonas reinhardtii</i> growing under osmotic stress. <i>Environmental and Experimental Botany</i> , 2020, 180, 104261.	2.0	2
12053	Insights from RNA-Seq analysis of Alzheimer's data suggest upregulation of GPCRs. <i>Gene Reports</i> , 2020, 21, 100921.	0.4	1
12054	The histone modification H3K4me3 marks functional genes in soybean nodules. <i>Genomics</i> , 2020, 112, 5282-5294.	1.3	8
12055	Comprehensive proteomic investigation of infectious and inflammatory changes in late preterm prelabour rupture of membranes. <i>Scientific Reports</i> , 2020, 10, 17696.	1.6	6
12056	Exploration in the Mechanism of Kaempferol for the Treatment of Gastric Cancer Based on Network Pharmacology. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	15
12057	Differential Modulation of Mouse Heart Gene Expression by Infection With Two <i>Trypanosoma cruzi</i> Strains: A Transcriptome Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 1031.	1.1	7
12058	FGF2 Affects Parkinson's Disease-Associated Molecular Networks Through Exosomal Rab8b/Rab31. <i>Frontiers in Genetics</i> , 2020, 11, 572058.	1.1	12
12059	Construction and Characterization of a Synergistic lncRNA-miRNA Network Reveals a Crucial and Prognostic Role of lncRNAs in Colon Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 572983.	1.1	5
12060	Functional network analysis reveals potential repurposing of $\beta$ -blocker atenolol for pancreatic cancer therapy. <i>DARU, Journal of Pharmaceutical Sciences</i> , 2020, 28, 685-699.	0.9	5
12061	Chinese herbal medicine promote tissue differentiation in colorectal cancer by activating HSD11B2. <i>Archives of Biochemistry and Biophysics</i> , 2020, 695, 108644.	1.4	8
12062	Defective cell proliferation is an attribute of overexpressed Notch1 receptor and impaired autophagy in Fanconi Anemia. <i>Genomics</i> , 2020, 112, 4628-4639.	1.3	4
12063	A Key Glycine in Bacterial Steroid-Degrading Acyl-CoA Dehydrogenases Allows Flavin-Ring Repositioning and Modulates Substrate Side Chain Specificity. <i>Biochemistry</i> , 2020, 59, 4081-4092.	1.2	5
12064	Systems analysis of avascular necrosis of femoral head using integrative data analysis and literature mining delineates pathways associated with disease. <i>Scientific Reports</i> , 2020, 10, 18099.	1.6	16
12065	Identification of Key Genes Involved in Acute Myocardial Infarction by Comparative Transcriptome Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	17
12066	Identification of Key Genes and Potential New Biomarkers for Ovarian Aging: A Study Based on RNA-Sequencing Data. <i>Frontiers in Genetics</i> , 2020, 11, 590660.	1.1	21
12067	Global Proteomic Analysis of Lysine Crotonylation in the Plant Pathogen <i>Botrytis cinerea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 564350.	1.5	9



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12068	Chemical Space Charting of Different Parts of <i>Inula nervosa</i> Wall.: Upregulation of Expression of Nrf2 and Correlated Antioxidants Enzymes. <i>Molecules</i> , 2020, 25, 4789.	1.7	5
12069	Horizontal meta-analysis identifies common deregulated genes across AML subgroups providing a robust prognostic signature. <i>Blood Advances</i> , 2020, 4, 5322-5335.	2.5	8
12070	Comprehensive Identification and Expression Profiling of Circular RNAs During Nodule Development in <i>Phaseolus vulgaris</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 587185.	1.7	10
12071	Network pharmacology-based investigation on the mechanisms of action of <i>Morinda officinalis</i> How. in the treatment of osteoporosis. <i>Computers in Biology and Medicine</i> , 2020, 127, 104074.	3.9	26
12072	Downregulation of Keap1 Confers Features of a Fasted Metabolic State. <i>IScience</i> , 2020, 23, 101638.	1.9	21
12073	Unravelling the molecular mechanisms of abscisic acid-mediated drought-stress alleviation in pomegranate ( <i>Punica granatum</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 157, 211-218.	2.8	12
12074	Different contribution of species sorting and exogenous species immigration from manure to soil fungal diversity and community assemblage under long-term fertilization. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108049.	4.2	53
12075	Increased RNA editing in maternal immune activation model of neurodevelopmental disease. <i>Nature Communications</i> , 2020, 11, 5236.	5.8	24
12076	Deciphering underlying mechanism of Sars-CoV-2 infection in humans and revealing the therapeutic potential of bioactive constituents from <i>Nigella sativa</i> to combat COVID19: <i>in-silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2417-2429.	2.0	27
12077	The adenoviral protein E4orf4: a probing tool to decipher mechanical stress-induced nuclear envelope remodeling in tumor cells. <i>Cell Cycle</i> , 2020, 19, 2963-2981.	1.3	0
12078	Islands in the sand: are all hypolithic microbial communities the same?. <i>FEMS Microbiology Ecology</i> , 2020, 97, .	1.3	4
12079	P0049IDENTIFYING HUB GENES ASSOCIATED WITH CLINICAL CHARACTERISTICS IN IGA NEPHROPATHY BYWGCNA. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, .	0.4	0
12080	Novel cytokine-antibody fusion protein, N-820, to enhance the functions of ex vivo expanded natural killer cells against Burkitt lymphoma. , 2020, 8, e001238.		11
12081	Identification of key genes and novel immune infiltration-associated biomarkers of sepsis. <i>Innate Immunity</i> , 2020, 26, 666-682.	1.1	29
12082	Molecular correlates and therapeutic targets in T cell-inflamed versus non-T cell-inflamed tumors across cancer types. <i>Genome Medicine</i> , 2020, 12, 90.	3.6	29
12083	Systematic Analysis of Lysine Lactylation in the Plant Fungal Pathogen <i>Botrytis cinerea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 594743.	1.5	47
12084	Coffee, Black Tea, and Green Tea Consumption in Relation to Plasma Metabolites in an Asian Population. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000527.	1.5	11
12085	Proteomics of regenerated tissue in response to a titanium implant with a bioactive surface in a rat tibial defect model. <i>Scientific Reports</i> , 2020, 10, 18493.	1.6	10



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12086	M.Âtuberculosis Reprograms Hematopoietic Stem Cells to Limit Myelopoiesis and Impair Trained Immunity. <i>Cell</i> , 2020, 183, 752-770.e22.	13.5	148
12087	InÂvitro Recapitulation of Murine Thymopoiesis from Single Hematopoietic Stem Cells. <i>Cell Reports</i> , 2020, 33, 108320.	2.9	20
12088	Systems biology approach suggests new miRNAs as phenotypic stability factors in the epithelialâ€mesenchymal transition. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200693.	1.5	30
12089	Identification of Hub Genes and Potential Molecular Mechanisms in Patients with HBV-Associated Acute Liver Failure. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432094390.	0.6	3
12090	RNA Profiling Reveals a Common Mechanism of Histone Gene Downregulation and Complementary Effects for Radioprotectants in Response to Ionizing Radiation. <i>Dose-Response</i> , 2020, 18, 155932582096843.	0.7	5
12091	Increased E2F2 predicts poor prognosis in patients with HCC based on TCGA data. <i>BMC Cancer</i> , 2020, 20, 1037.	1.1	14
12092	Identification and Validation of Novel Genes in Anaplastic Thyroid Carcinoma via Bioinformatics Analysis. <i>Cancer Management and Research</i> , 2020, Volume 12, 9787-9799.	0.9	10
12093	Early Protein Markers of Necrotizing Enterocolitis in Plasma of Preterm Pigs Exposed to Antibiotics. <i>Frontiers in Immunology</i> , 2020, 11, 565862.	2.2	8
12094	Transcriptomic Changes in Endothelial Cells Triggered by Na,K-ATPase Inhibition: A Search for Upstream Na <sup>+</sup> /K <sup>+</sup> Sensitive Genes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7992.	1.8	4
12095	Construction of novel mRNA-miRNA-lncRNA regulatory networks associated with prognosis of ovarian cancer. <i>Journal of Cancer</i> , 2020, 11, 7057-7072.	1.2	20
12096	Identification of lung cancer master genes triggered by smoking and their key pathways based on gene expression profiling. <i>Gene Reports</i> , 2020, 21, 100812.	0.4	1
12097	Local dynamic spontaneous brain activity changes in first-episode, treatment-naïve patients with major depressive disorder and their associated gene expression profiles. <i>Psychological Medicine</i> , 2022, 52, 2052-2061.	2.7	49
12098	Integration of gene profile to explore the hub genes of lung adenocarcinoma. <i>Medicine (United States)</i> , 2020, 99, e22861.	0.4	4
12099	Integrated TCGA and GEO analysis showed that SMAD7 is an independent prognostic factor for lung adenocarcinoma. <i>Medicine (United States)</i> , 2020, 99, e22861.	0.4	5
12100	Involvement of miR-126 rs4636297 and miR-146a rs2910164 polymorphisms in the susceptibility for diabetic retinopathy: a case-control study in a type 1 diabetes population. <i>Acta Ophthalmologica</i> , 2021, 99, e461-e469.	0.6	6
12101	Shared Mechanisms Govern HIV Transcriptional Suppression in Circulating CD103 <sup>+</sup> and Gut CD4 <sup>+</sup> T Cells. <i>Journal of Virology</i> , 2020, 95, .	1.5	4
12102	LL-37-Induced Autophagy Contributed to the Elimination of Live <i>Porphyromonas gingivalis</i> Internalized in Keratinocytes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 561761.	1.8	15
12103	Ovarian Circular RNAs Associated with High and Low Fertility in Large White Sows during the Follicular and Luteal Phases of the Estrous Cycle. <i>Animals</i> , 2020, 10, 696.	1.0	4

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12104	Involvement of Essential Signaling Cascades and Analysis of Gene Networks in Diabesity. <i>Genes</i> , 2020, 11, 1256.	1.0	32
12105	In Silico Analyses of Autophagy-Related Genes in Rapeseed ( <i>Brassica napus</i> L.) under Different Abiotic Stresses and in Various Tissues. <i>Plants</i> , 2020, 9, 1393.	1.6	5
12106	Genetic alteration and clinical significance of SUMOylation regulators in multiple cancer types. <i>Journal of Cancer</i> , 2020, 11, 6823-6833.	1.2	6
12107	Upregulation of miR-9 and miR-193b over human Th17 cell differentiation. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1538.	0.6	5
12108	Correlations Between Phenotypes and Biological Process Ontologies in Monogenic Human Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 547-554.	2.2	1
12109	Exploring the potential therapeutic effect of traditional Chinese medicine on coronavirus disease 2019 (COVID-19) through a combination of data mining and network pharmacology analysis. <i>European Journal of Integrative Medicine</i> , 2020, 40, 101242.	0.8	8
12110	Disease trajectory browser for exploring temporal, population-wide disease progression patterns in 7.2 million Danish patients. <i>Nature Communications</i> , 2020, 11, 4952.	5.8	70
12111	SynergyAge, a curated database for synergistic and antagonistic interactions of longevity-associated genes. <i>Scientific Data</i> , 2020, 7, 366.	2.4	16
12112	Evolutionary and ontogenetic changes of the anatomical organization and modularity in the skull of archosaurs. <i>Scientific Reports</i> , 2020, 10, 16138.	1.6	15
12113	Mechanistic insights into the loss-of-function mechanisms of rare human D-amino acid oxidase variants implicated in amyotrophic lateral sclerosis. <i>Scientific Reports</i> , 2020, 10, 17146.	1.6	8
12114	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. <i>Scientific Reports</i> , 2020, 10, 17198.	1.6	8
12115	Physiological demands and signaling associated with snake venom production and storage illustrated by transcriptional analyses of venom glands. <i>Scientific Reports</i> , 2020, 10, 18083.	1.6	11
12116	Genetic parameters and associated genomic regions for global immunocompetence and other health-related traits in pigs. <i>Scientific Reports</i> , 2020, 10, 18462.	1.6	23
12117	Dynamic transcriptional response of <i>Saccharomyces cerevisiae</i> cells to copper. <i>Scientific Reports</i> , 2020, 10, 18487.	1.6	8
12118	Clinical implications and nomogram prediction of long noncoding RNA FRGCA as diagnostic and prognostic indicators in colon adenocarcinoma. <i>Medicine (United States)</i> , 2020, 99, e22806.	0.4	1
12119	Proteomic Profiling Reveals Roles of Stress Response, Ca <sup>2+</sup> Transient Dysregulation, and Novel Signaling Pathways in Alcohol-Induced Cardiotoxicity. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 2187-2199.	1.4	6
12120	A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimer's Disease Through Expert Curation of Key Protein Targets. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 257-273.	1.2	7
12121	Systematic Identification of Hub Genes in Placenta Accreta Spectrum Based on Integrated Transcriptomic and Proteomic Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 551495.	1.1	6

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12122	Meta-analysis of Transcriptomic Data Reveals Pathophysiological Modules Involved with Atrial Fibrillation. <i>Molecular Diagnosis and Therapy</i> , 2020, 24, 737-751.	1.6	9
12123	A transaldolase-dependent sulfoglycolysis pathway in <i>Bacillus megaterium</i> DSM 1804. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 1109-1114.	1.0	19
12124	Identification of tumor-infiltrating immune cells and microenvironment-relevant genes in nasopharyngeal carcinoma based on gene expression profiling. <i>Life Sciences</i> , 2020, 263, 118620.	2.0	11
12125	Inhibition of enteric methanogenesis in dairy cows induces changes in plasma metabolome highlighting metabolic shifts and potential markers of emission. <i>Scientific Reports</i> , 2020, 10, 15591.	1.6	19
12126	Altered gene expression profiles of testicular tissues from azoospermic patients with maturation arrest. <i>Andrologia</i> , 2020, 52, e13812.	1.0	1
12127	Transcriptomic similarities and differences between the limb bud AER and unique carapacial ridge of turtle embryos. <i>Evolution &amp; Development</i> , 2020, 22, 370-383.	1.1	4
12128	Fungal heavy metal adaptation through single nucleotide polymorphisms and copy number variation. <i>Molecular Ecology</i> , 2020, 29, 4157-4169.	2.0	24
12129	Integrated Genome-Wide Methylation and Expression Analyses Reveal Key Regulators in Osteosarcoma. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-11.	0.7	7
12130	Comprehensive analysis of key genes associated with ceRNA networks in nasopharyngeal carcinoma based on bioinformatics analysis. <i>Cancer Cell International</i> , 2020, 20, 408.	1.8	11
12131	Copy Number Alterations in Papillary Thyroid Carcinomas: Does Loss of <i>SESN2</i> Have a Role in Age-related Different Prognoses?. <i>Cancer Genomics and Proteomics</i> , 2020, 17, 643-648.	1.0	1
12132	Discriminating miRNA Profiles between Endometrioid Well- and Poorly-Differentiated Tumours and Endometrioid and Serous Subtypes of Endometrial Cancers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6071.	1.8	10
12133	Interleukin-6 Gene Expression Changes after a 4-Week Intake of a Multispecies Probiotic in Major Depressive Disorder—Preliminary Results of the PROVIT Study. <i>Nutrients</i> , 2020, 12, 2575.	1.7	28
12134	Genome-wide identification and analysis of GRAS transcription factors in the bottle gourd genome. <i>Scientific Reports</i> , 2020, 10, 14338.	1.6	22
12135	Comparative Transcriptome Analysis of Pine Trees Treated with Resistance-Inducing Substances against the Nematode <i>Bursaphelenchus xylophilus</i> . <i>Genes</i> , 2020, 11, 1000.	1.0	9
12136	miR-183/96/182 cluster is an important morphogenetic factor targeting <i>PAX6</i> expression in differentiating human retinal organoids. <i>Stem Cells</i> , 2020, 38, 1557-1567.	1.4	26
12137	Multivariate gene expression-based survival predictor model in esophageal adenocarcinoma. <i>Thoracic Cancer</i> , 2020, 11, 2896-2908.	0.8	8
12138	Unveiling Crucivirus Diversity by Mining Metagenomic Data. <i>MBio</i> , 2020, 11, .	1.8	22
12139	Genomic landscape of the immune microenvironments of brain metastases in breast cancer. <i>Journal of Translational Medicine</i> , 2020, 18, 327.	1.8	14

#	ARTICLE	IF	CITATIONS
12140	Tubular ER Associates With Diacylglycerol-Rich Structures During Lipid Droplet Consumption. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 700.	1.8	4
12141	Identification of Prostate Cancer-Related Circular RNA Through Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 892.	1.1	18
12142	Adipose tissue from metabolic syndrome mice induces an aberrant miRNA signature highly relevant in prostate cancer development. <i>Molecular Oncology</i> , 2020, 14, 2868-2883.	2.1	6
12143	Milk somatic cell derived transcriptome analysis identifies regulatory genes and pathways during lactation in Indian Sahiwal cattle ( <i>Bos indicus</i> ). <i>Molecular Biology Reports</i> , 2020, 47, 7029-7038.	1.0	2
12144	Systematic screening of CTCF binding partners identifies that BHLHE40 regulates CTCF genome-wide distribution and long-range chromatin interactions. <i>Nucleic Acids Research</i> , 2020, 48, 9606-9620.	6.5	30
12145	Identification of new susceptibility loci associated with rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1565-1571.	0.5	27
12146	Integrative Analysis of MAPK14 as a Potential Biomarker for Cardioembolic Stroke. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	3
12147	Identification of potential biomarkers and candidate small molecule drugs in glioblastoma. <i>Cancer Cell International</i> , 2020, 20, 419.	1.8	12
12148	Comprehensive profiling of immune-related genes in soft tissue sarcoma patients. <i>Journal of Translational Medicine</i> , 2020, 18, 337.	1.8	18
12149	Assessing the Anti-cancer Therapeutic Mechanism of a Herbal Combination for Breast Cancer on System-level by a Network Pharmacological Approach. <i>Anticancer Research</i> , 2020, 40, 5097-5106.	0.5	5
12150	New Tricks with an Old Sponge: Feature-Based Molecular Networking Led to Fast Identification of New Styliamide L from <i>Stylissa caribica</i> . <i>Marine Drugs</i> , 2020, 18, 443.	2.2	15
12151	Lymphocyte infiltration and key differentially expressed genes in the ulcerative colitis. <i>Medicine (United States)</i> , 2020, 99, e21997.	0.4	7
12152	Bioinformatic Mapping of Opine-Like Zincophore Biosynthesis in Bacteria. <i>MSystems</i> , 2020, 5, .	1.7	26
12153	Transcriptome sequencing identifies genes associated with invasion of ovarian cancer. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095091.	0.4	9
12154	Molecular Evolutionary and Expression Pattern Analysis of AKR Genes Shed New Light on GalUR Functional Characteristics in <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5987.	1.8	3
12155	Dissecting Transcription Factor-Target Interaction in Bovine Coronavirus Infection. <i>Microorganisms</i> , 2020, 8, 1323.	1.6	5
12156	Expression profile analysis of circular RNAs in BmN cells ( <i>Bombyx mori</i> ) upon BmNPV infection. <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21735.	0.6	4
12157	Novel miRNA signature for predicting the stage of hepatocellular carcinoma. <i>Scientific Reports</i> , 2020, 10, 14452.	1.6	40

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12158	BdWRKY38 is required for the incompatible interaction of <i>Brachypodium distachyon</i> with the necrotrophic fungus <i>Rhizoctonia solani</i> . <i>Plant Journal</i> , 2020, 104, 995-1008.	2.8	18
12159	Prioritizing Candidates of Post-Myocardial Infarction Heart Failure Using Plasma Proteomics and Single-Cell Transcriptomics. <i>Circulation</i> , 2020, 142, 1408-1421.	1.6	50
12160	Microarray data analysis reveals gene expression changes in response to ionizing radiation in MCF7 human breast cancer cells. <i>Hereditas</i> , 2020, 157, 37.	0.5	7
12161	Secretome Proteomic Approaches for Biomarker Discovery: An Update on Colorectal Cancer. <i>Medicina (Lithuania)</i> , 2020, 56, 443.	0.8	7
12162	Human Milk Oligosaccharides Protect against Necrotizing Enterocolitis by Activating Intestinal Cell Differentiation. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000519.	1.5	27
12163	Multi-omics profiling reveals microRNA-mediated insulin signaling networks. <i>BMC Bioinformatics</i> , 2020, 21, 389.	1.2	3
12164	Selective Histone Deacetylase 6 Inhibitors Restore Cone Photoreceptor Vision or Outer Segment Morphology in Zebrafish and Mouse Models of Retinal Blindness. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 689.	1.8	22
12165	16S Metagenomics Reveals Dysbiosis of Nasal Core Microbiota in Children With Chronic Nasal Inflammation: Role of Adenoid Hypertrophy and Allergic Rhinitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 458.	1.8	21
12166	Metagenomic Profiling and Microbial Metabolic Potential of Perdido Fold Belt (NW) and Campeche Knolls (SE) in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2020, 11, 1825.	1.5	16
12167	Genetic Variability in Polish Lowland Sheepdogs Assessed by Pedigree and Genomic Data. <i>Animals</i> , 2020, 10, 1520.	1.0	3
12168	Ectopic release of nitric oxide modulates the onset of cardiac development in avian model. <i>In Vitro Cellular and Developmental Biology - Animal</i> , 2020, 56, 593-603.	0.7	2
12169	Multivalent Surface Cations Enhance Heterogeneous Freezing of Water on Muscovite Mica. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 8682-8689.	2.1	15
12170	Carotane sesquiterpenes from <i>Ferula vesceritensis</i> : <i>in silico</i> analysis as SARS-CoV-2 binding inhibitors. <i>RSC Advances</i> , 2020, 10, 34541-34548.	1.7	7
12171	Integrated meta-analysis, network pharmacology, and molecular docking to investigate the efficacy and potential pharmacological mechanism of Kai-Xin-San on Alzheimer's disease. <i>Pharmaceutical Biology</i> , 2020, 58, 932-943.	1.3	34
12172	Systematic Elucidation of the Mechanism of Quercetin against Gastric Cancer via Network Pharmacology Approach. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	18
12173	Exploring the Mechanism of Action Compound-Xueshuantong Capsule in Diabetic Retinopathy Treatment Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	11
12174	Identification of hub genes in diabetic kidney disease via multiple-microarray analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 997-997.	0.7	16
12175	Metabolomic Approaches to Study Chemical Exposure-Related Metabolism Alterations in Mammalian Cell Cultures. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6843.	1.8	16

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12176	The natural way forward: Molecular dynamics simulation analysis of phytochemicals from Indian medicinal plants as potential inhibitors of SARS-CoV-2 targets. <i>Phytotherapy Research</i> , 2020, 34, 3420-3433.	2.8	46
12177	Presynaptic dysfunction in CASK-related neurodevelopmental disorders. <i>Translational Psychiatry</i> , 2020, 10, 312.	2.4	28
12178	Prognostic effect of a novel long noncoding RNA signature and comparison with clinical staging systems for patients with hepatitis B virus-related hepatocellular carcinoma after hepatectomy. <i>Journal of Digestive Diseases</i> , 2020, 21, 650-663.	0.7	5
12179	Molecular classification and immunologic characteristics of immunoreactive high-grade serous ovarian cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 8103-8114.	1.6	2
12180	Development of Autophagy Signature-Based Prognostic Nomogram for Refined Glioma Survival Prognostication. <i>BioMed Research International</i> , 2020, 2020, 1-23.	0.9	7
12181	Bioinformatic screening for candidate biomarkers and their prognostic values in endometrial cancer. <i>BMC Genetics</i> , 2020, 21, 113.	2.7	3
12182	The Rhodamine Isothiocyanate Analogue as a Quorum Sensing Inhibitor Has the Potential to Control Microbially-Induced Biofouling. <i>Marine Drugs</i> , 2020, 18, 484.	2.2	3
12183	Intermittent leucine pulses during continuous feeding alters novel components involved in skeletal muscle growth of neonatal pigs. <i>Amino Acids</i> , 2020, 52, 1319-1335.	1.2	11
12184	Dissecting Molecular Principles of the Hsp90 Chaperone Regulation by Allosteric Modulators Using a Hierarchical Simulation Approach and Network Modeling of Allosteric Interactions: Conformational Selection Dictates the Diversity of Protein Responses and Ligand-Specific Functional Mechanisms. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 6656-6677.	2.3	3
12185	Functional gene networks reveal distinct mechanisms segregating in migraine families. <i>Brain</i> , 2020, 143, 2945-2956.	3.7	15
12186	GeneMates: an R package for detecting horizontal gene co-transfer between bacteria using gene-gene associations controlled for population structure. <i>BMC Genomics</i> , 2020, 21, 658.	1.2	9
12187	Comprehensive RNA-seq Analysis to Evaluate the Pigmentation-Related Genes Involved in Albinism of Cichlid Fish, <i>Aulonocara baenschi</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
12188	Transcriptomic Analysis Revealed an Emerging Role of Alternative Splicing in Embryonal Tumor with Multilayered Rosettes. <i>Genes</i> , 2020, 11, 1108.	1.0	2
12189	Maleic hydrazide elicits global transcriptomic changes in chemically topped tobacco to influence shoot bud development. <i>Planta</i> , 2020, 252, 64.	1.6	3
12190	Identifying Hub Genes, Key Pathways and Immune Cell Infiltration Characteristics in Pediatric and Adult Ulcerative Colitis by Integrated Bioinformatic Analysis. <i>Digestive Diseases and Sciences</i> , 2021, 66, 3002-3014.	1.1	15
12191	Integrated Omics of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2020, 38, 734-747.e9.	7.7	144
12192	Identifying Plasma Biomarkers with high specificity for major depressive disorder: A multi-level proteomics study. <i>Journal of Affective Disorders</i> , 2020, 277, 620-630.	2.0	16
12193	Functional compensation dominates the assembly of plant rhizospheric bacterial community. <i>Soil Biology and Biochemistry</i> , 2020, 150, 107968.	4.2	48



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12194	Multi-layered Spatial Transcriptomics Identify Secretary Factors Promoting Human Hematopoietic Stem Cell Development. <i>Cell Stem Cell</i> , 2020, 27, 822-839.e8.	5.2	51
12195	Molecular Characterization of the Coproduced Extracellular Vesicles in HEK293 during Virus-Like Particle Production. <i>Journal of Proteome Research</i> , 2020, 19, 4516-4532.	1.8	15
12196	A panel of 8 miRNAs as a novel diagnostic biomarker in pancreatic cancer. <i>Medicine (United States)</i> , 2020, 99, e22261.	0.4	5
12197	Multiple omics analysis reveals that high fiber diets promote gluconeogenesis and inhibit glycolysis in muscle. <i>BMC Genomics</i> , 2020, 21, 660.	1.2	10
12198	Identification of key genes and functions of circulating tumor cells in multiple cancers through bioinformatic analysis. <i>BMC Medical Genomics</i> , 2020, 13, 140.	0.7	10
12199	A single-cell survey of cellular hierarchy in acute myeloid leukemia. <i>Journal of Hematology and Oncology</i> , 2020, 13, 128.	6.9	45
12200	Exploring dynamic multilayer graphs for digital humanities. <i>Applied Network Science</i> , 2020, 5, .	0.8	4
12201	Altered vaginal microbiome and relative co-abundance network in pregnant women with penicillin allergy. <i>Allergy, Asthma and Clinical Immunology</i> , 2020, 16, 79.	0.9	4
12202	Rps27a might act as a controller of microglia activation in triggering neurodegenerative diseases. <i>PLoS ONE</i> , 2020, 15, e0239219.	1.1	27
12203	Immune-Related Hub Genes and the Competitive Endogenous RNA Network in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 1255-1265.	1.2	17
12204	Transcript Isoforms of SLC7A11-AS1 Are Associated With Varicocele-Related Male Infertility. <i>Frontiers in Genetics</i> , 2020, 11, 1015.	1.1	11
12205	Analyzing Gene Expression Profiles from Ataxia and Spasticity Phenotypes to Reveal Spastic Ataxia Related Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6722.	1.8	5
12206	Polysaccharide source altered ecological network, functional profile, and short-chain fatty acid production in a porcine gut microbiota. <i>Beneficial Microbes</i> , 2020, 11, 591-610.	1.0	9
12207	Identification and expression profile of microRNA in seven tissues of the Golden snub-nosed monkey ( <i>Rhinopithecus roxellanae</i> ). <i>Molecular Genetics and Genomics</i> , 2020, 295, 1547-1558.	1.0	2
12208	Identification of novel candidate genes by exome sequencing in Tunisian familial male breast cancer patients. <i>Molecular Biology Reports</i> , 2020, 47, 6507-6516.	1.0	4
12209	Molecular mechanisms underlying altered neurobehavioural development of female offspring of mothers with polycystic ovary syndrome: FOS-mediated regulation of neurotrophins in placenta. <i>EBioMedicine</i> , 2020, 60, 102993.	2.7	15
12210	In silico analysis predicting effects of deleterious SNPs of human RASSF5 gene on its structure and functions. <i>Scientific Reports</i> , 2020, 10, 14542.	1.6	51
12211	A carotenoid-deficient mutant of the plant-associated microbe <i>Pantoea</i> sp. YR343 displays an altered membrane proteome. <i>Scientific Reports</i> , 2020, 10, 14985.	1.6	6



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12212	Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. <i>Scientific Reports</i> , 2020, 10, 14701.	1.6	21
12213	Single-cell RNA-seq identifies unique transcriptional landscapes of human nucleus pulposus and annulus fibrosus cells. <i>Scientific Reports</i> , 2020, 10, 15263.	1.6	40
12214	Comprehensive analysis of ubiquitin-specific protease 1 reveals its importance in hepatocellular carcinoma. <i>Cell Proliferation</i> , 2020, 53, e12908.	2.4	31
12215	Study of the Mechanism of the Reyaning Mixture Involved in Treating Novel Coronavirus Pneumonia Based on Network Pharmacology. <i>Natural Product Communications</i> , 2020, 15, 1934578X2095459.	0.2	0
12216	Identification of KIF18B as a Hub Candidate Gene in the Metastasis of Clear Cell Renal Cell Carcinoma by Weighted Gene Co-expression Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 905.	1.1	10
12217	Clinical Correlation of Wnt2 and COL8A1 With Colon Adenocarcinoma Prognosis. <i>Frontiers in Oncology</i> , 2020, 10, 1504.	1.3	12
12218	Deep proteomics and phosphoproteomics reveal novel biological pathways perturbed by morphine, morphine-3- $\beta$ -glucuronide and morphine-6- $\beta$ -glucuronide in human astrocytes. <i>Journal of Neuroscience Research</i> , 2022, 100, 220-236.	1.3	10
12219	Matrisome Provides a Supportive Microenvironment for Skin Functions of Diverse Species. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 5720-5733.	2.6	10
12220	Multiple Sclerosis Atlas: A Molecular Map of Brain Lesion Stages in Progressive Multiple Sclerosis. <i>Network and Systems Medicine</i> , 2020, 3, 122-129.	2.7	12
12221	A meta-analysis of microRNA networks regulated by melatonin in cancer: Portrait of potential candidates for breast cancer treatment. <i>Journal of Pineal Research</i> , 2020, 69, e12693.	3.4	32
12222	A Prognostic Model Based on Six Metabolism-Related Genes in Colorectal Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	15
12223	Comprehensive Analysis of Differentially Expressed circRNAs Reveals a Colorectal Cancer-Related ceRNA Network. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-14.	0.7	6
12225	Dietary impact of a plant-derived microRNA on the gut microbiome. <i>ExRNA</i> , 2020, 2, .	1.0	18
12226	Cell signaling model for arterial mechanobiology. <i>PLoS Computational Biology</i> , 2020, 16, e1008161.	1.5	39
12227	Transcriptome analysis reveals key signature genes involved in the oncogenesis of lung cancer. <i>Cancer Biomarkers</i> , 2020, 29, 475-482.	0.8	5
12228	Comparative Analysis of Mouse Decidualization Models at the Molecular Level. <i>Genes</i> , 2020, 11, 935.	1.0	11
12229	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	9.0	650
12230	Transcriptomic analysis at organ and time scale reveals gene regulatory networks controlling the sulfate starvation response of <i>Solanum lycopersicum</i> . <i>BMC Plant Biology</i> , 2020, 20, 385.	1.6	13

#	ARTICLE	IF	CITATIONS
12231	Development and Analysis of a Stable, Reduced Complexity Model Soil Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 1987.	1.5	18
12232	Insights on the Structural and Metabolic Resistance of Potato ( <i>Solanum tuberosum</i> ) Cultivars to Tuber Black Dot ( <i>Colletotrichum coccodes</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 1287.	1.7	11
12233	Analysis of genes and metabolites associated with propamocarb hydrochloride response in tobacco. <i>Agronomy Journal</i> , 2020, 112, 4939-4950.	0.9	3
12234	Genetic diversity of MHC-B in 12 chicken populations in Korea revealed by single-nucleotide polymorphisms. <i>Immunogenetics</i> , 2020, 72, 367-379.	1.2	4
12235	A High-Density Human Mitochondrial Proximity Interaction Network. <i>Cell Metabolism</i> , 2020, 32, 479-497.e9.	7.2	124
12236	ATAC-seq footprinting unravels kinetics of transcription factor binding during zygotic genome activation. <i>Nature Communications</i> , 2020, 11, 4267.	5.8	318
12237	Molecular networking-based for the target discovery of potent antiproliferative polycyclic macrolactam ansamycins from <i>Streptomyces cacaoi</i> subsp. <i>asoensis</i> . <i>Organic Chemistry Frontiers</i> , 2020, 7, 4008-4018.	2.3	14
12238	Xylem systems genetics analysis reveals a key regulator of lignin biosynthesis in <i>Populus deltoides</i> . <i>Genome Research</i> , 2020, 30, 1131-1143.	2.4	18
12239	Integrative analysis of circRNAs, miRNAs, and mRNAs profiles to reveal ceRNAs networks in chicken intramuscular and abdominal adipogenesis. <i>BMC Genomics</i> , 2020, 21, 594.	1.2	28
12240	Identification and Analysis of Genes Underlying Bone Mineral Density by Integrating Microarray Data of Osteoporosis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 798.	1.8	8
12241	Transcriptome Analysis of <i>Bursaphelenchus xylophilus</i> Uncovers the Impact of <i>Stenotrophomonas maltophilia</i> on Nematode and Pine Wilt Disease. <i>Forests</i> , 2020, 11, 908.	0.9	2
12242	Identification, Expression and Co-Expression Analysis of R2R3-MYB Family Genes Involved in Graft Union Formation in Pecan ( <i>Carya illinoensis</i> ). <i>Forests</i> , 2020, 11, 917.	0.9	14
12243	Neurological manifestations of COVID-19: available evidences and a new paradigm. <i>Journal of NeuroVirology</i> , 2020, 26, 619-630.	1.0	75
12244	Study on Intervention Mechanism of Yiqi Huayu Jiedu Decoction on ARDS Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-16.	0.5	2
12245	Elucidation of the Mechanisms and Molecular Targets of Sanhuang Xiexin Decoction for Type 2 Diabetes Mellitus Based on Network Pharmacology. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	11
12246	The Construction and Analysis of ceRNA Network and Patterns of Immune Infiltration in Colon Adenocarcinoma Metastasis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 688.	1.8	33
12247	The Construction of Bone Metastasis-Specific Prognostic Model and Co-expressed Network of Alternative Splicing in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 790.	1.8	6
12248	Identification of a novel prognostic DNA methylation signature for lung adenocarcinoma based on consensus clustering method. <i>Cancer Medicine</i> , 2020, 9, 7488-7502.	1.3	6

#	ARTICLE	IF	CITATIONS
12249	Seven immune-related genes prognostic power and correlation with tumor-infiltrating immune cells in hepatocellular carcinoma. <i>Cancer Medicine</i> , 2020, 9, 7440-7452.	1.3	24
12250	Caveolin-1-mediated sphingolipid oncometabolism underlies a metabolic vulnerability of prostate cancer. <i>Nature Communications</i> , 2020, 11, 4279.	5.8	52
12251	Circadian clock mechanism driving mammalian photoperiodism. <i>Nature Communications</i> , 2020, 11, 4291.	5.8	42
12252	Osteoclast-associated receptor blockade prevents articular cartilage destruction via chondrocyte apoptosis regulation. <i>Nature Communications</i> , 2020, 11, 4343.	5.8	60
12253	Low protein intake during reproduction compromises the recovery of lactation-induced bone loss in female mouse dams without affecting skeletal muscles. <i>FASEB Journal</i> , 2020, 34, 11844-11859.	0.2	7
12254	Development and Validation of a Clinical Prognostic Model Based on Immune-Related Genes Expressed in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1496.	1.3	15
12255	Systems Analysis of Biliary Atresia Through Integration of High-Throughput Biological Data. <i>Frontiers in Physiology</i> , 2020, 11, 966.	1.3	3
12256	miR-205: A Potential Biomedicine for Cancer Therapy. <i>Cells</i> , 2020, 9, 1957.	1.8	31
12257	In silico analysis reveals interrelation of enriched pathways and genes in type 1 diabetes. <i>Immunogenetics</i> , 2020, 72, 399-412.	1.2	5
12258	A database of integrated molecular and phytochemical interactions of the foxm1 pathway for lung cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, , 1-13.	2.0	0
12259	Novel insights into the disease transcriptome of human diabetic glomeruli and tubulointerstitium. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, 2059-2072.	0.4	28
12260	DELTEX2 C-terminal domain recognizes and recruits ADP-ribosylated proteins for ubiquitination. <i>Science Advances</i> , 2020, 6, .	4.7	29
12261	Heat-Killed <i>Fusobacterium nucleatum</i> Triggers Varying Heme-Related Inflammatory and Stress Responses Depending on Primary Human Respiratory Epithelial Cell Type. <i>Molecules</i> , 2020, 25, 3839.	1.7	9
12262	Mortality Risk Profiling of <i>Staphylococcus aureus</i> Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures. <i>Cell</i> , 2020, 182, 1311-1327.e14.	13.5	58
12263	Systematic Transcriptome Analysis of Noise-Induced Hearing Loss Pathogenesis Suggests Inflammatory Activities and Multiple Susceptible Molecules and Pathways. <i>Frontiers in Genetics</i> , 2020, 11, 968.	1.1	10
12264	CeRNA Network Analysis Representing Characteristics of Different Tumor Environments Based on 1p/19q Codeletion in Oligodendrogliomas. <i>Cancers</i> , 2020, 12, 2543.	1.7	5
12265	Functional, proteomic and bioinformatic analyses of Nrf2 and Keap1-null skeletal muscle. <i>Journal of Physiology</i> , 2020, 598, 5427-5451.	1.3	34
12266	High-resolution analysis of differential gene expression during skeletal muscle atrophy and programmed cell death. <i>Physiological Genomics</i> , 2020, 52, 492-511.	1.0	8

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12267	Monocyte and Macrophage-Mediated Pathology and Protective Immunity During Schistosomiasis. <i>Frontiers in Microbiology</i> , 2020, 11, 1973.	1.5	15
12268	Potential mechanism of RRM2 for promoting Cervical Cancer based on weighted gene co-expression network analysis. <i>International Journal of Medical Sciences</i> , 2020, 17, 2362-2372.	1.1	13
12269	Clinical significance of long non-coding RNA DUXAP8 and its protein coding genes in hepatocellular carcinoma. <i>Journal of Cancer</i> , 2020, 11, 6140-6156.	1.2	11
12270	Caspase-8 mediates inflammation and disease in rodent malaria. <i>Nature Communications</i> , 2020, 11, 4596.	5.8	11
12271	Identification of MTHFD2 as a novel prognosis biomarker in esophageal carcinoma patients based on transcriptomic data and methylation profiling. <i>Medicine (United States)</i> , 2020, 99, e22194.	0.4	9
12272	Tunica-Specific Transcriptome of Abdominal Aortic Aneurysm and the Effect of Intraluminal Thrombus, Smoking, and Diameter Growth Rate. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2700-2713.	1.1	18
12273	Integrated analysis of lncRNA, miRNA and mRNA reveals novel insights into the fertility regulation of large white sows. <i>BMC Genomics</i> , 2020, 21, 636.	1.2	11
12274	Similar but Not Identical Binding Properties of LSU (Response to Low Sulfur) Proteins From <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1246.	1.7	15
12275	Both Soil Bacteria and Soil Chemical Property Affected the Micropredator Myxobacterial Community: Evidence from Natural Forest Soil and Greenhouse Rhizosphere Soil. <i>Microorganisms</i> , 2020, 8, 1387.	1.6	8
12276	Identification of potential mRNA panels for severe acute respiratory syndrome coronavirus 2 (COVID-19) diagnosis and treatment using microarray dataset and bioinformatics methods. <i>3 Biotech</i> , 2020, 10, 422.	1.1	31
12277	Integrative analysis of lncRNAs, miRNAs, and mRNAs-associated ceRNA network in a neonatal mouse model of bronchopulmonary dysplasia. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2021, 34, 3234-3245.	0.7	3
12278	Brain Transcriptomics of Wild and Domestic Rabbits Suggests That Changes in Dopamine Signaling and Ciliary Function Contributed to Evolution of Tameness. <i>Genome Biology and Evolution</i> , 2020, 12, 1918-1928.	1.1	17
12279	A Novel RNA-Seq-Based Model for Preoperative Prediction of Lymph Node Metastasis in Oral Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	7
12280	Signalosome-Regulated Serum Response Factor Phosphorylation Determining Myocyte Growth in Width Versus Length as a Therapeutic Target for Heart Failure. <i>Circulation</i> , 2020, 142, 2138-2154.	1.6	23
12281	MasterPATH: network analysis of functional genomics screening data. <i>BMC Genomics</i> , 2020, 21, 632.	1.2	3
12282	Mechanisms of indigo naturalis on treating ulcerative colitis explored by GEO gene chips combined with network pharmacology and molecular docking. <i>Scientific Reports</i> , 2020, 10, 15204.	1.6	45
12283	Gene co-expression analysis reveals transcriptome divergence between wild and cultivated chickpea under drought stress. <i>Plant Journal</i> , 2020, 104, 1195-1214.	2.8	22
12284	Identification of Key Prognostic Biomarker and Its Correlation with Immune Infiltrates in Pancreatic Ductal Adenocarcinoma. <i>Disease Markers</i> , 2020, 2020, 1-12.	0.6	23

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12285	Comparative analysis of maca ( <i>Lepidium meyenii</i> ) proteome profiles reveals insights into response mechanisms of herbal plants to high-temperature stress. <i>BMC Plant Biology</i> , 2020, 20, 431.	1.6	4
12286	Integrated Analyses of Mouse Stem Cell Transcriptomes Provide Clues for Stem Cell Maintenance and Transdifferentiation. <i>Frontiers in Genetics</i> , 2020, 11, 563798.	1.1	3
12287	Transcriptome Analyses in BV2 Microglial Cells Following Treatment With Amino-Terminal Fragments of Apolipoprotein E. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 256.	1.7	10
12288	Isolation and Characterization of the Novel Bacteriophage AXL3 against <i>Stenotrophomonas maltophilia</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 6338.	1.8	21
12289	The Expression Profile of mRNA and tRNA Genes in Splenocytes and Neutrophils after In Vivo Delivery of Antitumor Short Hairpin RNA of Indoleamine 2,3-Dioxygenase. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6703.	1.8	0
12290	Seminal fluid protein divergence among populations exhibiting postmating prezygotic reproductive isolation. <i>Molecular Ecology</i> , 2020, 29, 4428-4441.	2.0	12
12291	Deciphering the Underlying Mechanism of <i>Eucommia</i> Cortex against Osteoporotic Fracture by Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	7
12292	Culture-dependent and -independent methods revealed an abundant myxobacterial community shaped by other bacteria and pH in Dinghushan acidic soils. <i>PLoS ONE</i> , 2020, 15, e0238769.	1.1	4
12293	Determining the Molecular Background of Endometrial Receptivity in Adenomyosis. <i>Biomolecules</i> , 2020, 10, 1311.	1.8	12
12294	FRUITFULL Is a Repressor of Apical Hook Opening in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 6438.	1.8	4
12295	Inhibitions Dominate but Stimulations and Growth Rescues Are Not Rare Among Bacterial Isolates from Grains of Forest Soil. <i>Microbial Ecology</i> , 2020, 80, 872-884.	1.4	2
12296	Identification of a metabolism-related gene expression prognostic model in endometrial carcinoma patients. <i>BMC Cancer</i> , 2020, 20, 864.	1.1	21
12297	Impact of a weight loss and fitness intervention on exercise-associated plasma oxylipin patterns in obese, insulin-resistant, sedentary women. <i>Physiological Reports</i> , 2020, 8, e14547.	0.7	14
12298	Molecular Network and Culture Media Variation Reveal a Complex Metabolic Profile in <i>Pantoea</i> cf. <i>eucria</i> D2 Associated with an Acidified Marine Sponge. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6307.	1.8	14
12299	Genomic analysis suggests <i>Salinispora</i> is a rich source of novel lanthipeptides. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1529-1535.	1.0	1
12300	MassARRAY-based single nucleotide polymorphism analysis in breast cancer of north Indian population. <i>BMC Cancer</i> , 2020, 20, 861.	1.1	4
12301	Identification of Potential Biomarkers for CAD Using Integrated Expression and Methylation Data. <i>Frontiers in Genetics</i> , 2020, 11, 778.	1.1	5
12302	Similarities and Differences of Photosynthesis Establishment Related mRNAs and Novel lncRNAs in Early Seedlings ( <i>Coleoptile/Cotyledon</i> vs. <i>True Leaf</i> ) of Rice and <i>Arabidopsis</i> . <i>Frontiers in Genetics</i> , 2020, 11, 565006.	1.1	8

#	ARTICLE	IF	CITATIONS
12303	Comprehensive Metabolome Analysis of Fermented Aqueous Extracts of <i>Viscum album</i> L. by Liquid Chromatography-High Resolution Tandem Mass Spectrometry. <i>Molecules</i> , 2020, 25, 4006.	1.7	29
12304	Humic Acid Enhances the Growth of Tomato Promoted by Endophytic Bacterial Strains Through the Activation of Hormone-, Growth-, and Transcription-Related Processes. <i>Frontiers in Plant Science</i> , 2020, 11, 582267.	1.7	20
12305	Drug Vulnerabilities and Disease Prognosis Linked to the Stem Cell-Like Gene Expression Program Triggered by the RHO GTPase Activator VAV2 in Hyperplastic Keratinocytes and Head and Neck Cancers, 2020, 12, 2498.	1.7	6
12306	DEAD-Box Helicase 4 (Ddx4)+ Stem Cells Sustain Tumor Progression in Non-Serous Ovarian Cancers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6096.	1.8	2
12307	Identification of dysregulated miRNAs-genes network in ovarian cancer: An integrative approach to uncover the molecular interactions and oncomechanisms. <i>Cancer Reports</i> , 2020, 3, e1286.	0.6	6
12308	Jasmonate induced alternative splicing responses in <i>Arabidopsis</i> . <i>Plant Direct</i> , 2020, 4, e00245.	0.8	11
12309	Study on the Mechanisms of Banxia Xiexin Decoction in Treating Diabetic Gastroparesis Based on Network Pharmacology. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 487-498.	2.2	10
12310	Identifying Conserved Functional Gene Modules Underlying the Dynamic Regulation of Tea Plant Development and Secondary Metabolism. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 11026-11037.	2.4	4
12311	Metabolome of the <i>Phyllidiella pustulosa</i> Species Complex (Nudibranchia, Heterobranchia,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 and Undescribed Clade. <i>Journal of Natural Products</i> , 2020, 83, 2785-2796.	1.5	7
12312	Chromatin modifier MTA1 regulates mitotic transition and tumorigenesis by orchestrating mitotic mRNA processing. <i>Nature Communications</i> , 2020, 11, 4455.	5.8	20
12313	Floral transcriptomes reveal gene networks in pineapple floral growth and fruit development. <i>Communications Biology</i> , 2020, 3, 500.	2.0	34
12314	SMARCB1 loss interacts with neuronal differentiation state to block maturation and impact cell stability. <i>Genes and Development</i> , 2020, 34, 1316-1329.	2.7	30
12315	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	329
12316	Development of an Immune Infiltration-Related Eight-Gene Prognostic Signature in Colorectal Cancer Microenvironment. <i>BioMed Research International</i> , 2020, 2020, 1-43.	0.9	20
12317	Proteomic Analysis of Human Endometrial Tissues Reveals the Roles of PI3K/AKT/mTOR Pathway and Tumor Angiogenesis Molecules in the Pathogenesis of Endometrial Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	10
12318	Deciphering the Molecular Targets and Mechanisms of HGWD in the Treatment of Rheumatoid Arthritis via Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	19
12319	Immiscible inclusion bodies formed by polyglutamine and poly(glycine-alanine) are enriched with distinct proteomes but converge in proteins that are risk factors for disease and involved in protein degradation. <i>PLoS ONE</i> , 2020, 15, e0233247.	1.1	7
12320	Cancer proteome and metabolite changes linked to SHMT2. <i>PLoS ONE</i> , 2020, 15, e0237981.	1.1	18



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12321	Myocardial proteomic profile in pulmonary arterial hypertension. <i>Scientific Reports</i> , 2020, 10, 14351.	1.6	12
12322	Bioinformatics Analysis of Key Genes and circRNA-miRNA-mRNA Regulatory Network in Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	25
12323	Genome-wide identification, phylogeny and expression analysis of the SPL gene family in wheat. <i>BMC Plant Biology</i> , 2020, 20, 420.	1.6	38
12324	Circular HER2 RNA positive triple negative breast cancer is sensitive to Pertuzumab. <i>Molecular Cancer</i> , 2020, 19, 142.	7.9	96
12325	Personalized cancer therapy prioritization based on driver alteration co-occurrence patterns. <i>Genome Medicine</i> , 2020, 12, 78.	3.6	10
12326	Nanoparticle treatment of maize analyzed through the metatranscriptome: compromised nitrogen cycling, possible phytopathogen selection, and plant hormesis. <i>Microbiome</i> , 2020, 8, 127.	4.9	26
12327	Time-series transcriptomic analysis reveals novel gene modules that control theanine biosynthesis in tea plant ( <i>Camellia sinensis</i> ). <i>PLoS ONE</i> , 2020, 15, e0238175.	1.1	2
12328	Human transcription factor and protein kinase gene fusions in human cancer. <i>Scientific Reports</i> , 2020, 10, 14169.	1.6	9
12329	A Novel Mechanism for NF- $\kappa$ B-activation via I $\kappa$ B-aggregation: Implications for Hepatic Mallory-Denk-Body Induced Inflammation. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1968-1986.	2.5	17
12330	Strict network analysis of evolutionary conserved and brain-expressed genes reveals new putative candidates implicated in Intellectual Disability and in Global Development Delay. <i>World Journal of Biological Psychiatry</i> , 2021, 22, 1-11.	1.3	1
12331	Repetitive Elements Contribute to the Diversity and Evolution of Centromeres in the Fungal Genus <i>Verticillium</i> . <i>MBio</i> , 2020, 11, .	1.8	26
12332	Identification of Biomarkers to Construct a Competing Endogenous RNA Network and Establishment of a Genomic-Clinicopathologic Nomogram to Predict Survival for Children with Rhabdoid Tumors of the Kidney. <i>BioMed Research International</i> , 2020, 2020, 1-27.	0.9	1
12333	Construction of circRNA-Associated ceRNA Network Reveals Novel Biomarkers for Esophageal Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-12.	0.7	13
12334	Novel genes associated with folic acid-mediated metabolism in mouse: A bioinformatics study. <i>PLoS ONE</i> , 2020, 15, e0238940.	1.1	4
12335	Comparative Transcriptome Analysis of the Regenerating Zebrafish Telencephalon Unravels a Resource With Key Pathways During Two Early Stages and Activation of Wnt/ $\beta$ -Catenin Signaling at the Early Wound Healing Stage. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 584604.	1.8	18
12336	VapC21 Toxin Contributes to Drug-Tolerance and Interacts With Non-cognate VapB32 Antitoxin in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 2037.	1.5	21
12337	Ontogeny of arterial macrophages defines their functions in homeostasis and inflammation. <i>Nature Communications</i> , 2020, 11, 4549.	5.8	54
12338	Presence of Gastric Pepsinogen in the Trachea Is Associated with Altered Inflammation and Microbial Composition. <i>Infection and Immunity</i> , 2020, 88, .	1.0	2



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12339	Integrated Bioinformatics Analysis Reveals Function and Regulatory Network of miR-200b-3p in Endometriosis. <i>BioMed Research International</i> , 2020, 2020, 1-7.	0.9	14
12340	Prognostic lncRNA, miRNA, and mRNA Signatures in Papillary Thyroid Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 805.	1.1	9
12341	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1740.	1.5	27
12342	Post-translational formation of strained cyclophanes in bacteria. <i>Nature Chemistry</i> , 2020, 12, 1042-1053.	6.6	62
12343	ReDU: a framework to find and reanalyze public mass spectrometry data. <i>Nature Methods</i> , 2020, 17, 901-904.	9.0	79
12344	Randomised, double-blind, placebo-controlled trial of oral probiotic <i>Streptococcus salivarius</i> M18 on head and neck cancer patients post-radiotherapy: a pilot study. <i>Scientific Reports</i> , 2020, 10, 13201.	1.6	11
12345	Discovery of small molecules that normalize the transcriptome and enhance cysteine cathepsin activity in progranulin-deficient microglia. <i>Scientific Reports</i> , 2020, 10, 13688.	1.6	13
12346	Omics Application in Animal Science—A Special Emphasis on Stress Response and Damaging Behaviour in Pigs. <i>Genes</i> , 2020, 11, 920.	1.0	31
12347	The AAA+ATPase valosin-containing protein (VCP)/p97/Cdc48 interaction network in <i>Leishmania</i> . <i>Scientific Reports</i> , 2020, 10, 13135.	1.6	3
12348	The Somatic Mutation Landscape and RNA Prognostic Markers in Stomach Adenocarcinoma. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 7735-7746.	1.0	24
12349	The Immune Landscape and Prognostic Immune Key Genes Potentially Involved in Modulating Synaptic Functions in Prostate Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1330.	1.3	8
12350	Using Micro- and Macro-Level Network Metrics Unveils Top Communicative Gene Modules in Psoriasis. <i>Genes</i> , 2020, 11, 914.	1.0	2
12351	A Linear Regression and Deep Learning Approach for Detecting Reliable Genetic Alterations in Cancer Using DNA Methylation and Gene Expression Data. <i>Genes</i> , 2020, 11, 931.	1.0	24
12352	The Expression of Cold-Inducible RNA-Binding Protein mRNA in Sow Genital Tract Is Modulated by Natural Mating, But Not by Seminal Plasma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5333.	1.8	8
12353	Integrated Framework of the Immune-Defense Transcriptional Signatures in the Arabidopsis Shoot Apical Meristem. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5745.	1.8	0
12354	Solving the Conundrum: Widespread Proteins Annotated for Urea Metabolism in Bacteria Are Carboxyguanidine Deiminases Mediating Nitrogen Assimilation from Guanidine. <i>Biochemistry</i> , 2020, 59, 3258-3270.	1.2	27
12355	Isolation of Isotrichophycin C and Trichophycins G-I from a Collection of <i>Trichodesmium thiebautii</i> . <i>Journal of Natural Products</i> , 2020, 83, 2664-2671.	1.5	7
12356	The DUF328 family member YaaA is a DNA-binding protein with a novel fold. <i>Journal of Biological Chemistry</i> , 2020, 295, 14236-14247.	1.6	6

#	ARTICLE	IF	CITATIONS
12357	Potential Antigenic Cross-reactivity Between Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Dengue Viruses. <i>Clinical Infectious Diseases</i> , 2021, 73, e2444-e2449.	2.9	137
12358	Networks of inbreeding coefficients in a selected population of rabbits. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 599-608.	0.8	4
12359	Potential Molecular Mechanism of the <i>NPPB</i> Gene in Postischemic Heart Failure with and without T2DM. <i>BioMed Research International</i> , 2020, 2020, 1-17.	0.9	2
12360	Construction and Investigation of MicroRNA-mRNA Regulatory Network of Gastric Cancer with <i>Helicobacter pylori</i> Infection. <i>Biochemistry Research International</i> , 2020, 2020, 1-10.	1.5	2
12361	To bloom once or more times: the reblooming mechanisms of <i>Iris germanica</i> revealed by transcriptome profiling. <i>BMC Genomics</i> , 2020, 21, 553.	1.2	9
12362	The current landscape of coronavirus-host protein-protein interactions. <i>Journal of Translational Medicine</i> , 2020, 18, 319.	1.8	66
12363	Dynamic nanopore long-read sequencing analysis of HIV-1 splicing events during the early steps of infection. <i>Retrovirology</i> , 2020, 17, 25.	0.9	23
12364	Effects of Gut Microbiome and Short-Chain Fatty Acids (SCFAs) on Finishing Weight of Meat Rabbits. <i>Frontiers in Microbiology</i> , 2020, 11, 1835.	1.5	26
12365	Uncovering the Mechanisms of Cryptotanshinone as a Therapeutic Agent Against Hepatocellular Carcinoma. <i>Frontiers in Pharmacology</i> , 2020, 11, 1264.	1.6	17
12366	LncRNA-SLC16A1-AS1 induces metabolic reprogramming during Bladder Cancer progression as target and co-activator of E2F1. <i>Theranostics</i> , 2020, 10, 9620-9643.	4.6	58
12367	Dual Host-Intracellular Parasite Transcriptome of Enucleated Cells Hosting <i>Leishmania amazonensis</i> : Control of Half-Life of Host Cell Transcripts by the Parasite. <i>Infection and Immunity</i> , 2020, 88, .	1.0	5
12368	The Integrated Analyses of Driver Genes Identify Key Biomarkers in Thyroid Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382094044.	0.8	4
12369	<p></p>Construction and Comprehensive Analysis of a ceRNA Network to Reveal Potential Novel Biomarkers for Triple-Negative Breast Cancer</p>. <i>Cancer Management and Research</i> , 2020, Volume 12, 7061-7075.	0.9	6
12370	Transcriptomic analysis delineates potential signature genes and miRNAs associated with the pathogenesis of asthma. <i>Scientific Reports</i> , 2020, 10, 13354.	1.6	20
12371	Metabolomic and Signaling Programs Induced by Immobilized versus Soluble IFN $\gamma$ in Neural Stem Cells. <i>Bioconjugate Chemistry</i> , 2020, 31, 2125-2135.	1.8	7
12372	Molecular Networking-Guided Discovery and Characterization of Stechlisins, a Group of Cyclic Lipopeptides from a <i>Pseudomonas</i> sp.. <i>Journal of Natural Products</i> , 2020, 83, 2607-2617.	1.5	17
12373	The ancient roots of nicotianamine: diversity, role, regulation and evolution of nicotianamine-like metallophores. <i>Metallomics</i> , 2020, 12, 1480-1493.	1.0	23
12374	Covariation patterns of phytoplankton and bacterioplankton in hypertrophic shallow lakes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	5

#	ARTICLE	IF	CITATIONS
12375	Plasmin Cascade Mediates Thrombotic Events in SARS-CoV-2 Infection via Complement and Platelet-Activating Systems. <i>IEEE Open Journal of Engineering in Medicine and Biology</i> , 2020, 1, 220-227.	1.7	12
12376	EffectorK, a comprehensive resource to mine for <i>Ralstonia</i> , <i>Xanthomonas</i> , and other published effector interactors in the <i>Arabidopsis</i> proteome. <i>Molecular Plant Pathology</i> , 2020, 21, 1257-1270.	2.0	38
12377	Phosphorylation-Dependent Assembly of a 14-3-3 Mediated Signaling Complex during Red Blood Cell Invasion by <i>Plasmodium falciparum</i> Merozoites. <i>MBio</i> , 2020, 11, .	1.8	13
12378	Brain microenvironment-driven resistance to immune and targeted therapies in acral melanoma. <i>ESMO Open</i> , 2020, 5, e000707.	2.0	3
12379	Gene Expression and RNA Splicing Imputation Identifies Novel Candidate Genes Associated with Osteoporosis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e4742-e4757.	1.8	12
12380	Association Analysis of Peripheral and CSF Biomarkers in Late Mild Cognitive Impairment. <i>Frontiers in Genetics</i> , 2020, 11, 834.	1.1	1
12381	Establishment of Optogenetic Modulation of cAMP for Analyzing Growth, Biofilm Formation, and Virulence Pathways of Bacteria Using a Light-Gated Cyclase. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 5535.	1.3	2
12382	Gene Regulatory Network Analysis of Perivascular Adipose Tissue of Abdominal Aortic Aneurysm Identifies Master Regulators of Key Pathogenetic Pathways. <i>Biomedicine</i> , 2020, 8, 288.	1.4	11
12383	Detecting Interactive Gene Groups for Single-Cell RNA-Seq Data Based on Co-Expression Network Analysis and Subgraph Learning. <i>Cells</i> , 2020, 9, 1938.	1.8	11
12384	Inhibition of miRNA-34a Promotes M2 Macrophage Polarization and Improves LPS-Induced Lung Injury by Targeting Klf4. <i>Genes</i> , 2020, 11, 966.	1.0	22
12385	Network Pharmacology-Oriented Identification of Key Proteins and Signaling Pathways Targeted by Xihuang Pill in the Treatment of Breast Cancer. <i>Breast Cancer: Targets and Therapy</i> , 2020, Volume 12, 267-277.	1.0	5
12386	Deep Learning on High-Throughput Transcriptomics to Predict Drug-Induced Liver Injury. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 562677.	2.0	24
12387	Multi-Approach Bioinformatics Analysis of Curated Omics Data Provides a Gene Expression Panorama for Multiple Cancer Types. <i>Frontiers in Genetics</i> , 2020, 11, 586602.	1.1	14
12388	Comprehensive Analysis Reveals Novel Interactions between Circulating MicroRNAs and Gut Microbiota Composition in Human Obesity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9509.	1.8	20
12389	Application of Differential Network Enrichment Analysis for Deciphering Metabolic Alterations. <i>Metabolites</i> , 2020, 10, 479.	1.3	5
12390	Radix Rehmanniae and Corni Fructus against Diabetic Nephropathy via AGE-RAGE Signaling Pathway. <i>Journal of Diabetes Research</i> , 2020, 2020, 1-15.	1.0	20
12391	The identification of co-expressed gene modules in <i>Streptococcus pneumoniae</i> from colonization to infection to predict novel potential virulence genes. <i>BMC Microbiology</i> , 2020, 20, 376.	1.3	0
12392	A comprehensive study of the proteins involved in salinity stress response in roots and shoots of the FL478 genotype of rice ( <i>Oryza sativa</i> L. ssp. indica). <i>Crop Journal</i> , 2021, 9, 1154-1168.	2.3	11

#	ARTICLE	IF	CITATIONS
12393	SON inhibits megakaryocytic differentiation via repressing RUNX1 and the megakaryocytic gene expression program in acute megakaryoblastic leukemia. <i>Cancer Gene Therapy</i> , 2021, 28, 1000-1015.	2.2	5
12394	A reference catalog of DNA palindromes in the human genome and their variations in 1000 Genomes. <i>Human Genome Variation</i> , 2020, 7, 40.	0.4	15
12395	Intron retention is a robust marker of intertumoral heterogeneity in pancreatic ductal adenocarcinoma. <i>Npj Genomic Medicine</i> , 2020, 5, 55.	1.7	10
12396	A methodology for predicting tissue-specific metabolic roles of receptors applied to subcutaneous adipose. <i>Scientific Reports</i> , 2020, 10, 19535.	1.6	2
12397	Network-based approach highlighting interplay among anti-hypertensives: target coding-genes: diseases. <i>Scientific Reports</i> , 2020, 10, 20152.	1.6	0
12398	Transcriptional signatures of the small intestinal mucosa in response to ethanol in transgenic mice rich in endogenous n3 fatty acids. <i>Scientific Reports</i> , 2020, 10, 19930.	1.6	3
12399	Bacterial diversity and functional analysis of severe early childhood caries and recurrence in India. <i>Scientific Reports</i> , 2020, 10, 21248.	1.6	19
12400	Transcriptome comparison between pluripotent and non-pluripotent calli derived from mature rice seeds. <i>Scientific Reports</i> , 2020, 10, 21257.	1.6	10
12401	Network analysis reveals essential proteins that regulate sodium-iodide symporter expression in anaplastic thyroid carcinoma. <i>Scientific Reports</i> , 2020, 10, 21440.	1.6	4
12402	Identification of Hub Genes of Mesio Temporal Lobe Epilepsy and Prognostic Biomarkers of Brain Low-grade Gliomas Based on Bioinformatics Analysis. <i>Cell Transplantation</i> , 2020, 29, 096368972097872.	1.2	4
12403	Preparing for Life: Plasma Proteome Changes and Immune System Development During the First Week of Human Life. <i>Frontiers in Immunology</i> , 2020, 11, 578505.	2.2	23
12404	Tomato Spotted Wilt Virus Benefits Its Thrips Vector by Modulating Metabolic and Plant Defense Pathways in Tomato. <i>Frontiers in Plant Science</i> , 2020, 11, 575564.	1.7	26
12405	Butyrate-containing structured lipids inhibit RAC1 and epithelial-to-mesenchymal transition markers: a chemopreventive mechanism against hepatocarcinogenesis. <i>Journal of Nutritional Biochemistry</i> , 2020, 86, 108496.	1.9	8
12406	Network-theoretic analysis and the exploration of stylistic development in Haydn's string quartets. <i>Journal of Mathematics and Music</i> , 2022, 16, 18-28.	0.3	1
12407	Novel Branch Centrality Measures for Electrical Power Systems Considering Both Load-serving and Circulating Currents. , 2020, , .		2
12408	Identification of miRNAs as the Crosstalk in the Interaction between Neural Stem/Progenitor Cells and Endothelial Cells. <i>Disease Markers</i> , 2020, 2020, 1-29.	0.6	2
12409	<i>BPI</i> and <i>KIR6.1</i> as significant hub genes for vein graft restenosis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052096933.	0.4	0
12410	Identification of Key Modules and Hub Genes Involved in Esophageal Squamous Cell Carcinoma Tumorigenesis Using WCGNA. <i>Cancer Control</i> , 2020, 27, 107327482097881.	0.7	15

#	ARTICLE	IF	CITATIONS
12411	Prognostic Significance of Prostaglandin-Endoperoxide Synthase-2 Expressions in Human Breast Carcinoma: A Multiomic Approach. <i>Cancer Informatics</i> , 2020, 19, 117693512096969.	0.9	4
12412	Alteration in Gene Pair Correlations in Tryptophan Metabolism as a Hallmark in Cancer Diagnosis. <i>International Journal of Tryptophan Research</i> , 2020, 13, 117864692097701.	1.0	5
12413	Systems Pharmacology Study of the Anticervical Cancer Mechanisms of FDY003. <i>Natural Product Communications</i> , 2020, 15, 1934578X2097736.	0.2	1
12414	Inferring directional relationships in microbial communities using signed Bayesian networks. <i>BMC Genomics</i> , 2020, 21, 663.	1.2	13
12415	Weighted gene co-expression network analysis identifies FCER1G as a key gene associated with diabetic kidney disease. <i>Annals of Translational Medicine</i> , 2020, 8, 1427-1427.	0.7	15
12416	Kinetics of Phenotypic and Functional Changes in Mouse Models of Sponge Implants: Rational Selection to Optimize Protocols for Specific Biomolecules Screening Purposes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 538203.	2.0	0
12417	Key Modules and Hub Genes Identified by Coexpression Network Analysis for Revealing Novel Biomarkers for Spina Bifida. <i>Frontiers in Genetics</i> , 2020, 11, 583316.	1.1	6
12418	Genome-Wide Identification and Capsaicinoid Biosynthesis-Related Expression Analysis of the R2R3-MYB Gene Family in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2020, 11, 598183.	1.1	23
12419	Machine Learning Models to Predict Primary Sites of Metastatic Cervical Carcinoma From Unknown Primary. <i>Frontiers in Genetics</i> , 2020, 11, 614823.	1.1	1
12420	Screening and Identification of Prognostic Tumor-Infiltrating Immune Cells and Genes of Endometrioid Endometrial Adenocarcinoma: Based on The Cancer Genome Atlas Database and Bioinformatics. <i>Frontiers in Oncology</i> , 2020, 10, 554214.	1.3	9
12421	Differentiation of Tracheary Elements in Sugarcane Suspension Cells Involves Changes in Secondary Wall Deposition and Extensive Transcriptional Reprogramming. <i>Frontiers in Plant Science</i> , 2020, 11, 617020.	1.7	10
12422	Inhibition of FGF and TGF- $\beta$ Pathways in hESCs Identify STOX2 as a Novel SMAD2/4 Cofactor. <i>Biology</i> , 2020, 9, 470.	1.3	3
12423	Genome-Wide Survey and Expression Analysis of the KT/HAK/KUP Family in <i>Brassica napus</i> and Its Potential Roles in the Response to K <sup>+</sup> Deficiency. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9487.	1.8	11
12424	Novel Liver X Receptor Ligand GAC0001E5 Disrupts Glutamine Metabolism and Induces Oxidative Stress in Pancreatic Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9622.	1.8	9
12425	From miRNA Target Gene Network to miRNA Function: miR-375 Might Regulate Apoptosis and Actin Dynamics in the Heart Muscle via Rho-GTPases-Dependent Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9670.	1.8	7
12426	Revealing the Role of Divergent Thinking and Fluid Intelligence in Children's Semantic Memory Organization. <i>Journal of Intelligence</i> , 2020, 8, 43.	1.3	7
12427	The Rheumatoid Arthritis Gene Expression Signature Among Women Who Improve or Worsen During Pregnancy: A Pilot Study. <i>Journal of Rheumatology</i> , 2021, 48, 985-991.	1.0	2
12428	Systems biology drug screening identifies statins as enhancers of current therapies in chronic lymphocytic leukemia. <i>Scientific Reports</i> , 2020, 10, 22153.	1.6	16

#	ARTICLE	IF	CITATIONS
12429	Long Noncoding RNA THAP9-AS1 and TSPOAP1-AS1 Provide Potential Diagnostic Signatures for Pediatric Septic Shock. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	7
12430	Gallinacin ameliorates colitis-associated inflammation and barrier function in mice based on network pharmacology prediction. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095102.	0.4	6
12431	Meshness of sewer networks and its implications for flooding occurrence. <i>Water Science and Technology</i> , 2020, 81, 40-51.	1.2	12
12432	Alteration of Proteotranscriptomic Landscape Reveals the Transcriptional Regulatory Circuits Controlling Key-Signaling Pathways and Metabolic Reprogramming During Tumor Evolution. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 586479.	1.8	6
12433	Systematic Pharmacology and GEO Database Mining Revealed the Therapeutic Mechanism of Xuefu Zhuyu Decoration for Atherosclerosis Cardiovascular Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 592201.	1.1	8
12434	CRFK and Primary Macrophages Transcriptomes in Response to Feline Coronavirus Infection Differ Significantly. <i>Frontiers in Genetics</i> , 2020, 11, 584744.	1.1	1
12435	A Novel XGBoost Method to Identify Cancer Tissue-of-Origin Based on Copy Number Variations. <i>Frontiers in Genetics</i> , 2020, 11, 585029.	1.1	19
12436	Down-Regulation of MiR-181c-5p Promotes Epithelial-to-Mesenchymal Transition in Laryngeal Squamous Cell Carcinoma via Targeting SERPINE1. <i>Frontiers in Oncology</i> , 2020, 10, 544476.	1.3	11
12437	Systems View of Deconditioning During Spaceflight Simulation in the PlanHab Project: The Departure of Urine 1 H-NMR Metabolomes From Healthy State in Young Males Subjected to Bedrest Inactivity and Hypoxia. <i>Frontiers in Physiology</i> , 2020, 11, 532271.	1.3	9
12438	Molecular Mechanism Underlying Derepressed Male Production in Hexaploid Persimmon. <i>Frontiers in Plant Science</i> , 2020, 11, 567249.	1.7	8
12439	Interdependence of Sectors of Economic Activities for World Countries from the Reduced Google Matrix Analysis of WTO Data. <i>Entropy</i> , 2020, 22, 1407.	1.1	6
12440	Intergenerational Metabolomic Analysis of Mothers with a History of Gestational Diabetes Mellitus and Their Offspring. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9647.	1.8	7
12441	Evidence for Divergent Selection on Immune Genes between the African Malaria Vectors, <i>Anopheles coluzzii</i> and <i>A. gambiae</i> . <i>Insects</i> , 2020, 11, 893.	1.0	3
12442	Comparative Microbiome and Metabolome Analyses of the Marine Tunicate <i>Ciona intestinalis</i> from Native and Invaded Habitats. <i>Microorganisms</i> , 2020, 8, 2022.	1.6	17
12443	An Integrated In Silico and In Vivo Approach to Identify Protective Effects of Palonosetron in Cisplatin-Induced Nephrotoxicity. <i>Pharmaceuticals</i> , 2020, 13, 480.	1.7	6
12444	Comparative Transcriptome Analysis of Iron and Zinc Deficiency in Maize ( <i>Zea mays</i> L.). <i>Plants</i> , 2020, 9, 1812.	1.6	26
12445	Characteristics of banana B genome MADS-box family demonstrate their roles in fruit development, ripening, and stress. <i>Scientific Reports</i> , 2020, 10, 20840.	1.6	2
12446	Elucidating the regulatory mechanism of Swi1 prion in global transcription and stress responses. <i>Scientific Reports</i> , 2020, 10, 21838.	1.6	5



#	ARTICLE	IF	CITATIONS
12447	Identifying Potential Candidate Hub Genes and Functionally Enriched Pathways in the Immune Responses to Quadrivalent Inactivated Influenza Vaccines in the Elderly Through Co-Expression Network Analysis. <i>Frontiers in Immunology</i> , 2020, 11, 603337.	2.2	1
12448	Platelet microparticles load a repertory of miRNAs programmed to drive osteogenic phenotype. <i>Journal of Biomedical Materials Research - Part A</i> , 2021, 109, 1502-1511.	2.1	6
12449	Gene expression profiling of chromosome 10 in PTEN-knockout ( $\hat{\sim}/\hat{\sim}$ ) human neural and mesenchymal stem cells: A system biology study. <i>Gene Reports</i> , 2020, 21, 100895.	0.4	0
12450	Macrophages and brown adipocytes cross-communicate to modulate a thermogenic program following methamphetamine exposure. <i>International Journal of Hyperthermia</i> , 2020, 37, 1368-1382.	1.1	6
12451	A Network Pharmacology Approach to Explore the Potential Mechanisms of Yifei Sanjie Formula in Treating Pulmonary Fibrosis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	5
12452	ILDGDB: a manually curated database of genomics, transcriptomics, proteomics and drug information for interstitial lung diseases. <i>BMC Pulmonary Medicine</i> , 2020, 20, 323.	0.8	3
12453	Differential Co-Expression Analyses Allow the Identification of Critical Signalling Pathways Altered during Tumour Transformation and Progression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9461.	1.8	27
12454	Engineered Ripening-Specific Accumulation of Polyamines Spermidine and Spermine in Tomato Fruit Upregulates Clustered C/D Box snoRNA Gene Transcripts in Concert with Ribosomal RNA Biogenesis in the Red Ripe Fruit. <i>Plants</i> , 2020, 9, 1710.	1.6	5
12455	NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index". <i>Viruses</i> , 2020, 12, 1424.	1.5	3
12456	Transcriptional Circuits Regulating Developmental Processes in <i>Candida albicans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 605711.	1.8	26
12457	Structural and Functional Characteristics of miRNAs in Five Strategic Millet Species and Their Utility in Drought Tolerance. <i>Frontiers in Genetics</i> , 2020, 11, 608421.	1.1	14
12458	Genome-Wide Identification of <i>Populus</i> Malectin/Malectin-Like Domain-Containing Proteins and Expression Analyses Reveal Novel Candidates for Signaling and Regulation of Wood Development. <i>Frontiers in Plant Science</i> , 2020, 11, 588846.	1.7	8
12459	SARS-Cov-2 Interactome with Human Ghost Proteome: A Neglected World Encompassing a Wealth of Biological Data. <i>Microorganisms</i> , 2020, 8, 2036.	1.6	2
12460	Mining of gene modules and identification of key genes in head and neck squamous cell carcinoma based on gene co-expression network analysis. <i>Medicine (United States)</i> , 2020, 99, e22655.	0.4	5
12461	Identification of the Biomarkers and Pathological Process of Heterotopic Ossification: Weighted Gene Co-Expression Network Analysis. <i>Frontiers in Endocrinology</i> , 2020, 11, 581768.	1.5	9
12462	Comparative Expression Analysis of Stress-Inducible Candidate Genes in Response to Cold and Drought in Tea Plant [ <i>Camellia sinensis</i> (L.) Kuntze]. <i>Frontiers in Genetics</i> , 2020, 11, 611283.	1.1	25
12463	Quantifying the influence of mutation detection on tumour subclonal reconstruction. <i>Nature Communications</i> , 2020, 11, 6247.	5.8	10
12464	Identification of Potential Hub Genes Related to Diagnosis and Prognosis of Hepatitis B Virus-Related Hepatocellular Carcinoma via Integrated Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-19.	0.9	29



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12465	Analysis of Crucial Genes and Pathways Associated with Spared Nerve Injury-Induced Neuropathic Pain. <i>Neural Plasticity</i> , 2020, 2020, 1-12.	1.0	0
12466	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. <i>Cell Reports</i> , 2020, 32, 108176.	2.9	75
12467	Dominance network analysis of the healthy human vaginal microbiome not dominated by <i>Lactobacillus</i> species. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3447-3456.	1.9	12
12468	Association is not prediction: A landscape of confused reporting in diabetes â€œ A systematic review. <i>Diabetes Research and Clinical Practice</i> , 2020, 170, 108497.	1.1	44
12470	Network pharmacology of AYUSH recommended immune-boosting medicinal plants against COVID-19. <i>Journal of Ayurveda and Integrative Medicine</i> , 2022, 13, 100374.	0.9	33
12471	Temporal regulation of alternative splicing events in rice memory under drought stress. <i>Plant Diversity</i> , 2022, 44, 116-125.	1.8	10
12472	Assessing the Influence of Generational Variety on Product Family Structures. <i>Procedia CIRP</i> , 2020, 91, 796-801.	1.0	4
12473	Introduction and Preliminaries. , 2020, , 1-49.		0
12474	Prediction and analysis of humanâ€œherpes simplex virus type 1 proteinâ€œprotein interactions by integrating multiple methods. <i>Quantitative Biology</i> , 2020, 8, 312-324.	0.3	11
12475	Comparative proteomic analysis highlights metabolic dysfunction in Î±-synucleinopathy. <i>Npj Parkinson's Disease</i> , 2020, 6, 40.	2.5	16
12476	Hostâ€œViral Interactions Revealed among Shared Transcriptomics Signatures of ARDS and Thrombosis: A Clue into COVID-19 Pathogenesis. <i>TH Open</i> , 2020, 04, e403-e412.	0.7	13
12477	SUMMER, a shiny utility for metabolomics and multiomics exploratory research. <i>Metabolomics</i> , 2020, 16, 126.	1.4	4
12478	Cell-Type-Specific Gene Regulatory Networks Underlying Murine Neonatal Heart Regeneration at Single-Cell Resolution. <i>Cell Reports</i> , 2020, 33, 108472.	2.9	99
12479	Targeting aurora kinases as a potential prognostic and therapeutic biomarkers in pediatric acute lymphoblastic leukaemia. <i>Scientific Reports</i> , 2020, 10, 21272.	1.6	13
12480	Interaction of indole-3-acetic acid with horseradish peroxidase as a potential anticancer agent: from docking to molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4188-4196.	2.0	3
12481	nMAGMA: a network-enhanced method for inferring risk genes from GWAS summary statistics and its application to schizophrenia. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
12482	Characterization of mRNA Profiles of Exosomes from Diverse Forms of M2 Macrophages. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	4
12483	Identification of Functional Genes in Pterygium Based on Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	7

#	ARTICLE	IF	CITATIONS
12484	Pathway Maps of Orphan and Complex Diseases Using an Integrative Computational Approach. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	1
12485	Bioinformatics Analysis Identifies Key Genes and Pathways in Acute Myeloid Leukemia Associated with DNMT3A Mutation. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	9
12486	A systems biology framework integrating GWAS and RNA-seq to shed light on the molecular basis of sperm quality in swine. <i>Genetics Selection Evolution</i> , 2020, 52, 72.	1.2	25
12487	The effect of a novel glycolysis-related gene signature on progression, prognosis and immune microenvironment of renal cell carcinoma. <i>BMC Cancer</i> , 2020, 20, 1207.	1.1	40
12488	Exploration of predictive and prognostic alternative splicing signatures in lung adenocarcinoma using machine learning methods. <i>Journal of Translational Medicine</i> , 2020, 18, 463.	1.8	11
12489	<p>A Seven-NF- $\kappa$ B-Related Gene Signature May Distinguish Patients with Ulcerative Colitis-Associated Colorectal Carcinoma</p>. <i>Pharmacogenomics and Personalized Medicine</i> , 2020, Volume 13, 707-718.	0.4	4
12490	Identification of Candidate Circular RNAs Underlying Intramuscular Fat Content in the Donkey. <i>Frontiers in Genetics</i> , 2020, 11, 587559.	1.1	16
12491	Integrative Analysis of Transcriptome-Wide Association Study and mRNA Expression Profiles Identifies Candidate Genes Associated With Idiopathic Pulmonary Fibrosis. <i>Frontiers in Genetics</i> , 2020, 11, 604324.	1.1	6
12492	A Network-Based Analysis Reveals the Mechanism Underlying Vitamin D in Suppressing Cytokine Storm and Virus in SARS-CoV-2 Infection. <i>Frontiers in Immunology</i> , 2020, 11, 590459.	2.2	46
12493	Identification of CHRN4 as a Diagnostic/Prognostic Indicator and Therapeutic Target in Human Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 571167.	1.3	3
12494	RNA-Seq Whole Transcriptome Analysis of Bovine Mammary Epithelial Cells in Response to Intracellular <i>Staphylococcus aureus</i> . <i>Frontiers in Veterinary Science</i> , 2020, 7, 642.	0.9	9
12495	Inhibition of miR-152 during In Vitro Maturation Enhances the Developmental Potential of Porcine Embryos. <i>Animals</i> , 2020, 10, 2289.	1.0	1
12496	Network and Evolutionary Analysis of Human Epigenetic Regulators to Unravel Disease Associations. <i>Genes</i> , 2020, 11, 1457.	1.0	4
12497	An Automated Functional Annotation Pipeline That Rapidly Prioritizes Clinically Relevant Genes for Autism Spectrum Disorder. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9029.	1.8	1
12498	Specificity of Interactions between Components of Two Zinc ABC Transporters in <i>Paracoccus denitrificans</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9098.	1.8	2
12499	Effects of Sphingosine-1-Phosphate on Cell Viability, Differentiation, and Gene Expression of Adipocytes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9284.	1.8	3
12500	Integration of transcriptomic profile of SARS-CoV-2 infected normal human bronchial epi-thelial cells with metabolic and protein-protein interaction networks. <i>Turkish Journal of Biology</i> , 2020, 44, 168-177.	2.1	8
12501	Underpinning miRNA-miRNA co-functional interaction patterns in the metabolism of <i>Oryza sativa</i> by genome-scale network analysis. <i>Heliyon</i> , 2020, 6, e05496.	1.4	5

#	ARTICLE	IF	CITATIONS
12502	Kinetic and Bioinformatic Characterization of <sc>d</sc>-2-Hydroxyglutarate Dehydrogenase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemistry</i> , 2020, 59, 4833-4844.	1.2	5
12503	Identification of prognostic and metastasis-related alternative splicing signatures in hepatocellular carcinoma. <i>Bioscience Reports</i> , 2020, 40, .	1.1	14
12504	Modeling and simulation of atrazine biodegradation in bacteria and its effect in other living systems. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3285-3295.	2.0	33
12505	NetCoMi: network construction and comparison for microbiome data in R. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	222
12506	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	6.0	24
12507	Germline variation networks in the PI3K/AKT pathway corresponding to familial high-incidence lung cancer pedigrees. <i>BMC Cancer</i> , 2020, 20, 1209.	1.1	4
12508	A Multi-Pronged Computational Pipeline for Prioritizing Drug Target Strategies for Latent Tuberculosis. <i>Frontiers in Chemistry</i> , 2020, 8, 593497.	1.8	9
12509	Identification of Transcriptional Variation in Aortic Remodeling Using a Murine Transverse Aortic Constriction (TAC) Model. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 581362.	1.1	3
12510	Multi-Omics Analysis of Diabetic Nephropathy Reveals Potential New Mechanisms and Drug Targets. <i>Frontiers in Genetics</i> , 2020, 11, 616435.	1.1	20
12511	An in-silico method leads to recognition of hub genes and crucial pathways in survival of patients with breast cancer. <i>Scientific Reports</i> , 2020, 10, 18770.	1.6	18
12512	Integrative genomic analysis of the bioprospection of regulators and accessory enzymes associated with cellulose degradation in a filamentous fungus ( <i>Trichoderma harzianum</i> ) BMC Genomics, 2020, 21, 757.	1.2	5
12513	Urinary Metabolomics around Parturition Identifies Metabolite Alterations in Dairy Cows Affected Postpartum by Lameness: Preliminary Study. <i>Dairy</i> , 2020, 1, 2.	0.7	9
12514	Genome-Wide Identification and Coexpression Network Analysis of DNA Methylation Pathway Genes and Their Differentiated Functions in <i>Ginkgo biloba</i> L.. <i>Forests</i> , 2020, 11, 1076.	0.9	6
12515	<i>Campylobacter jejuni</i> Cas9 Modulates the Transcriptome in Caco-2 Intestinal Epithelial Cells. <i>Genes</i> , 2020, 11, 1193.	1.0	12
12516	m6A RNA Methylation in Marine Plants: First Insights and Relevance for Biological Rhythms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7508.	1.8	10
12517	OsteoBLAST: Computational Routine of Global Molecular Analysis Applied to Biomaterials Development. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 565901.	2.0	4
12518	The Landscape of Coronavirus Disease 2019 (COVID-19) and Integrated Analysis SARS-CoV-2 Receptors and Potential Inhibitors in Lung Adenocarcinoma Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 577032.	1.8	6
12519	Transcriptome Analyses of $\beta$ -Thalassemia $\alpha$ 28(A&G) Mutation Using Isogenic Cell Models Generated by CRISPR/Cas9 and Asymmetric Single-Stranded Oligodeoxynucleotides (assODNs). <i>Frontiers in Genetics</i> , 2020, 11, 577053.	1.1	5

#	ARTICLE	IF	CITATIONS
12520	Sulfate Alters the Competition Among Microbiome Members of Sediments Chronically Exposed to Asphalt. <i>Frontiers in Microbiology</i> , 2020, 11, 556793.	1.5	5
12521	Much More Than a Cytoskeletal Protein: Physiological and Pathological Functions of the Non-microtubule Binding Region of Tau. <i>Frontiers in Neurology</i> , 2020, 11, 590059.	1.1	45
12522	Genomic and transcriptomic landscapes and evolutionary dynamics of molluscan glycoside hydrolase families with implications for algae-feeding biology. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2744-2756.	1.9	2
12523	CircPlant: An Integrated Tool for circRNA Detection and Functional Prediction in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 352-358.	3.0	13
12524	Temperature differentially modulates the transcriptome response in <i>Oryza sativa</i> to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> infection. <i>Genomics</i> , 2020, 112, 4842-4852.	1.3	11
12525	Screening and identification of key genes and pathways in metastatic uveal melanoma based on gene expression using bioinformatic analysis. <i>Medicine (United States)</i> , 2020, 99, e22974.	0.4	6
12526	Modified base-binding EVE and DCD domains: striking diversity of genomic contexts in prokaryotes and predicted involvement in a variety of cellular processes. <i>BMC Biology</i> , 2020, 18, 159.	1.7	4
12527	Genome-Wide Identification of Circular RNAs in Response to Low-Temperature Stress in Tomato Leaves. <i>Frontiers in Genetics</i> , 2020, 11, 591806.	1.1	13
12528	The Role of Circular RNAs in Pancreatic Ductal Adenocarcinoma and Biliary-Tract Cancers. <i>Cancers</i> , 2020, 12, 3250.	1.7	22
12529	The structure of the cytokine gene network in uterine fibroids. , 2020, , .		2
12530	Construction of a Potential Breast Cancer-Related miRNA-mRNA Regulatory Network. <i>BioMed Research International</i> , 2020, 2020, 1-18.	0.9	8
12531	Identification of prognosis-associated immune genes and exploration of immune cell infiltration in colorectal cancer. <i>Biomarkers in Medicine</i> , 2020, 14, 1353-1369.	0.6	5
12532	Gene Expression and Co-expression Networks Are Strongly Altered Through Stages in Clear Cell Renal Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 578679.	1.1	19
12533	RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach. <i>Frontiers in Microbiology</i> , 2020, 11, 567471.	1.5	6
12534	Is Crocin a Potential Anti-tumor Candidate Targeting Microtubules? Computational Insights From Molecular Docking and Dynamics Simulations. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 586970.	1.6	4
12535	Humans Dominate the Social Interaction Networks of Urban Free-Ranging Dogs in India. <i>Frontiers in Psychology</i> , 2020, 11, 2153.	1.1	13
12536	Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. <i>Cancer Cell</i> , 2020, 38, 829-843.e4.	7.7	40
12537	Plasma extracellular vesicle miRNAs as potential biomarkers of superstimulatory response in cattle. <i>Scientific Reports</i> , 2020, 10, 19130.	1.6	10

#	ARTICLE	IF	CITATIONS
12538	Investigation of Hepatocellular Carcinoma Molecular Mechanisms via in Silico Analyses. , 2020, , .		0
12539	An Autophagy-Related Long Noncoding RNA Signature Contributes to Poor Prognosis in Colorectal Cancer. <i>Journal of Oncology</i> , 2020, 2020, 1-13.	0.6	40
12540	Investigation of hub genes involved in diabetic nephropathy using biological informatics methods. <i>Annals of Translational Medicine</i> , 2020, 8, 1087-1087.	0.7	10
12541	Revealing Prognosis-Related Pathways at the Individual Level by a Comprehensive Analysis of Different Cancer Transcription Data. <i>Genes</i> , 2020, 11, 1281.	1.0	5
12542	Mapping a Circular RNAâ€“microRNAâ€“mRNA-Signaling Regulatory Axis that Modulates Stemness Properties of Cancer Stem Cell Populations in Colorectal Cancer Spheroid Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7864.	1.8	27
12543	Changes in Honey Bee Head Proteome in Response to Dietary 24-Methylenecholesterol. <i>Insects</i> , 2020, 11, 743.	1.0	1
12544	Novel Modular Rhodopsins from Green Algae Hold Great Potential for Cellular Optogenetic Modulation Across the Biological Model Systems. <i>Life</i> , 2020, 10, 259.	1.1	5
12545	Diversity and Bioactive Potential of Actinobacteria Isolated from a Coastal Marine Sediment in Northern Portugal. <i>Microorganisms</i> , 2020, 8, 1691.	1.6	20
12546	Hsp90 Co-chaperones Form Plastic Genetic Networks Adapted to Client Maturation. <i>Cell Reports</i> , 2020, 32, 108063.	2.9	29
12547	Transcriptomic analysis of glioblastoma multiforme providing new insights into GPR17 signaling communication. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2586-2599.	2.0	13
12548	Phosphoproteomic Analysis of Platelets in Severe Obesity Uncovers Platelet Reactivity and Signaling Pathways Alterations. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 478-490.	1.1	12
12549	Microbiota Analysis of Chickens Raised Under Stressed Conditions. <i>Frontiers in Veterinary Science</i> , 2020, 7, 482637.	0.9	8
12550	UPEFinder: A Bioinformatic Tool for the Study of Uncharacterized Proteins Based on Gene Expression Correlation and the PageRank Algorithm. <i>Journal of Proteome Research</i> , 2020, 19, 4795-4807.	1.8	3
12551	Injury triggers fascia fibroblast collective cell migration to drive scar formation through N-cadherin. <i>Nature Communications</i> , 2020, 11, 5653.	5.8	66
12552	COSIFER: a Python package for the consensus inference of molecular interaction networks. <i>Bioinformatics</i> , 2021, 37, 2070-2072.	1.8	4
12553	Bioinformatics-based identification of miRNA-, lncRNA-, and mRNA-associated ceRNA networks and potential biomarkers for preeclampsia. <i>Medicine (United States)</i> , 2020, 99, e22985.	0.4	12
12554	System biology approach to identify critical host genes for dengue infection. , 2020, , .		0
12555	Potential Molecular Mechanisms of Plantain in the Treatment of Gout and Hyperuricemia Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-20.	0.5	20

#	ARTICLE	IF	CITATIONS
12556	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. <i>Environmental Microbiomes</i> , 2020, 15, 18.	2.2	16
12557	LncRNA MYLK-AS1 facilitates tumor progression and angiogenesis by targeting miR-424-5p/E2F7 axis and activating VEGFR-2 signaling pathway in hepatocellular carcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2020, 39, 235.	3.5	80
12558	Multimiomics Study of Gut Bacteria and Host Metabolism in Irritable Bowel Syndrome and Depression Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 580980.	1.8	11
12559	Key Molecules and Pathways Underlying Sporadic Amyotrophic Lateral Sclerosis: Integrated Analysis on Gene Expression Profiles of Motor Neurons. <i>Frontiers in Genetics</i> , 2020, 11, 578143.	1.1	11
12560	Comparison of the Performance and Microbial Community Structure of Two Outdoor Pilot-Scale Photobioreactors Treating Digestate. <i>Microorganisms</i> , 2020, 8, 1754.	1.6	10
12561	Differential Protein Expression in Striatal D1- and D2-Dopamine Receptor-Expressing Medium Spiny Neurons. <i>Proteomes</i> , 2020, 8, 27.	1.7	6
12562	Assessment of Intratumoral and Peritumoral Computed Tomography Radiomics for Predicting Pathological Complete Response to Neoadjuvant Chemoradiation in Patients With Esophageal Squamous Cell Carcinoma. <i>JAMA Network Open</i> , 2020, 3, e2015927.	2.8	83
12563	Comparative Leaf Proteomics of Brassica napus Genotypes with Distinctive Levels of Early Cold Acclimation. <i>Plant Molecular Biology Reporter</i> , 2020, 39, 317.	1.0	3
12564	Transcriptomic data-driven discovery of global regulatory features of rice seeds developing under heat stress. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2556-2567.	1.9	7
12565	Bioinformatics analysis of a three-gene signature as an independent prediction of survival in follicular gastritis developing into gastric cancer. <i>Gene Reports</i> , 2020, 21, 100861.	0.4	1
12566	Multi-omic comparison of Alzheimer's variants in human ESC-derived microglia reveals convergence at APOE. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	41
12567	Differences in biomarkers and molecular pathways according to age for patients with HFREF. <i>Cardiovascular Research</i> , 2021, 117, 2228-2236.	1.8	8
12568	Adintoviruses: a proposed animal-tropic family of midsize eukaryotic linear dsDNA (MELD) viruses. <i>Virus Evolution</i> , 2021, 7, veaa055.	2.2	28
12569	Network pharmacology and molecular docking analyses on Lianhua Qingwen capsule indicate Akt1 is a potential target to treat and prevent COVID-19. <i>Cell Proliferation</i> , 2020, 53, e12949.	2.4	161
12570	Transcriptome Analysis Reveals Candidate Genes Involved in Low Temperature Stress in Bell Pepper. <i>Russian Journal of Plant Physiology</i> , 2020, 67, 1116-1125.	0.5	1
12571	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
12572	Bioinformatics analysis of key genes and miRNAs associated with Stanford type A aortic dissection. <i>Journal of Thoracic Disease</i> , 2020, 12, 4842-4853.	0.6	9
12573	Perversely expressed long noncoding RNAs can alter host response and viral proliferation in SARS-CoV-2 infection. <i>Future Virology</i> , 2020, 15, 577-593.	0.9	35



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12574	Exploration of Sorafenib Influences on Gene Expression of Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 577000.	1.1	0
12575	Integrated Analysis of Distant Metastasis-Associated Genes and Potential Drugs in Colon Adenocarcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 576615.	1.3	8
12576	Maize Response to Low Temperatures at the Gene Expression Level: A Critical Survey of Transcriptomic Studies. <i>Frontiers in Plant Science</i> , 2020, 11, 576941.	1.7	16
12577	Network Building with the Cytoscape BioGateway App Explained in Five Use Cases. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e106.	25.8	4
12578	Clinical and genetic features of PEHO and PEHO-Like syndromes: A scoping review. <i>Biomedicine and Pharmacotherapy</i> , 2020, 131, 110793.	2.5	3
12579	Transcriptome profiling reveals differential expression of genes potentially involved in muscle and adipose tissue development of cattle. <i>Electronic Journal of Biotechnology</i> , 2020, 48, 72-77.	1.2	2
12580	Ubiquitinome Profiling Reveals the Landscape of Ubiquitination Regulation in Rice Young Panicles. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 305-320.	3.0	18
12581	Mutational analysis revealed 97 key cancer metastasis genes from extracellular vesicles associated with patient survival. <i>Meta Gene</i> , 2020, 26, 100781.	0.3	0
12582	Network vaccinology. <i>Seminars in Immunology</i> , 2020, 50, 101420.	2.7	3
12583	MicroRNA-100 Enhances Autophagy and Suppresses Migration and Invasion of Renal Cell Carcinoma Cells via Disruption of NOX4-Dependent mTOR Pathway. <i>Clinical and Translational Science</i> , 2022, 15, 567-575.	1.5	15
12584	Diatoms Are Selective Segregators in Global Ocean Planktonic Communities. <i>MSystems</i> , 2020, 5, .	1.7	38
12585	NEK10 interactome and depletion reveal new roles in mitochondria. <i>Proteome Science</i> , 2020, 18, 4.	0.7	17
12586	Conjoint analysis of lncRNA and mRNA expression in rotator cuff tendinopathy. <i>Annals of Translational Medicine</i> , 2020, 8, 335-335.	0.7	13
12587	Analysis of potential hub genes involved in the pathogenesis of Chinese type 1 diabetic patients. <i>Annals of Translational Medicine</i> , 2020, 8, 295-295.	0.7	12
12588	Integrated analysis of immunocyte infiltration and differential gene expression in tricuspid aortic valve-associated thoracic aortic aneurysms. <i>Annals of Translational Medicine</i> , 2020, 8, 285-285.	0.7	2
12589	Whole-Genome Sequencing and Target Validation Analysis of Malignant Adenosarcoma: A Tumor With Complex but Specific Genetic Alterations. <i>Frontiers in Oncology</i> , 2020, 10, 538.	1.3	8
12590	Identification of molecular markers for superior quantitative traits in a novel sea cucumber strain by comparative microRNA-mRNA expression profiling. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100686.	0.4	3
12591	Identifying potential treatments of COVID-19 from Traditional Chinese Medicine (TCM) by using a data-driven approach. <i>Journal of Ethnopharmacology</i> , 2020, 258, 112932.	2.0	98



#	ARTICLE	IF	CITATIONS
12592	Rottlerin acts as a therapeutic in primary open-angle glaucoma by targeting the trabecular meshwork via activation of Rap1 signaling. <i>Pharmacological Research</i> , 2020, 159, 104780.	3.1	8
12593	Rusty sink of rhizodeposits and associated keystone microbiomes. <i>Soil Biology and Biochemistry</i> , 2020, 147, 107840.	4.2	73
12594	A Cross-linking Mass Spectrometry Approach Defines Protein Interactions in Yeast Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1161-1178.	2.5	38
12595	Metal-induced bacterial interactions promote diversity in river-sediment microbiomes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	14
12596	Comparative Genomic Analysis of Third-Generation-Cephalosporin-Resistant <i>Escherichia coli</i> Harboring the <i>bla</i> <sub>CMY-2</sub> -Positive Inc1 Group, IncB/O/K/Z, and IncC Plasmids Isolated from Healthy Broilers in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	11
12597	Hepatitis B Virus Core Particles Containing a Conserved Region of the G Protein Combined with Interleukin-35 Protected Mice against Respiratory Syncytial Virus Infection without Vaccine-Enhanced Immunopathology. <i>Journal of Virology</i> , 2020, 94, .	1.5	10
12598	Horizontally Acquired Quorum-Sensing Regulators Recruited by the PhoP Regulatory Network Expand the Host Adaptation Repertoire in the Phytopathogen <i>Pectobacterium brasiliense</i> . <i>MSystems</i> , 2020, 5, .	1.7	11
12599	Metagenome Mining Reveals Hidden Genomic Diversity of Pelagimyophages in Aquatic Environments. <i>MSystems</i> , 2020, 5, .	1.7	23
12600	Prenet: Predictive network from ATAC-SEQ data. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040003.	0.3	2
12601	Characterizing rhizome bud dormancy in <i>Polygonatum kingianum</i> : Development of novel chill models and determination of dormancy release mechanisms by weighted correlation network analysis. <i>PLoS ONE</i> , 2020, 15, e0231867.	1.1	5
12602	Tumor-Infiltrating CD8 T Cells Predict Clinical Breast Cancer Outcomes in Young Women. <i>Cancers</i> , 2020, 12, 1076.	1.7	31
12603	The Hippo Pathway Transducers YAP1/TEAD Induce Acquired Resistance to Trastuzumab in HER2-Positive Breast Cancer. <i>Cancers</i> , 2020, 12, 1108.	1.7	13
12604	Comparative Transcriptomic Analysis to Identify the Genes Related to Delayed Gland Morphogenesis in <i>Gossypium bickii</i> . <i>Genes</i> , 2020, 11, 472.	1.0	7
12605	Deciphering the Cold Adaptive Mechanisms in <i>Pseudomonas psychrophila</i> MTCC12324 Isolated from the Arctic at 79° N. <i>Current Microbiology</i> , 2020, 77, 2345-2355.	1.0	14
12606	Shifts in the bacterial community along with root-associated compartments of maize as affected by goethite. <i>Biology and Fertility of Soils</i> , 2020, 56, 1201-1210.	2.3	15
12607	Heightened Innate Immune Responses in the Respiratory Tract of COVID-19 Patients. <i>Cell Host and Microbe</i> , 2020, 27, 883-890.e2.	5.1	811
12608	A Feasible Dashboard to predict Patent Mining Using Classification Algorithms. <i>Procedia Computer Science</i> , 2020, 167, 2011-2021.	1.2	1
12609	Individual differences in stereotypy and neuron subtype translome with TrkB deletion. <i>Molecular Psychiatry</i> , 2021, 26, 1846-1859.	4.1	24

#	ARTICLE	IF	CITATIONS
12610	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202.	5.8	95
12611	Landscape of Dysregulated Placental RNA Editing Associated With Preeclampsia. <i>Hypertension</i> , 2020, 75, 1532-1541.	1.3	10
12612	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. <i>PLoS Genetics</i> , 2020, 16, e1008754.	1.5	27
12613	An Integrative Pharmacology-Based Analysis of Refined Qingkailing Injection Against Cerebral Ischemic Stroke: A Novel Combination of Baicalin, Geniposide, Cholic Acid, and Hydoxycholic Acid. <i>Frontiers in Pharmacology</i> , 2020, 11, 519.	1.6	24
12614	Metabolomics and Multi-Omics Integration: A Survey of Computational Methods and Resources. <i>Metabolites</i> , 2020, 10, 202.	1.3	69
12615	Comparative transcriptome analysis reveals the sexual dimorphic expression profiles of mRNAs and non-coding RNAs in the Asian yellow pond turtle ( <i>Meuremys mutica</i> ). <i>Gene</i> , 2020, 750, 144756.	1.0	12
12616	Scutellaria barbata and Hedyotis diffusa herb pair for breast cancer treatment: Potential mechanism based on network pharmacology. <i>Journal of Ethnopharmacology</i> , 2020, 259, 112929.	2.0	30
12617	Network pharmacology used to decode potential active ingredients in <i>Ferula assafoetida</i> and mechanisms for the application to Alzheimer's disease. <i>Journal of Traditional Chinese Medical Sciences</i> , 2020, 7, 199-209.	0.1	1
12618	A directed network analysis of the cardiome identifies molecular pathways contributing to the development of HFpEF. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 144, 66-75.	0.9	16
12619	Identifying Cell Type Specific TF Combinatorial Regulation via a Two-Stage Statistical Method. , 2020, , .		0
12620	SpoT Induces Intracellular Salmonella Virulence Programs in the Phagosome. <i>MBio</i> , 2020, 11, .	1.8	17
12621	CSN: unsupervised approach for inferring biological networks based on the genome alone. <i>BMC Bioinformatics</i> , 2020, 21, 190.	1.2	1
12622	Discovery of GLO1 New Related Genes and Pathways by RNA-Seq on A2E-Stressed Retinal Epithelial Cells Could Improve Knowledge on Retinitis Pigmentosa. <i>Antioxidants</i> , 2020, 9, 416.	2.2	28
12623	Nasal Microbiota in RSV Bronchiolitis. <i>Microorganisms</i> , 2020, 8, 731.	1.6	19
12624	Grazing does not increase soil antibiotic resistome in two types of grasslands in Inner Mongolia, China. <i>Applied Soil Ecology</i> , 2020, 155, 103644.	2.1	8
12625	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. <i>Journal of Alzheimer's Disease</i> , 2020, 75, 1417-1435.	1.2	18
12626	Identification of Prognostic miRNA Signature and Lymph Node Metastasis-Related Key Genes in Cervical Cancer. <i>Frontiers in Pharmacology</i> , 2020, 11, 544.	1.6	29
12627	Sulfoxide-Containing Polymer-Coated Nanoparticles Demonstrate Minimal Protein Fouling and Improved Blood Circulation. <i>Advanced Science</i> , 2020, 7, 2000406.	5.6	43

#	ARTICLE	IF	CITATIONS
12628	Large-scale network analysis captures biological features of bacterial plasmids. <i>Nature Communications</i> , 2020, 11, 2452.	5.8	78
12629	Plant terpenoid metabolism co-opts a component of the cell wall biosynthesis machinery. <i>Nature Chemical Biology</i> , 2020, 16, 740-748.	3.9	67
12630	Shared proteomic effects of cerebral atherosclerosis and Alzheimer's disease on the human brain. <i>Nature Neuroscience</i> , 2020, 23, 696-700.	7.1	86
12631	Transcriptomic profiles reveal differences in zinc metabolism, inflammation, and tight junction proteins in duodenum from cholesterol gallstone subjects. <i>Scientific Reports</i> , 2020, 10, 7448.	1.6	6
12632	Chinese Medicine for Psoriasis Vulgaris Based on Syndrome Pattern: A Network Pharmacological Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-16.	0.5	4
12633	The microbiome of alpine snow algae shows a specific inter-kingdom connectivity and algae-bacteria interactions with supportive capacities. <i>ISME Journal</i> , 2020, 14, 2197-2210.	4.4	46
12634	Gene regulatory networks associated with lateral root and nodule development in soybean. <i>In Silico Plants</i> , 2020, 2, .	0.8	3
12635	The Architecture of Metabolism Maximizes Biosynthetic Diversity in the Largest Class of Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2838-2856.	3.5	33
12636	webPSN v2.0: a webserver to infer fingerprints of structural communication in biomacromolecules. <i>Nucleic Acids Research</i> , 2020, 48, W94-W103.	6.5	56
12637	Transcriptional regulatory networks of methanol-independent protein expression in <i>Pichia pastoris</i> under the AOX1 promoter with trans-acting elements engineering. <i>Bioresources and Bioprocessing</i> , 2020, 7, .	2.0	4
12638	Identification of Immune Cell Landscape and Construction of a Novel Diagnostic Nomogram for Crohn's Disease. <i>Frontiers in Genetics</i> , 2020, 11, 423.	1.1	13
12639	Isolation and Identification of Three New Sterigmatocystin Derivatives from the Fungus <i>Aspergillus versicolor</i> Guided by Molecular Networking Approach. <i>Chemistry and Biodiversity</i> , 2020, 17, e2000208.	1.0	7
12640	Identification of drought stress-responsive genes in rice ( <i>Oryza sativa</i> ) by meta-analysis of microarray data. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	13
12641	Generation and Profiling of 2,135 Human ESC Lines for the Systematic Analyses of Cell States Perturbed by Inducing Single Transcription Factors. <i>Cell Reports</i> , 2020, 31, 107655.	2.9	28
12642	Prochlorococcus phage ferredoxin: structural characterization and electron transfer to cyanobacterial sulfite reductases. <i>Journal of Biological Chemistry</i> , 2020, 295, 10610-10623.	1.6	10
12643	Multimiomics-based characterization of specialized metabolites biosynthesis in <i>Cornus Officinalis</i> . <i>DNA Research</i> , 2020, 27, .	1.5	8
12644	NetConfer: a web application for comparative analysis of multiple biological networks. <i>BMC Biology</i> , 2020, 18, 53.	1.7	8
12645	Muscle transcriptome analysis identifies genes involved in ciliogenesis and the molecular cascade associated with intramuscular fat content in Large White heavy pigs. <i>PLoS ONE</i> , 2020, 15, e0233372.	1.1	25

#	ARTICLE	IF	CITATIONS
12646	Comparative (Within Species) Genomics of the <i>Vitis vinifera</i> L. Terpene Synthase Family to Explore the Impact of Genotypic Variation Using Phased Diploid Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 421.	1.1	8
12647	Harnessing Gene Expression Profiles for the Identification of Ex Vivo Drug Response Genes in Pediatric Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 1247.	1.7	8
12648	Characterization of Stem-like Circulating Tumor Cells in Pancreatic Cancer. <i>Diagnostics</i> , 2020, 10, 305.	1.3	7
12649	Identification of Differentially Expressed Gene Transcripts in Porcine Endometrium during Early Stages of Pregnancy. <i>Life</i> , 2020, 10, 68.	1.1	5
12650	Comparison of the Vitreous Fluid Bacterial Microbiomes between Individuals with Post Fever Retinitis and Healthy Controls. <i>Microorganisms</i> , 2020, 8, 751.	1.6	9
12651	Exosomes Derived from the Human Primary Colorectal Cancer Cell Line SW480 Orchestrate Fibroblast-Mediated Cancer Invasion. <i>Proteomics</i> , 2020, 20, e2000016.	1.3	25
12652	Effects of Drought-Tolerant Ea-DREB2B Transgenic Sugarcane on Bacterial Communities in Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 704.	1.5	29
12653	The WD40 Gene Family in Potato ( <i>Solanum Tuberosum</i> L.): Genome-Wide Analysis and Identification of Anthocyanin and Drought-Related WD40s. <i>Agronomy</i> , 2020, 10, 401.	1.3	19
12654	Role of microRNAs in epidermal growth factor receptor signaling pathway in cervical cancer. <i>Molecular Biology Reports</i> , 2020, 47, 4553-4568.	1.0	15
12655	RIC-seq for global in situ profiling of RNA-RNA spatial interactions. <i>Nature</i> , 2020, 582, 432-437.	13.7	176
12656	Exosomal miR-9-5p secreted by bone marrow-derived mesenchymal stem cells alleviates osteoarthritis by inhibiting syndecan-1. <i>Cell and Tissue Research</i> , 2020, 381, 99-114.	1.5	63
12657	Transcriptomic signatures of treatment response to the combination of escitalopram and memantine or placebo in late-life depression. <i>Molecular Psychiatry</i> , 2021, 26, 5171-5179.	4.1	4
12658	Enrichment of damaging missense variants in genes related with axonal guidance signalling in sporadic Meniere's disease. <i>Journal of Medical Genetics</i> , 2020, 57, 82-88.	1.5	21
12659	Nitrogen and water addition regulate soil fungal diversity and co-occurrence networks. <i>Journal of Soils and Sediments</i> , 2020, 20, 3192-3203.	1.5	18
12660	Adipogenesis of skeletal muscle fibro/adipogenic progenitors is affected by the WNT5a/GSK3 $\beta$ -catenin axis. <i>Cell Death and Differentiation</i> , 2020, 27, 2921-2941.	5.0	69
12661	Phosphotyrosine-based Phosphoproteomics for Target Identification and Drug Response Prediction in AML Cell Lines. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 884-899.	2.5	29
12662	Cinobufagin Triggers Defects in Spindle Formation and Cap-Dependent Translation in Liver Cancer Cells by Inhibiting the AURKA-mTOR-eIF4E Axis. <i>The American Journal of Chinese Medicine</i> , 2020, 48, 651-678.	1.5	13
12663	ProNetView-RCC: A Web-Based Portal to Interactively Explore Clear Cell Renal Cell Carcinoma Proteogenomics Networks. <i>Proteomics</i> , 2020, 20, e2000043.	1.3	6

#	ARTICLE	IF	CITATIONS
12664	Single-cell RNA sequencing demonstrates the molecular and cellular reprogramming of metastatic lung adenocarcinoma. <i>Nature Communications</i> , 2020, 11, 2285.	5.8	565
12665	Pooled CRISPR screens with imaging on microarray reveals stress granule-regulatory factors. <i>Nature Methods</i> , 2020, 17, 636-642.	9.0	60
12666	Targeted isolation of two disesquiterpenoid macrocephadiolides A and B from <i>Ainsliaea macrocephala</i> using a molecular networking-based dereplication strategy. <i>Organic Chemistry Frontiers</i> , 2020, 7, 1481-1489.	2.3	18
12667	A Comprehensive Repertoire of Transfer RNA-Derived Fragments and Their Regulatory Networks in Colorectal Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 1644-1655.	0.8	17
12668	Identification of miRNA-mRNA Regulatory Network and Construction of Prognostic Signature in Cervical Cancer. <i>DNA and Cell Biology</i> , 2020, 39, 1023-1040.	0.9	10
12669	In Silico Identification of Crucial Genes and Specific Pathways in Hepatocellular Cancer. <i>Genetic Testing and Molecular Biomarkers</i> , 2020, 24, 296-308.	0.3	9
12670	Analysis of genes associated with prognosis of lung adenocarcinoma based on GEO and TCGA databases. <i>Medicine (United States)</i> , 2020, 99, e20183.	0.4	26
12671	Potential genes and pathways along with immune cells infiltration in the progression of atherosclerosis identified via microarray gene expression dataset re-analysis. <i>Vascular</i> , 2020, 28, 643-654.	0.4	21
12672	Elevated TNFRSF4 gene expression is a predictor of poor prognosis in non-M3 acute myeloid leukemia. <i>Cancer Cell International</i> , 2020, 20, 146.	1.8	11
12673	Transcriptome Analysis Reveals the Flexibility of Cordycepin Network in <i>Cordyceps militaris</i> Activated by L-Alanine Addition. <i>Frontiers in Microbiology</i> , 2020, 11, 577.	1.5	23
12674	Identification and Annotation of Potential Function of Regulatory Antisense Long Non-Coding RNAs Related to Feed Efficiency in <i>Bos taurus</i> Bulls. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3292.	1.8	10
12675	Genome-Wide Analysis of the DNA Methylation Profile Identifies the Fragile Histidine Triad (FHIT) Gene as a New Promising Biomarker of Crohn's Disease. <i>Journal of Clinical Medicine</i> , 2020, 9, 1338.	1.0	9
12676	The Bacterial Gut Microbiota of Adult Patients Infected, Colonized or Noncolonized by <i>Clostridioides difficile</i> . <i>Microorganisms</i> , 2020, 8, 677.	1.6	25
12677	Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving -Omics Era. <i>Plants</i> , 2020, 9, 591.	1.6	25
12678	High-dimensional analyses reveal a distinct role of T cell subsets in the immune microenvironment of gastric cancer. <i>Clinical and Translational Immunology</i> , 2020, 9, e1127.	1.7	21
12679	MicroRNA Profiling of Highly Enriched Human Corneal Epithelial Stem Cells by Small RNA Sequencing. <i>Scientific Reports</i> , 2020, 10, 7418.	1.6	8
12680	A selective autophagy cargo receptor NBR1 modulates abscisic acid signalling in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2020, 10, 7778.	1.6	26
12681	Cyber-Physical Stress-Testing Platform for Water Distribution Networks. <i>Journal of Environmental Engineering, ASCE</i> , 2020, 146, .	0.7	34

#	ARTICLE	IF	CITATIONS
12682	Short- and Long-Term Transcriptomic Responses of <i>Escherichia coli</i> to Biocides: a Systems Analysis. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
12683	The tapeworm interactome: inferring confidence scored protein-protein interactions from the proteome of <i>Hymenolepis microstoma</i> . <i>BMC Genomics</i> , 2020, 21, 346.	1.2	4
12684	The seasonal development dynamics of the yak hair cycle transcriptome. <i>BMC Genomics</i> , 2020, 21, 355.	1.2	14
12685	Comparison of a human neuronal model proteome upon Japanese encephalitis or West Nile Virus infection and potential role of mosquito saliva in neuropathogenesis. <i>PLoS ONE</i> , 2020, 15, e0232585.	1.1	4
12686	Investigating gene-microRNA networks in atrial fibrillation patients with mitral valve regurgitation. <i>PLoS ONE</i> , 2020, 15, e0232719.	1.1	14
12687	A Signaling Pathway to Mediate the Combined Immunomodulation of Acetylcholine and Enkephalin in Oyster <i>Crassostrea gigas</i> . <i>Frontiers in Immunology</i> , 2020, 11, 616.	2.2	3
12688	Targeting Cellular Metabolism in Acute Myeloid Leukemia and the Role of Patient Heterogeneity. <i>Cells</i> , 2020, 9, 1155.	1.8	25
12689	Synergistic effect of <i>Lactobacillus gasseri</i> and <i>Cudrania tricuspidata</i> on the modulation of body weight and gut microbiota structure in diet-induced obese mice. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6273-6285.	1.7	17
12690	Analysis of cerebrovascular dysfunction caused by chronic social defeat in mice. <i>Brain, Behavior, and Immunity</i> , 2020, 88, 735-747.	2.0	24
12691	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	2.9	78
12692	TASL is the SLC15A4-associated adaptor for IRF5 activation by TLR7. <i>Nature</i> , 2020, 581, 316-322.	13.7	117
12693	Reproducible molecular networking of untargeted mass spectrometry data using GNPS. <i>Nature Protocols</i> , 2020, 15, 1954-1991.	5.5	344
12694	Onset of hippocampal network aberration and memory deficits in P301S tau mice are associated with an early gene signature. <i>Brain</i> , 2020, 143, 1889-1904.	3.7	12
12695	Phages Actively Challenge Niche Communities in Antarctic Soils. <i>MSystems</i> , 2020, 5, .	1.7	17
12696	Improvement of steatotic rat liver function with a defatting cocktail during ex situ normothermic machine perfusion is not directly related to liver fat content. <i>PLoS ONE</i> , 2020, 15, e0232886.	1.1	18
12697	Online searching platform for the antibiotic resistome in bacterial tree of life and global habitats. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
12698	Dissecting the Genetic Architecture of Cystatin C in Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2529-2541.	0.8	9
12699	MicroRNA-mRNA Co-sequencing Identifies Transcriptional and Post-transcriptional Regulatory Networks Underlying Muscle Wasting in Cancer Cachexia. <i>Frontiers in Genetics</i> , 2020, 11, 541.	1.1	19



#	ARTICLE	IF	CITATIONS
12700	A fourâ€long noncoding RNA signature predicts survival of hepatocellular carcinoma patients. <i>Journal of Clinical Laboratory Analysis</i> , 2020, 34, e23377.	0.9	4
12701	Two way network construction and analysis of mRNA, miRNA and lncRNA reveals critical regulators and regulatory modules in cardiovascular diseases. <i>Genes and Genomics</i> , 2020, 42, 855-867.	0.5	4
12702	Genetic variants entail type 2 diabetes as an innate immune disorder. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140458.	1.1	4
12703	The Parkinsonâ€™s Disease Protein LRRK2 Interacts with the GARP Complex to Promote Retrograde Transport to the trans-Golgi Network. <i>Cell Reports</i> , 2020, 31, 107614.	2.9	49
12704	Zebrafish brain RNA sequencing reveals that cell adhesion molecules are critical in brain aging. <i>Neurobiology of Aging</i> , 2020, 94, 164-175.	1.5	7
12705	Epigenetics factors in nonalcoholic fatty liver disease. <i>Expert Review of Gastroenterology and Hepatology</i> , 2022, 16, 521-536.	1.4	17
12706	Proteinâ€“protein interactions of HPVâ€<i>Chlamydia trachomatis</i>â€“humanâ€and their potential in cervical cancer. <i>Future Microbiology</i> , 2020, 15, 509-520.	1.0	14
12707	Traditional rice beer depletes butyric acid-producing gut bacteria <i>Faecalibacterium</i> and <i>Roseburia</i> along with fecal butyrate levels in the ethnic groups of Northeast India. <i>3 Biotech</i> , 2020, 10, 283.	1.1	9
12708	Functional Divergence of the Arabidopsis Florigen-Interacting bZIP Transcription Factors FD and FDP. <i>Cell Reports</i> , 2020, 31, 107717.	2.9	49
12709	Can network pharmacology identify the anti-virus and anti-inflammatory activities of Shuanghuanglian oral liquid used in Chinese medicine for respiratory tract infection?. <i>European Journal of Integrative Medicine</i> , 2020, 37, 101139.	0.8	32
12710	Identification of microRNA biomarkers in serum of patients at different stages of atrial fibrillation. <i>Heart and Lung: Journal of Acute and Critical Care</i> , 2020, 49, 902-908.	0.8	8
12711	Proteomics analysis reveals the effect of <i>Aeromonas hydrophila</i> sirtuin CobB on biological functions. <i>Journal of Proteomics</i> , 2020, 225, 103848.	1.2	17
12712	A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
12713	Can network science reveal structure in a complex healthcare system? A network analysis using data from emergency surgical services. <i>BMJ Open</i> , 2020, 10, e034265.	0.8	15
12714	Insights of Molecular Mechanism of Xylem Development in Five Black Poplar Cultivars. <i>Frontiers in Plant Science</i> , 2020, 11, 620.	1.7	14
12715	Guizhi Fuling Decoction inhibiting the PI3K and MAPK pathways in breast cancer cells revealed by HTS2 technology and systems pharmacology. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1121-1136.	1.9	27
12716	Immunostimulatory efficacy and protective potential of putative TgERK7 protein in mice experimentally infected by <i>Toxoplasma gondii</i> . <i>International Journal of Medical Microbiology</i> , 2020, 310, 151432.	1.5	3
12717	The four dimensions of social network analysis: An overview of research methods, applications, and software tools. <i>Information Fusion</i> , 2020, 63, 88-120.	11.7	143



#	ARTICLE	IF	CITATIONS
12718	Exploring Mechanisms of Communication Switching in the Hsp90-Cdc37 Regulatory Complexes with Client Kinases through Allosteric Coupling of Phosphorylation Sites: Perturbation-Based Modeling and Hierarchical Community Analysis of Residue Interaction Networks. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 4706-4725.	2.3	15
12719	miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. <i>Nucleic Acids Research</i> , 2020, 48, W244-W251.	6.5	461
12720	Identifying the mRNAs associated with Bladder cancer recurrence. <i>Cancer Biomarkers</i> , 2020, 28, 429-437.	0.8	6
12721	Identification of the Biosynthetic Gene Cluster of Thermoactinoamides and Discovery of New Congeners by Integrated Genome Mining and MS-Based Molecular Networking. <i>Frontiers in Chemistry</i> , 2020, 8, 397.	1.8	11
12722	The Integrated Landscape of Biological Candidate Causal Genes in Coronary Artery Disease. <i>Frontiers in Genetics</i> , 2020, 11, 320.	1.1	12
12723	Establishment and Validation of an Individualized Cell Cycle Process-Related Gene Signature to Predict Cancer-Specific Survival in Patients with Bladder Cancer. <i>Cancers</i> , 2020, 12, 1146.	1.7	8
12724	Srebf1 Controls Midbrain Dopaminergic Neurogenesis. <i>Cell Reports</i> , 2020, 31, 107601.	2.9	20
12725	Construction of a human cell landscape at single-cell level. <i>Nature</i> , 2020, 581, 303-309.	13.7	695
12726	Coding Variants in HOOK2 and GTPBP3 May Contribute to Risk of Primary Angle Closure Glaucoma. <i>DNA and Cell Biology</i> , 2020, 39, 949-957.	0.9	2
12727	Henipavirus W Proteins Interact with 14-3-3 To Modulate Host Gene Expression. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
12728	Gene networks and expression quantitative trait loci associated with adjuvant chemotherapy response in high-grade serous ovarian cancer. <i>BMC Cancer</i> , 2020, 20, 413.	1.1	6
12729	Protein phosphorylation networks in spargana of <i>Spirometra erinaceieuropaei</i> revealed by phosphoproteomic analysis. <i>Parasites and Vectors</i> , 2020, 13, 248.	1.0	8
12730	OPTN recruitment to a Golgi-proximal compartment regulates immune signalling and cytokine secretion. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	15
12731	Esophageal microbiome signature in patients with Barrett's esophagus and esophageal adenocarcinoma. <i>PLoS ONE</i> , 2020, 15, e0231789.	1.1	58
12732	Transcriptome analysis identifies genes involved with the development of umbilical hernias in pigs. <i>PLoS ONE</i> , 2020, 15, e0232542.	1.1	10
12733	Systematic Identification and Analysis of Light-Responsive Circular RNA and Co-expression Networks in Lettuce ( <i>Lactuca sativa</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2397-2410.	0.8	6
12734	miR-196B-5P and miR-200B-3P Are Differentially Expressed in Medulloblastomas of Adults and Children. <i>Diagnostics</i> , 2020, 10, 265.	1.3	6
12735	Genome-Wide Transcriptome and Metabolome Analyses Provide Novel Insights and Suggest a Sex-Specific Response to Heat Stress in Pigs. <i>Genes</i> , 2020, 11, 540.	1.0	11

#	ARTICLE	IF	CITATIONS
12736	Diversity of Glutathione S-Transferases (GSTs) in Cyanobacteria with Reference to Their Structures, Substrate Recognition and Catalytic Functions. <i>Microorganisms</i> , 2020, 8, 712.	1.6	11
12737	Comparative analysis of ROS-scavenging gene families in finger millet, rice, sorghum, and foxtail millet revealed potential targets for antioxidant activity and drought tolerance improvement. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	6
12738	Insights into the histopathology and microbiome of Pacific white shrimp, <i>Penaeus vannamei</i> , suffering from white feces syndrome. <i>Aquaculture</i> , 2020, 527, 735447.	1.7	35
12739	Network pharmacology-based strategy to investigate pharmacological mechanisms of <i>Tinospora sinensis</i> for treatment of Alzheimer's disease. <i>Journal of Ethnopharmacology</i> , 2020, 259, 112940.	2.0	25
12740	Evaluating the "triggering response"™ in soils, using <sup>13</sup> C-glucose, and effects on dynamics of microbial biomass. <i>Soil Biology and Biochemistry</i> , 2020, 147, 107843.	4.2	7
12741	Nutrient dose-responsive transcriptome changes driven by Michaelis-Menten kinetics underlie plant growth rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12531-12540.	3.3	38
12742	Network-based strategies in metabolomics data analysis and interpretation: from molecular networking to biological interpretation. <i>Expert Review of Proteomics</i> , 2020, 17, 243-255.	1.3	70
12743	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. <i>Nucleic Acids Research</i> , 2020, 48, W104-W109.	6.5	51
12744	A Knowledge-Driven Network-Based Analytical Framework for the Identification of Rumen Metabolites. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 518-526.	2.2	4
12745	Common cancer biomarkers of breast and ovarian types identified through artificial intelligence. <i>Chemical Biology and Drug Design</i> , 2020, 96, 995-1004.	1.5	3
12746	Identification of microRNAs associated with the survival of patients with gallbladder carcinoma. <i>Journal of International Medical Research</i> , 2020, 48, 030006052091806.	0.4	5
12747	Corticosterone and testosterone treatment influence expression of gene pathways linked to meiotic segregation in preovulatory follicles of the domestic hen. <i>PLoS ONE</i> , 2020, 15, e0232120.	1.1	3
12748	Ablation of non-coding RNAs affects bovine leukemia virus B lymphocyte proliferation and abrogates oncogenesis. <i>PLoS Pathogens</i> , 2020, 16, e1008502.	2.1	16
12749	Analyzing the prognostic value of DKK1 expression in human cancers based on bioinformatics. <i>Annals of Translational Medicine</i> , 2020, 8, 552-552.	0.7	12
12750	Global Proteomic Analysis of Lysine Malonylation in <i>Toxoplasma gondii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 776.	1.5	16
12751	AFB1 Induced Transcriptional Regulation Related to Apoptosis and Lipid Metabolism in Liver of Chicken. <i>Toxins</i> , 2020, 12, 290.	1.5	32
12752	Panel-based targeted exome sequencing reveals novel candidate susceptibility loci for age-related cataracts in Chinese Cohort. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1218.	0.6	4
12753	Comprehensive transcriptomic analysis identifies novel regulators of lung adenocarcinoma. <i>Journal of Cell Communication and Signaling</i> , 2020, 14, 453-465.	1.8	17

#	ARTICLE	IF	CITATIONS
12754	Luteolin inhibits melanoma growth in vitro and in vivo via regulating ECM and oncogenic pathways but not ROS. <i>Biochemical Pharmacology</i> , 2020, 177, 114025.	2.0	25
12755	Microbiota-Induced Type I Interferons Instruct a Poised Basal State of Dendritic Cells. <i>Cell</i> , 2020, 181, 1080-1096.e19.	13.5	139
12756	Host transcriptomic signature as alternative test-of-cure in visceral leishmaniasis patients co-infected with HIV. <i>EBioMedicine</i> , 2020, 55, 102748.	2.7	16
12757	Differentially expressed circular RNAs in orbital adipose/connective tissue from patients with thyroid-associated ophthalmopathy. <i>Experimental Eye Research</i> , 2020, 196, 108036.	1.2	22
12758	Digging deeper in the proteome of different regions from schizophrenia brains. <i>Journal of Proteomics</i> , 2020, 223, 103814.	1.2	17
12759	Identification of circular RNAs in porcine sperm and evaluation of their relation to sperm motility. <i>Scientific Reports</i> , 2020, 10, 7985.	1.6	27
12760	Genetic and molecular features for hepadnavirus and plague infections in the Himalayan marmot. <i>Genome</i> , 2020, 63, 307-317.	0.9	2
12761	Long-term transcriptional memory in rice plants submitted to salt shock. <i>Planta</i> , 2020, 251, 111.	1.6	11
12762	Integrative In Silico Analysis of Genome-Wide DNA Methylation Profiles in Schizophrenia. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1887-1893.	1.1	10
12763	Analysis of sequence diversity and selection pressure in HIV-1 clade C gp41 from India. <i>VirusDisease</i> , 2020, 31, 277-291.	1.0	1
12764	Metabolomics and the Microbiome: Characterizing Molecular Diversity in Complex Microbial Communities. , 2020, , 502-518.		2
12765	Expression of RUNX1-ETO Rapidly Alters the Chromatin Landscape and Growth of Early Human Myeloid Precursor Cells. <i>Cell Reports</i> , 2020, 31, 107691.	2.9	20
12766	Bacterioplankton assembly and interspecies interactions follow trajectories of <i>Gymnodinium</i> diatom bloom. <i>Marine Environmental Research</i> , 2020, 160, 105010.	1.1	4
12767	MyomirDB: A unified database and server platform for muscle atrophy myomiRs, coregulatory networks and regulons. <i>Scientific Reports</i> , 2020, 10, 8593.	1.6	3
12768	Whole blood transcriptome profile at hospital admission discriminates between patients with ST-segment elevation and non-ST-segment elevation acute myocardial infarction. <i>Scientific Reports</i> , 2020, 10, 8731.	1.6	11
12769	BatchLayout: A Batch-Parallel Force-Directed Graph Layout Algorithm in Shared Memory. , 2020, , .		5
12770	EBST: An Evolutionary Multi-Objective Optimization Based Tool for Discovering Potential Biomarkers in Ovarian Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	13
12771	Aligning functional network constraint to evolutionary outcomes. <i>BMC Evolutionary Biology</i> , 2020, 20, 58.	3.2	7

#	ARTICLE	IF	CITATIONS
12772	Multipathway synergy promotes testicular transition from growth to spermatogenesis in early-puberty goats. <i>BMC Genomics</i> , 2020, 21, 372.	1.2	19
12773	Comparative transcriptome analysis between inbred and hybrids reveals molecular insights into yield heterosis of upland cotton. <i>BMC Plant Biology</i> , 2020, 20, 239.	1.6	28
12774	Phylogenomic synteny network analyses reveal ancestral transpositions of auxin response factor genes in plants. <i>Plant Methods</i> , 2020, 16, 70.	1.9	8
12775	Establishment of a CALU, AURKA, and MCM2 gene panel for discrimination of metastasis from primary colon and lung cancers. <i>PLoS ONE</i> , 2020, 15, e0233717.	1.1	15
12776	CXCL8 is a potential biomarker for predicting disease progression in gastric carcinoma. <i>Translational Cancer Research</i> , 2020, 9, 1053-1062.	0.4	6
12777	The identification of highly upregulated genes in claudin-low breast cancer through an integrative bioinformatics approach. <i>Computers in Biology and Medicine</i> , 2020, 127, 103806.	3.9	7
12778	Epigenetics in non-classical monocytes support their pro-inflammatory gene expression. <i>Immunobiology</i> , 2020, 225, 151958.	0.8	6
12779	Human Glial Progenitor Cells Effectively Remyelinate the Demyelinated Adult Brain. <i>Cell Reports</i> , 2020, 31, 107658.	2.9	27
12780	Research Techniques Made Simple: Whole-Transcriptome Sequencing by RNA-Seq for Diagnosis of Monogenic Disorders. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1117-1126.e1.	0.3	46
12781	miRReg: A Framework for Studying miRNA Regulation in Tetralogy of Fallot. <i>IEEE Access</i> , 2020, 8, 103454-103461.	2.6	1
12782	Phylogenomic analysis of the APETALA2 transcription factor subfamily across angiosperms reveals both deep conservation and lineage-specific patterns. <i>Plant Journal</i> , 2020, 103, 1516-1524.	2.8	22
12783	An Analysis of the Anti-Neuropathic Effects of Qi She Pill Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	6
12784	Identification and Verification of Core Genes in Colorectal Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	18
12785	Construction and Analysis of a ceRNA Network Reveals Potential Prognostic Markers in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 418.	1.1	13
12786	Self-selecting peer groups formed within the laboratory environment have a lasting effect on individual student attainment and working practices. <i>FEBS Open Bio</i> , 2020, 10, 1194-1209.	1.0	6
12787	Identification of genes associated with cancer stem cell characteristics in head and neck squamous cell carcinoma through co-expression network analysis. <i>Head and Neck</i> , 2020, 42, 2460-2472.	0.9	2
12788	Multicopper oxidases: modular structure, sequence space, and evolutionary relationships. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1329-1339.	1.5	22
12789	Combinational approach of retrospective clinical evidence and transcriptomics highlight AMH superiority to FSH, as successful ICSI outcome predictor. <i>Journal of Assisted Reproduction and Genetics</i> , 2020, 37, 1623-1635.	1.2	4

#	ARTICLE	IF	CITATIONS
12790	Abiotic-stress tolerance in plants-system biology approach. , 2020, , 577-609.		6
12791	The microbiome driving anaerobic digestion and microbial analysis. <i>Advances in Bioenergy</i> , 2020, 5, 1-61.	0.5	50
12792	MKRN2 Physically Interacts with GLE1 to Regulate mRNA Export and Zebrafish Retinal Development. <i>Cell Reports</i> , 2020, 31, 107693.	2.9	11
12793	Proteomic profiling of MIN6 cell-derived exosomes. <i>Journal of Proteomics</i> , 2020, 224, 103841.	1.2	4
12794	PINE: An Automation Tool to Extract and Visualize Protein-Centric Functional Networks. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1410-1421.	1.2	14
12795	Photothermal modulation of human stem cells using light-responsive 2D nanomaterials. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13329-13338.	3.3	47
12796	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	4.3	22
12797	A microRNAâ€‘Messenger RNA Regulatory Network and Its Prognostic Value in Cervical Cancer. <i>DNA and Cell Biology</i> , 2020, 39, 1328-1346.	0.9	11
12798	PaCRISPR: a server for predicting and visualizing anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2020, 48, W348-W357.	6.5	37
12799	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, 7279-7297.	6.5	4
12800	Mu opioid receptors in the medial preoptic area govern social play behavior in adolescent male rats. <i>Genes, Brain and Behavior</i> , 2020, 19, e12662.	1.1	19
12801	Proteomics of intracellular freezing survival. <i>PLoS ONE</i> , 2020, 15, e0233048.	1.1	1
12802	Neutrophils, Crucial, or Harmful Immune Cells Involved in Coronavirus Infection: A Bioinformatics Study. <i>Frontiers in Genetics</i> , 2020, 11, 641.	1.1	71
12803	Genome-Wide Analysis of Basic Helix-Loop-Helix Transcription Factors to Elucidate Candidate Genes Related to Fruit Ripening and Stress in Banana ( <i>Musa acuminata</i> L. AAA Group, cv. Cavendish). <i>Frontiers in Plant Science</i> , 2020, 11, 650.	1.7	15
12804	MAT2A as Key Regulator and Therapeutic Target in MLLr Leukemogenesis. <i>Cancers</i> , 2020, 12, 1342.	1.7	16
12805	Insights into the Metabolome of the Cyanobacterium <i>Leibleinia gracilis</i> from the Lagoon of Tahiti and First Inspection of Its Variability. <i>Metabolites</i> , 2020, 10, 215.	1.3	7
12806	Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107897.	4.2	68
12807	Differences in pig respiratory tract and peripheral blood immune responses to <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2020, 247, 108755.	0.8	9

#	ARTICLE	IF	CITATIONS
12808	Identification of prognostic alternative splicing signatures in hepatitis B or/and C viruses related hepatocellular carcinoma. <i>Genomics</i> , 2020, 112, 3396-3406.	1.3	6
12809	Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. <i>Horticulture Research</i> , 2020, 7, 90.	2.9	38
12810	ACE2 Expression Is Increased in the Lungs of Patients With Comorbidities Associated With Severe COVID-19. <i>Journal of Infectious Diseases</i> , 2020, 222, 556-563.	1.9	302
12811	Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. <i>Nucleic Acids Research</i> , 2020, 48, 7079-7098.	6.5	12
12812	PINOT: an intuitive resource for integrating protein-protein interactions. <i>Cell Communication and Signaling</i> , 2020, 18, 92.	2.7	21
12813	VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. <i>Microbiome</i> , 2020, 8, 90.	4.9	482
12814	Exploring the Impact of PARK2 Mutations on the Total and Mitochondrial Proteome of Human Skin Fibroblasts. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 423.	1.8	11
12815	Novel Insights Into Triple-Negative Breast Cancer Prognosis by Comprehensive Characterization of Aberrant Alternative Splicing. <i>Frontiers in Genetics</i> , 2020, 11, 534.	1.1	10
12816	Host Gene Expression of Macrophages in Response to Feline Coronavirus Infection. <i>Cells</i> , 2020, 9, 1431.	1.8	19
12817	Long Non-Coding RNA HAND2-AS1 Acts as a Tumor Suppressor in High-Grade Serous Ovarian Carcinoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4059.	1.8	18
12818	Identification of Core Genes and Pathways in Medulloblastoma by Integrated Bioinformatics Analysis. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1702-1712.	1.1	6
12819	Temporal Integrative Omics Reveals an Increase in Nondegradative Ubiquitylation during Primary Hepatocyte Dedifferentiation. <i>Engineering</i> , 2020, 6, 1302-1314.	3.2	1
12820	Anti-Helicobacter pylori-associated gastritis effect of the ethyl acetate extract of <i>Alpinia officinarum</i> Hance through MAPK signaling pathway. <i>Journal of Ethnopharmacology</i> , 2020, 260, 113100.	2.0	8
12821	Mucosa-associated microbiota in the jejunum of patients with morbid obesity: alterations in states of insulin resistance and metformin treatment. <i>Surgery for Obesity and Related Diseases</i> , 2020, 16, 1575-1585.	1.0	8
12822	Metabolomics in plant protection product research and development. , 2020, , 163-194.		0
12823	High throughput sequencing of 18S rRNA and its gene to characterize a <i>Prorocentrum shikokuense</i> (Dinophyceae) bloom. <i>Harmful Algae</i> , 2020, 94, 101809.	2.2	10
12824	Differential regulation of the immune system in a brain-liver-fats organ network during short-term fasting. <i>Molecular Metabolism</i> , 2020, 40, 101038.	3.0	7
12825	Structural basis for divergent C-H hydroxylation selectivity in two Rieske oxygenases. <i>Nature Communications</i> , 2020, 11, 2991.	5.8	34



#	ARTICLE	IF	CITATIONS
12826	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , 2020, 11, 3013.	5.8	29
12827	Fluxer: a web application to compute, analyze and visualize genome-scale metabolic flux networks. <i>Nucleic Acids Research</i> , 2020, 48, W427-W435.	6.5	27
12828	Weighted Gene Coexpression Network Analysis Reveals the Dynamic Transcriptome Regulation and Prognostic Biomarkers of Hepatocellular Carcinoma. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432092056.	0.6	4
12829	Molecular Network-Guided Alkaloid Profiling of Aerial Parts of <i>Papaver nudicaule</i> L. Using LC-HRMS. <i>Molecules</i> , 2020, 25, 2636.	1.7	10
12830	Mining and predicting protein-drug interaction network of breast cancer risk genes. <i>Gene Reports</i> , 2020, 20, 100753.	0.4	0
12831	Determination of novel biomarkers and pathways shared by colorectal cancer and endometrial cancer via comprehensive bioinformatics analysis. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100376.	1.9	7
12832	Covariance in diurnal patterns of suicide-related expressions on Twitter and recorded suicide deaths. <i>Social Science and Medicine</i> , 2020, 253, 112960.	1.8	15
12833	Whole-genome sequencing provides new insights into genetic mechanisms of tropical adaptation in Nellore ( <i>Bos primigenius indicus</i> ). <i>Scientific Reports</i> , 2020, 10, 9412.	1.6	20
12834	Understanding the Landscape of X-linked Variants Causing Intellectual Disability in Females Through Extreme X Chromosome Inactivation Skewing. <i>Molecular Neurobiology</i> , 2020, 57, 3671-3684.	1.9	21
12835	Differential expression of lung adenocarcinoma transcriptome with signature of tobacco exposure. <i>Journal of Applied Genetics</i> , 2020, 61, 421-437.	1.0	10
12836	Exploring multiple mechanisms of Qingjie Fanggan prescription for prevention and treatment of influenza based on systems pharmacology. <i>Computational Biology and Chemistry</i> , 2020, 88, 107307.	1.1	2
12837	CRISPR-assisted detection of RNA-protein interactions in living cells. <i>Nature Methods</i> , 2020, 17, 685-688.	9.0	82
12838	Cardiac transcriptional and metabolic changes following thoracotomy. <i>Scientific Reports</i> , 2020, 10, 9673.	1.6	0
12839	A novel prognostic signature of immune-related genes for patients with colorectal cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 8491-8504.	1.6	46
12840	Mechanism of YuPingFeng in the Treatment of COPD Based on Network Pharmacology. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	5
12841	RNA Sequencing for Gene Expression Profiles in Peripheral Blood Mononuclear Cells with Ankylosing Spondylitis RNA. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3
12842	Use of AMSTAR-2 in the methodological assessment of systematic reviews: protocol for a methodological study. <i>Annals of Translational Medicine</i> , 2020, 8, 652-652.	0.7	27
12843	Identification of CDC5L as bridge gene between chronic obstructive pulmonary disease and lung adenocarcinoma. <i>Epigenomics</i> , 2020, 12, 1515-1529.	1.0	4



#	ARTICLE	IF	CITATIONS
12844	A two-step human culture system replicates intestinal monocyte maturation cascade: Conversion of tissue-like inflammatory monocytes into macrophages. <i>European Journal of Immunology</i> , 2020, 50, 1676-1690.	1.6	6
12845	MicroRNA comparison between poplar and larch provides insight into the different mechanism of wood formation. <i>Plant Cell Reports</i> , 2020, 39, 1199-1217.	2.8	13
12846	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	2.1	13
12847	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. <i>Current Biology</i> , 2020, 30, 2887-2900.e7.	1.8	22
12848	Genome-wide mRNA and miRNA analysis in the early stages of germ tube outgrowth in <i>Coprinopsis cinerea</i> . <i>Fungal Genetics and Biology</i> , 2020, 142, 103416.	0.9	11
12849	Huangbai Liniment Accelerated Wound Healing by Activating Nrf2 Signaling in Diabetes. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-20.	1.9	14
12850	Construction and analysis of a lncRNA-miRNA-mRNA network based on competitive endogenous RNA reveal functional lncRNAs in oral cancer. <i>BMC Medical Genomics</i> , 2020, 13, 84.	0.7	28
12851	Genome wide meta-analysis of cDNA datasets reveals new target gene signatures of colorectal cancer based on systems biology approach. <i>Journal of Biological Research</i> , 2020, 27, 8.	2.2	13
12852	Comprehensive analysis of lncRNA-associated competing endogenous RNA network and immune infiltration in idiopathic pulmonary fibrosis. <i>Journal of Thoracic Disease</i> , 2020, 12, 1856-1865.	0.6	9
12853	A computational approach to validate novel drug targets of gentianine from <i>Swertia chirayita</i> in <i>Plasmodium falciparum</i> . <i>BioSystems</i> , 2020, 196, 104175.	0.9	3
12854	Directed evolution approach to enhance efficiency and speed of outgrowth during single cell subcloning of Chinese Hamster Ovary cells. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1320-1329.	1.9	15
12855	Silencing of aquaporin1 activates the Wnt signaling pathway to improve cognitive function in a mouse model of Alzheimer's disease. <i>Gene</i> , 2020, 755, 144904.	1.0	10
12856	Analysis of Inflammatory and Homeostatic Roles of Tissue-resident Macrophages in the Progression of Cholesteatoma by RNA-Seq. <i>Immunological Investigations</i> , 2021, 50, 609-621.	1.0	5
12857	Comparative Genomics and Metabolomics in the Genus <i>Nocardia</i> . <i>MSystems</i> , 2020, 5, .	1.7	39
12858	Proteomic analysis of human synovial fluid reveals potential diagnostic biomarkers for ankylosing spondylitis. <i>Clinical Proteomics</i> , 2020, 17, 20.	1.1	19
12859	Identification and characterization of male reproduction-related genes in pig ( <i>Sus scrofa</i> ) using transcriptome analysis. <i>BMC Genomics</i> , 2020, 21, 381.	1.2	7
12860	Cadmium, Smoking, and Human Blood DNA Methylation Profiles in Adults from the Strong Heart Study. <i>Environmental Health Perspectives</i> , 2020, 128, 67005.	2.8	57
12861	Transcriptomic stratification of late-onset Alzheimer's cases reveals novel genetic modifiers of disease pathology. <i>PLoS Genetics</i> , 2020, 16, e1008775.	1.5	31

#	ARTICLE	IF	CITATIONS
12862	An investigation into the beneficial effects and molecular mechanisms of humic acid on foxtail millet under drought conditions. <i>PLoS ONE</i> , 2020, 15, e0234029.	1.1	9
12863	Rhizosphere Soil Fungal Communities of Aluminum-Tolerant and -Sensitive Soybean Genotypes Respond Differently to Aluminum Stress in an Acid Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 1177.	1.5	23
12864	Microbiome structure of ecologically important bioeroding sponges (family Clionaidae): the role of host phylogeny and environmental plasticity. <i>Coral Reefs</i> , 2020, 39, 1285-1298.	0.9	16
12865	LncPRYP4-3 serves as a novel diagnostic biomarker for dissecting subtypes of metabolic associated fatty liver disease by targeting RPS4Y2. <i>Clinical and Experimental Medicine</i> , 2020, 20, 587-600.	1.9	10
12866	MicroRNA expression in relation with clinical evolution of osteosarcoma. <i>Pathology Research and Practice</i> , 2020, 216, 153038.	1.0	7
12867	Integrated miRNA-mRNA network revealing the key molecular characteristics of ossification of the posterior longitudinal ligament. <i>Medicine (United States)</i> , 2020, 99, e20268.	0.4	6
12868	Unexpected conservation and global transmission of agrobacterial virulence plasmids. <i>Science</i> , 2020, 368, .	6.0	56
12869	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. <i>MSystems</i> , 2020, 5, .	1.7	14
12870	In vitro analysis of the renin-angiotensin system and inflammatory gene transcripts in human bronchial epithelial cells after infection with severe acute respiratory syndrome coronavirus. <i>JRAAS - Journal of the Renin-Angiotensin-Aldosterone System</i> , 2020, 21, 147032032092887.	1.0	12
12871	Transcriptional profiling of multiple system atrophy cerebellar tissue highlights differences between the parkinsonian and cerebellar sub-types of the disease. <i>Acta Neuropathologica Communications</i> , 2020, 8, 76.	2.4	20
12872	Differential Secretome Profiling of Human Osteoarthritic Synoviocytes Treated with Biotechnological Unsulfated and Marine Sulfated Chondroitins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3746.	1.8	15
12873	T54R mutation destabilizes the dimer of superoxide dismutase 1 <sup>T54R</sup> by inducing steric clashes at the dimer interface. <i>RSC Advances</i> , 2020, 10, 10776-10788.	1.7	14
12874	Digging Deeper for the Eye Proteome in Vitreous Substructures: A High-Resolution Proteome Map of the Normal Human Vitreous Base. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 379-389.	1.0	6
12875	Preclinical Molecular Signatures of Spinal Cord Functional Restoration: Optimizing the Metamorphic Axolotl ( <i>Ambystoma mexicanum</i> ) Model in Regenerative Medicine. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 370-378.	1.0	8
12876	Systems Genetics for Mechanistic Discovery in Heart Diseases. <i>Circulation Research</i> , 2020, 126, 1795-1815.	2.0	8
12877	RNA-seq reveals downregulated osteochondral genes potentially related to tibia bacterial chondronecrosis with osteomyelitis in broilers. <i>BMC Genetics</i> , 2020, 21, 58.	2.7	4
12878	Precursor peptide-targeted mining of more than one hundred thousand genomes expands the lanthipeptide natural product family. <i>BMC Genomics</i> , 2020, 21, 387.	1.2	102
12879	A mouse SWATH-MS reference spectral library enables deconvolution of species-specific proteomic alterations in human tumour xenografts. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	16

#	ARTICLE	IF	CITATIONS
12880	The Osmotin-Like Protein Gene PdOLP1 Is Involved in Secondary Cell Wall Biosynthesis during Wood Formation in Poplar. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3993.	1.8	9
12881	16S rRNA sequencing analysis of the correlation between the intestinal microbiota and body-mass of grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100699.	0.4	8
12882	Host genotype explains rhizospheric microbial community composition: the case of wild cotton metapopulations ( <i>Gossypium hirsutum</i> L.) in Mexico. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	7
12883	The Central Role of Nondisclosed Men Who Have Sex With Men in Human Immunodeficiency Virus-1 Transmission Networks in Guangzhou, China. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa154.	0.4	14
12884	Transcriptomic Analysis of circRNAs and mRNAs Reveals a Complex Regulatory Network That Participate in Follicular Development in Chickens. <i>Frontiers in Genetics</i> , 2020, 11, 503.	1.1	15
12885	Dark response genes: a group of endogenous pendulum/timing players in maize?. <i>Planta</i> , 2020, 252, 1.	1.6	64
12886	Bacterial profiles and volatile flavor compounds in commercial Suancai with varying salt concentration from Northeastern China. <i>Food Research International</i> , 2020, 137, 109384.	2.9	47
12887	Identification of novel class I and class IIb histone deacetylase inhibitor for Alzheimer's disease therapeutics. <i>Life Sciences</i> , 2020, 256, 117912.	2.0	13
12888	Integrated analysis of mRNA and miRNA in testis and cauda epididymidis reveals candidate molecular markers associated with reproduction in Dezhou donkey. <i>Livestock Science</i> , 2020, 234, 103885.	0.6	14
12889	A New TTZ Feature Extracting Algorithm to Decipher Tobacco Related Mutation Signature Genes for the Personalized Lung Adenocarcinoma Treatment. <i>IEEE Access</i> , 2020, 8, 89031-89040.	2.6	7
12890	Fish Skin and Gut Microbiomes Show Contrasting Signatures of Host Species and Habitat. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	62
12891	Consistent gene signature of schizophrenia identified by a novel feature selection strategy from comprehensive sets of transcriptomic data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1058-1068.	3.2	177
12892	RWRMTN: a tool for predicting disease-associated microRNAs based on a microRNA-target gene network. <i>BMC Bioinformatics</i> , 2020, 21, 244.	1.2	5
12893	Genome-wide analysis of proline-rich extension-like receptor protein kinase (PERK) in <i>Brassica rapa</i> and its association with the pollen development. <i>BMC Genomics</i> , 2020, 21, 401.	1.2	16
12894	Clinical significance and biological mechanisms of glutathione S-transferase mu gene family in colon adenocarcinoma. <i>BMC Medical Genetics</i> , 2020, 21, 130.	2.1	9
12895	Comprehensive analysis of LDHAP5 pseudogene expression and potential pathogenesis in ovarian serous cystadenocarcinoma. <i>Cancer Cell International</i> , 2020, 20, 229.	1.8	6
12896	A lncRNA-miRNA-mRNA network for human primed, naive and extended pluripotent stem cells. <i>PLoS ONE</i> , 2020, 15, e0234628.	1.1	8
12897	Does 24-h Activity Cycle Influence Plasma PCSK9 Concentration? A Systematic Review and Meta-Analysis. <i>Current Atherosclerosis Reports</i> , 2020, 22, 30.	2.0	2

#	ARTICLE	IF	CITATIONS
12898	Rewired functional regulatory networks among miRNA isoforms (isomiRs) from let-7 and miR-10 gene families in cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1238-1248.	1.9	11
12899	Single molecule real-time sequencing and RNA-seq unravel the role of long non-coding and circular RNA in the regulatory network during Nile tilapia ( <i>Oreochromis niloticus</i> ) infection with <i>Streptococcus agalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 104, 640-653.	1.6	13
12900	Systems Studies Uncover miR-146a as a Target in <i>Leishmania major</i> Infection Model. <i>ACS Omega</i> , 2020, 5, 12516-12526.	1.6	21
12901	A comprehensive map of disease networks and molecular drug discoveries for glaucoma. <i>Scientific Reports</i> , 2020, 10, 9719.	1.6	3
12902	DNA methylation-based diagnostic and prognostic biomarkers of nasopharyngeal carcinoma patients. <i>Medicine (United States)</i> , 2020, 99, e20682.	0.4	11
12903	A <i>Vibrio cholerae</i> Core Genome Multilocus Sequence Typing Scheme To Facilitate the Epidemiological Study of Cholera. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	16
12904	Alterations in the Ocular Surface Microbiome in Traumatic Corneal Ulcer Patients. , 2020, 61, 35.		21
12905	A systematic evaluation of <i>Mycobacterium tuberculosis</i> Genome-Scale Metabolic Networks. <i>PLoS Computational Biology</i> , 2020, 16, e1007533.	1.5	17
12906	Unveiling prognostics biomarkers of tyrosine metabolism reprogramming in liver cancer by cross-platform gene expression analyses. <i>PLoS ONE</i> , 2020, 15, e0229276.	1.1	29
12907	An automated pipeline for the discovery of conspiracy and conspiracy theory narrative frameworks: Bridgegate, Pizzagate and storytelling on the web. <i>PLoS ONE</i> , 2020, 15, e0233879.	1.1	48
12908	Construction and Analysis of a Long Non-Coding RNA-Associated Competing Endogenous RNA Network Identified Potential Prognostic Biomarkers in Luminal Breast Cancer. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 4271-4282.	1.0	8
12909	Candidate Genes Associated With Neurological Findings in a Patient With Trisomy 4p16.3 and Monosomy 5p15.2. <i>Frontiers in Genetics</i> , 2020, 11, 561.	1.1	4
12910	Gene Expression and Metabolite Profiling of Thirteen Nigerian Cassava Landraces to Elucidate Starch and Carotenoid Composition. <i>Agronomy</i> , 2020, 10, 424.	1.3	7
12911	RNA Binding Proteins as Drivers and Therapeutic Target Candidates in Pancreatic Ductal Adenocarcinoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4190.	1.8	16
12912	Identification of the key genes and microRNAs in adult acute myeloid leukemia with FLT3 mutation by bioinformatics analysis. <i>International Journal of Medical Sciences</i> , 2020, 17, 1269-1280.	1.1	11
12913	Flexibility in an emergency life-history stage: acute food deprivation prevents sickness behaviour but not the immune response. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200842.	1.2	6
12914	Coexpression enrichment analysis at the single-cell level reveals convergent defects in neural progenitor cells and their cell-type transitions in neurodevelopmental disorders. <i>Genome Research</i> , 2020, 30, 835-848.	2.4	25
12915	Comparative Genomics Identified a Genetic Locus in Plant-Associated <i>Pseudomonas</i> spp. That Is Necessary for Induced Systemic Susceptibility. <i>MBio</i> , 2020, 11, .	1.8	9

#	ARTICLE	IF	CITATIONS
12916	Initial Mapping of the New York City Wastewater Virome. <i>MSystems</i> , 2020, 5, .	1.7	26
12917	Thapsigargin and induced chemical defence in <i>Thapsia garganica</i> . <i>Chemoecology</i> , 2020, 30, 255-267.	0.6	1
12918	Assessing functional propagation patterns in COVID-19. <i>Chaos, Solitons and Fractals</i> , 2020, 138, 109993.	2.5	9
12919	Deconstructing sarcomeric structureâ€“function relations in titin-BioID knock-in mice. <i>Nature Communications</i> , 2020, 11, 3133.	5.8	39
12920	A Transcriptome Analysis Reveals that Hepatic Glycolysis and Lipid Synthesis Are Negatively Associated with Feed Efficiency in DLY Pigs. <i>Scientific Reports</i> , 2020, 10, 9874.	1.6	8
12921	Identification of potential key genes and key pathways related to clear cell renal cell carcinoma through bioinformatics analysis. <i>Acta Biochimica Et Biophysica Sinica</i> , 2020, 52, 853-863.	0.9	4
12922	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	1.1	13
12923	Micro-Transcriptome Analysis Reveals Immune-Related MicroRNA Regulatory Networks of <i>Paralichthys olivaceus</i> Induced by <i>Vibrio anguillarum</i> Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4252.	1.8	13
12924	Lipotoxic Injury Differentially Regulates Brain Microvascular Gene Expression in Male Mice. <i>Nutrients</i> , 2020, 12, 1771.	1.7	12
12925	Multilevel regulation of muscle-specific transcription factor <i>hhl-1</i> during <i>Caenorhabditis elegans</i> embryogenesis. <i>Development Genes and Evolution</i> , 2020, 230, 265-278.	0.4	3
12926	Prokaryotic communities vary with floc size in a biofloc-technology based aquaculture system. <i>Aquaculture</i> , 2020, 529, 735632.	1.7	28
12927	An integrated analysis of testis miRNA and mRNA transcriptome reveals important functional miRNA-targets in reproduction traits of roosters. <i>Reproductive Biology</i> , 2020, 20, 433-440.	0.9	6
12928	A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020, 15, 2247-2276.	5.5	553
12929	An Interaction Network of RNA-Binding Proteins Involved in <i>Drosophila</i> Oogenesis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1485-1502.	2.5	13
12930	Temporal patterns in the interaction between photosynthetic picoeukaryotes and their attached fungi in Lake Chaohu. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	7
12931	Gene Similarity Networks Unveil a Potential Novel Unicellular Group Closely Related to Animals from the Tara Oceans Expedition. <i>Genome Biology and Evolution</i> , 2020, 12, 1664-1678.	1.1	9
12932	Human milk fungi: environmental determinants and inter-kingdom associations with milk bacteria in the CHILD Cohort Study. <i>BMC Microbiology</i> , 2020, 20, 146.	1.3	28
12933	Identification of Hub Genes Associated With Development of Head and Neck Squamous Cell Carcinoma by Integrated Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 681.	1.3	56

#	ARTICLE	IF	CITATIONS
12934	Transcriptome and Network Analyses of Heterostyly in <i>Turnera subulata</i> Provide Mechanistic Insights: Are S-Loci a Red-Light for Pistil Elongation?. <i>Plants</i> , 2020, 9, 713.	1.6	9
12935	Gene ontology enrichment analysis of Î±-amylase inhibitors from <i>Duranta repens</i> in diabetes mellitus. <i>Journal of Diabetes and Metabolic Disorders</i> , 2020, 19, 735-747.	0.8	26
12936	Semantic characterization of adverse outcome pathways. <i>Aquatic Toxicology</i> , 2020, 222, 105478.	1.9	6
12937	Protection against COVID-19 injury by qingfei paidu decoction via anti-viral, anti-inflammatory activity and metabolic programming. <i>Biomedicine and Pharmacotherapy</i> , 2020, 129, 110281.	2.5	91
12938	GreenCircRNA: a database for plant circRNAs that act as miRNA decoys. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	23
12939	Transcriptomic Study of Substrate-Specific Transport Mechanisms for Iron and Carbon in the Marine Copiotroph <i>Alteromonas macleodii</i> . <i>MSystems</i> , 2020, 5, .	1.7	19
12940	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
12941	The Methodology of Extraction and Analysis of Event Log Social Graph. , 2020, , .		0
12942	Gene regulation could be attributed to TCF3 and other key transcription factors in the muscle of pubertal heifers. <i>Veterinary Medicine and Science</i> , 2020, 6, 695-710.	0.6	6
12943	Four genes predict the survival of osteosarcoma patients based on TARGET database. <i>Journal of Bioenergetics and Biomembranes</i> , 2020, 52, 291-299.	1.0	7
12944	Network analysis of the hot spring microbiome sketches out possible niche differentiations among ecological guilds. <i>Ecological Modelling</i> , 2020, 431, 109147.	1.2	7
12945	Expression of SARS-CoV-2 receptor ACE2 and coincident host response signature varies by asthma inflammatory phenotype. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 315-324.e7.	1.5	90
12946	The Nuclear SUMO-Targeted Ubiquitin Quality Control Network Regulates the Dynamics of Cytoplasmic Stress Granules. <i>Molecular Cell</i> , 2020, 79, 54-67.e7.	4.5	73
12947	Connection of miR-185 and miR-320a expression levels with response to interferon-beta in multiple sclerosis patients. <i>Multiple Sclerosis and Related Disorders</i> , 2020, 44, 102264.	0.9	6
12948	The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020, 11, 2902.	5.8	118
12949	Screening novel drug candidates for Alzheimer's disease by an integrated network and transcriptome analysis. <i>Bioinformatics</i> , 2020, 36, 4626-4632.	1.8	26
12950	Molecular alterations in the extracellular matrix in the brains of newborns with congenital Zika syndrome. <i>Science Signaling</i> , 2020, 13, .	1.6	39
12951	Genome-wide DNA methylation profiles may reveal new possible epigenetic pathogenesis of sporadic congenital cataract. <i>Epigenomics</i> , 2020, 12, 771-788.	1.0	4



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12952	Identification and Validation of Potential Biomarkers and Their Functions in Acute Kidney Injury. <i>Frontiers in Genetics</i> , 2020, 11, 411.	1.1	23
12953	Bioinformatics Analysis of Prognostic miRNA Signature and Potential Critical Genes in Colon Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 478.	1.1	30
12954	Interactions Among Expressed MicroRNAs and mRNAs in the Early Stages of Fowl Adenovirus Aerotype 4-Infected Leghorn Male Hepatocellular Cells. <i>Frontiers in Microbiology</i> , 2020, 11, 831.	1.5	9
12955	Personalized Mapping of Drug Metabolism by the Human Gut Microbiome. <i>Cell</i> , 2020, 181, 1661-1679.e22.	13.5	239
12956	Spatial Compartmentalization of the Microbiome between the Lumen and Crypts Is Lost in the Murine Cecum following the Process of Surgery, Including Overnight Fasting and Exposure to Antibiotics. <i>MSystems</i> , 2020, 5, .	1.7	21
12957	Systems biology approaches toward autosomal dominant polycystic kidney disease (ADPKD). <i>Clinical and Translational Medicine</i> , 2020, 9, 1.	1.7	21
12958	Profiling and Functional Analysis of Circular RNAs in Porcine Fast and Slow Muscles. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 322.	1.8	24
12959	Clinical Proteomics Profiling for Biomarker Identification Among Patients Suffering With Indian Post Kala Azar Dermal Leishmaniasis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 251.	1.8	2
12960	Patterns of Sequence and Expression Diversification Associate Members of the PADRE Gene Family With Response to Fungal Pathogens. <i>Frontiers in Genetics</i> , 2020, 11, 491.	1.1	9
12961	Dynamics of Gene Co-expression Networks in Time-Series Data: A Case Study in <i>Drosophila melanogaster</i> Embryogenesis. <i>Frontiers in Genetics</i> , 2020, 11, 517.	1.1	5
12962	A Comparative Analysis of Ash Leaf-Colonizing Bacterial Communities Identifies Putative Antagonists of <i>Hymenoscypus fraxineus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 966.	1.5	25
12963	Crop Management Impacts the Soybean ( <i>Glycine max</i> ) Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 1116.	1.5	48
12964	Loss of <i>Arid1a</i> Promotes Neuronal Survival Following Optic Nerve Injury. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 131.	1.8	4
12965	Genes Bound by $\hat{I}$ FosB in Different Conditions With Recurrent Seizures Regulate Similar Neuronal Functions. <i>Frontiers in Neuroscience</i> , 2020, 14, 472.	1.4	8
12966	Ex vivo Quantitative Proteomic Analysis of Serotonin Transporter Interactome: Network Impact of the SERT Ala56 Coding Variant. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 89.	1.4	16
12967	The Landscape of Iron Metabolism-Related and Methylated Genes in the Prognosis Prediction of Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 788.	1.3	19
12968	LPAR1, Correlated With Immune Infiltrates, Is a Potential Prognostic Biomarker in Prostate Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 846.	1.3	59
12969	Centralization Within Sub-Experiments Enhances the Biological Relevance of Gene Co-expression Networks: A Plant Mitochondrial Case Study. <i>Frontiers in Plant Science</i> , 2020, 11, 524.	1.7	1



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12970	Analysis of Dynamic Global Transcriptional Atlas Reveals Common Regulatory Networks of Hormones and Photosynthesis Across Nicotiana Varieties in Response to Long-Term Drought. <i>Frontiers in Plant Science</i> , 2020, 11, 672.	1.7	13
12971	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10
12972	Structural Studies of Glutamate Dehydrogenase (Isoform 1) From <i>Arabidopsis thaliana</i> , an Important Enzyme at the Branch-Point Between Carbon and Nitrogen Metabolism. <i>Frontiers in Plant Science</i> , 2020, 11, 754.	1.7	30
12973	SPOP Deregulation Improves the Radiation Response of Prostate Cancer Models by Impairing DNA Damage Repair. <i>Cancers</i> , 2020, 12, 1462.	1.7	8
12974	The Progression of Acute Myeloid Leukemia from First Diagnosis to Chemoresistant Relapse: A Comparison of Proteomic and Phosphoproteomic Profiles. <i>Cancers</i> , 2020, 12, 1466.	1.7	33
12975	Identification of miRNA-mRNA-TFs Regulatory Network and Crucial Pathways Involved in Tetralogy of Fallot. <i>Frontiers in Genetics</i> , 2020, 11, 552.	1.1	17
12976	Compound craniosynostosis, intellectual disability, and Noonan-like facial dysmorphism associated with 7q32.3-q35 deletion. <i>Birth Defects Research</i> , 2020, 112, 740-748.	0.8	4
12977	Anti-infective nitazoxanide disrupts transcription of ribosome biogenesis-related genes in yeast. <i>Genes and Genomics</i> , 2020, 42, 915-926.	0.5	6
12978	Beneficial effect of phospholipase A2 group IIA inhibitors from <i>Acacia suma</i> in obesity: an in silico and in vitro study. <i>Advances in Traditional Medicine</i> , 2020, 20, 599-608.	1.0	4
12979	Hydrogen bond network analysis reveals the pathway for the proton transfer in the E-channel of <i>T. thermophilus</i> Complex I. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2020, 1861, 148240.	0.5	20
12980	Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. <i>Cancer Cell</i> , 2020, 38, 129-143.e7.	7.7	57
12981	Genome-wide profiling of host-encoded circular RNAs highlights their potential role during the Japanese encephalitis virus-induced neuroinflammatory response. <i>BMC Genomics</i> , 2020, 21, 409.	1.2	13
12982	Genomic diversity of bacteriophages infecting <i>Microbacterium</i> spp. <i>PLoS ONE</i> , 2020, 15, e0234636.	1.1	50
12983	Comparative Transcriptome Analysis of Two Contrasting Soybean Varieties in Response to Aluminum Toxicity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4316.	1.8	16
12984	Moss biocrusts buffer the negative effects of karst rocky desertification on soil properties and soil microbial richness. <i>Plant and Soil</i> , 2022, 475, 153-168.	1.8	26
12985	Transcriptome Analysis of iPSC-Derived Neurons from Rubinstein-Taybi Patients Reveals Deficits in Neuronal Differentiation. <i>Molecular Neurobiology</i> , 2020, 57, 3685-3701.	1.9	15
12986	Insight into potent leads for alzheimer's disease by using several artificial intelligence algorithms. <i>Biomedicine and Pharmacotherapy</i> , 2020, 129, 110360.	2.5	10
12987	DDX3X Suppresses the Susceptibility of Hindbrain Lineages to Medulloblastoma. <i>Developmental Cell</i> , 2020, 54, 455-470.e5.	3.1	47

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12988	Sequence-based bioprospecting of myo-inositol oxygenase (Miox) reveals new homologues that increase glucaric acid production in <i>Saccharomyces cerevisiae</i> . <i>Enzyme and Microbial Technology</i> , 2020, 140, 109623.	1.6	12
12989	Targeting pheochromocytoma/paraganglioma with polyamine inhibitors. <i>Metabolism: Clinical and Experimental</i> , 2020, 110, 154297.	1.5	11
12990	Interactome overlap between schizophrenia and cognition. <i>Schizophrenia Research</i> , 2020, 222, 167-174.	1.1	13
12991	Altered Gut Archaea Composition and Interaction With Bacteria Are Associated With Colorectal Cancer. <i>Gastroenterology</i> , 2020, 159, 1459-1470.e5.	0.6	87
12992	Identification of Host Trafficking Genes Required for HIV-1 Virological Synapse Formation in Dendritic Cells. <i>Journal of Virology</i> , 2020, 94, .	1.5	13
12993	Transcriptional signatures of participant-derived neural progenitor cells and neurons implicate altered Wnt signaling in Phelan-McDermid syndrome and autism. <i>Molecular Autism</i> , 2020, 11, 53.	2.6	24
12994	Lipid Annotation by Combination of UHPLC-HRMS (MS), Molecular Networking, and Retention Time Prediction: Application to a Lipidomic Study of In Vitro Models of Dry Eye Disease. <i>Metabolites</i> , 2020, 10, 225.	1.3	16
12995	Insights into the Natural Defenses of a Coral Reef Fish Against Gill Ectoparasites: Integrated Metabolome and Microbiome Approach. <i>Metabolites</i> , 2020, 10, 227.	1.3	3
12996	Proteomics analysis of zebrafish larvae exposed to 3,4-dichloroaniline using the fish embryo acute toxicity test. <i>Environmental Toxicology</i> , 2020, 35, 849-860.	2.1	16
12997	Multi-level and lineage-specific interactomes of the Hox transcription factor Ubx contribute to its functional specificity. <i>Nature Communications</i> , 2020, 11, 1388.	5.8	24
12998	Evolutionary transcriptomics of metazoan biphasic life cycle supports a single intercalation origin of metazoan larvae. <i>Nature Ecology and Evolution</i> , 2020, 4, 725-736.	3.4	39
12999	Novel pathways of HIV latency reactivation revealed by integrated analysis of transcriptome and target profile of bryostatin. <i>Scientific Reports</i> , 2020, 10, 3511.	1.6	11
13000	Expression and prognostic potential of GPX1 in human cancers based on data mining. <i>Annals of Translational Medicine</i> , 2020, 8, 124-124.	0.7	45
13001	Alterations in Gut Microbiota of Gestational Diabetes Patients During the First Trimester of Pregnancy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 58.	1.8	64
13002	Genome-Wide Identification and Characterization of DNA Methylation and Long Non-Coding RNA Expression in Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 91.	1.1	13
13003	Overexpression of the Selective Autophagy Cargo Receptor NBR1 Modifies Plant Response to Sulfur Deficit. <i>Cells</i> , 2020, 9, 669.	1.8	18
13004	Identification of key genes and pathways of diagnosis and prognosis in cervical cancer by bioinformatics analysis. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1200.	0.6	29
13005	End-stage renal disease is different from chronic kidney disease in upregulating ROS-modulated proinflammatory secretome in PBMCs - A novel multiple-hit model for disease progression. <i>Redox Biology</i> , 2020, 34, 101460.	3.9	62

#	ARTICLE	IF	CITATIONS
13006	Elevated serum chemokine CCL22 levels in first-episode psychosis: associations with symptoms, peripheral immune state and in vivo brain glial cell function. <i>Translational Psychiatry</i> , 2020, 10, 94.	2.4	16
13007	Lifting the veil on arid-to-hyperarid Antarctic soil microbiomes: a tale of two oases. <i>Microbiome</i> , 2020, 8, 37.	4.9	22
13008	Integrative Analysis of MicroRNA and Gene Interactions for Revealing Candidate Signatures in Prostate Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 176.	1.1	41
13009	From Chloroplast Biogenesis to Chlorophyll Accumulation: The Interplay of Light and Hormones on Gene Expression in <i>Camellia sinensis</i> cv. Shuchazao Leaves. <i>Frontiers in Plant Science</i> , 2020, 11, 256.	1.7	58
13010	Systems toxicology assessment revealed the impact of graphene-based materials on cell cycle regulators. <i>Journal of Biomedical Materials Research - Part A</i> , 2020, 108, 1520-1533.	2.1	8
13011	Functional Characterization of Cj1427, a Unique Ping-Pong Dehydrogenase Responsible for the Oxidation of GDP-glycero- $\pm$ -manno-heptose in <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2020, 59, 1328-1337.	1.2	12
13012	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
13013	Cardiopoeitic stem cell therapy restores infarction-altered cardiac proteome. <i>Npj Regenerative Medicine</i> , 2020, 5, 5.	2.5	21
13014	Transcriptomic and metabolomic analyses of <i>Lycium ruthenicum</i> and <i>Lycium barbarum</i> fruits during ripening. <i>Scientific Reports</i> , 2020, 10, 4354.	1.6	17
13015	Structure and upstream region analysis of phenylalanine ammonia-lyase gene in rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT/Overlock 10 <i>Phytopathology and Plant Protection</i> , 2020, 53, 355-378.	0.6	3
13016	Multimiomics Analysis Coupled with Text Mining Identify Novel Biomarker Candidates for Recurrent Cardiovascular Events. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 205-215.	1.0	3
13017	Resource availability drives bacterial succession during leaf-litter decomposition in a bromeliad ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
13018	Using GARDEN-NET and ChAseR to explore human haematopoietic 3D chromatin interaction networks. <i>Nucleic Acids Research</i> , 2020, 48, 4066-4080.	6.5	18
13019	Rewiring of gene networks underlying mite allergen-induced CD4 <sup>+</sup> Th <sub>1</sub> cell responses during immunotherapy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2330-2341.	2.7	11
13020	Chitosan-triggered immunity to <i>Fusarium</i> in chickpea is associated with changes in the plant extracellular matrix architecture, stomatal closure and remodeling of the plant metabolome and proteome. <i>Plant Journal</i> , 2020, 103, 561-583.	2.8	29
13021	Identification and integrated analysis of glyphosate stress-responsive microRNAs, lncRNAs, and mRNAs in rice using genome-wide high-throughput sequencing. <i>BMC Genomics</i> , 2020, 21, 238.	1.2	18
13022	CANcer bioMarker Prediction Pipeline (CAMPP) – A standardized framework for the analysis of quantitative biological data. <i>PLoS Computational Biology</i> , 2020, 16, e1007665.	1.5	10
13023	Diversity and biogeography of picoplankton communities from the Straits of Malacca to the South China Sea. <i>Oceanological and Hydrobiological Studies</i> , 2020, 49, 23-33.	0.3	2

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13024	Potential Biomarkers for Feed Efficiency-Related Traits in Nelore Cattle Identified by Co-expression Network and Integrative Genomics Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 189.	1.1	23
13025	Genomic and Transcriptomic Landscape of Tumor Clonal Evolution in Cholangiocarcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 195.	1.1	4
13026	Plant Growth-Promoting Methylobacteria Selectively Increase the Biomass of Biotechnologically Relevant Microalgae. <i>Frontiers in Microbiology</i> , 2020, 11, 427.	1.5	26
13027	Boosting the Biogenesis and Secretion of Mesenchymal Stem Cell-Derived Exosomes. <i>Cells</i> , 2020, 9, 660.	1.8	97
13028	Reveals of New Candidate Active Components in <i>Hemerocallis Radix</i> and Its Anti-Depression Action of Mechanism Based on Network Pharmacology Approach. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1868.	1.8	25
13029	Agroforestry Management Systems Drive the Composition, Diversity, and Function of Fungal and Bacterial Endophyte Communities in <i>Theobroma Cacao</i> Leaves. <i>Microorganisms</i> , 2020, 8, 405.	1.6	20
13030	RNA markers for ultra-rapid molecular antimicrobial susceptibility testing in fluoroquinolone-treated <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1747-1755.	1.3	10
13031	Immune-related prognosis biomarkers associated with osteosarcoma microenvironment. <i>Cancer Cell International</i> , 2020, 20, 83.	1.8	45
13032	Translating traditional herbal formulas into modern drugs: a network-based analysis of Xiaoyao decoction. <i>Chinese Medicine</i> , 2020, 15, 25.	1.6	16
13033	&lt;p&gt;A Protein Corona Adsorbed to a Bacterial Magnetosome Affects Its Cellular Uptake&lt;/p&gt;. <i>International Journal of Nanomedicine</i> , 2020, Volume 15, 1481-1498.	3.3	18
13034	A Comparative Analysis of Tumors and Plasma Circulating Tumor DNA in 145 Advanced Cancer Patients Annotated by 3 Core Cellular Processes. <i>Cancers</i> , 2020, 12, 701.	1.7	5
13035	MicroRNAs association with azoospermia, oligospermia, asthenozoospermia, and teratozoospermia: a systematic review. <i>Journal of Assisted Reproduction and Genetics</i> , 2020, 37, 763-775.	1.2	26
13036	Spectrum-specific encephalography standardized low-resolution brain electromagnetic tomography network and gray matter correlations in vascular dementia patients. <i>International Journal of Distributed Sensor Networks</i> , 2020, 16, 155014771989596.	1.3	1
13037	&lt;scp>KCMML&lt;/scp> : a machine&Elearning framework for inference of multi&Escale gene functions from genetic perturbation screens. <i>Molecular Systems Biology</i> , 2020, 16, e9083.	3.2	11
13038	A Novel Long Non-coding RNA, MSTRG.51053.2 Regulates Cisplatin Resistance by Sponging the miR-432-5p in Non-small Cell Lung Cancer Cells. <i>Frontiers in Oncology</i> , 2020, 10, 215.	1.3	33
13039	Valproic Acid Promotes Early Neural Differentiation in Adult Mesenchymal Stem Cells Through Protein Signalling Pathways. <i>Cells</i> , 2020, 9, 619.	1.8	23
13040	Global Survey and Expressions of the Phosphate Transporter Gene Families in <i>Brassica napus</i> and Their Roles in Phosphorus Response. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1752.	1.8	14
13041	A Network-Based Approach to Explore the Mechanisms of <i>Uncaria Alkaloids</i> in Treating Hypertension and Alleviating Alzheimer&E™s Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1766.	1.8	25

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13042	Modeling a global regulatory network of <i>Methanothermobacter thermautotrophicus</i> strain $\hat{H}$ . <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	15
13043	ANGPTL3 deficiency alters the lipid profile and metabolism of cultured hepatocytes and human lipoproteins. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2020, 1865, 158679.	1.2	7
13044	Large-scale profiling of the proteome and dual transcriptome in Nile tilapia ( <i>Oreochromis niloticus</i> ) challenged with low- and high-virulence strains of <i>Streptococcus agalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 100, 386-396.	1.6	12
13045	Network-based meta-analysis for the identification of potential target for human anaplastic thyroid carcinoma. <i>Meta Gene</i> , 2020, 24, 100690.	0.3	0
13046	Comprehensive analyses of the annexin (ANN) gene family in <i>Brassica rapa</i> , <i>Brassica oleracea</i> and <i>Brassica napus</i> reveals their roles in stress response. <i>Scientific Reports</i> , 2020, 10, 4295.	1.6	39
13047	Long noncoding RNA and messenger RNA abnormalities in pediatric sepsis: a preliminary study. <i>BMC Medical Genomics</i> , 2020, 13, 36.	0.7	9
13048	Post-Transcriptional Dysregulation of microRNA and Alternative Polyadenylation in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 64.	1.1	31
13049	Development of a Novel Six-miRNA-Based Model to Predict Overall Survival Among Colon Adenocarcinoma Patients. <i>Frontiers in Oncology</i> , 2020, 10, 26.	1.3	17
13050	Genome-Wide Detection of Key Genes and Epigenetic Markers for Chicken Fatty Liver. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1800.	1.8	11
13051	Visualizing Human Protein-Protein Interactions and Subcellular Localizations on Cell Images Through CellMap. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e97.	25.8	6
13052	Synovial fibroblast-derived exosomal microRNA-106b suppresses chondrocyte proliferation and migration in rheumatoid arthritis via down-regulation of PDK4. <i>Journal of Molecular Medicine</i> , 2020, 98, 409-423.	1.7	31
13053	Basement membrane ligands initiate distinct signalling networks to direct cell shape. <i>Matrix Biology</i> , 2020, 90, 61-78.	1.5	38
13054	Phosphoproteome Analysis Reveals Dynamic Heat Shock Protein 27 Phosphorylation in Tanshinone IIA-Induced Cell Death. <i>Journal of Proteome Research</i> , 2020, 19, 1620-1634.	1.8	8
13055	Hippocampal subfield transcriptome analysis in schizophrenia psychosis. <i>Molecular Psychiatry</i> , 2021, 26, 2577-2589.	4.1	25
13056	Edgetic perturbation signatures represent known and novel cancer biomarkers. <i>Scientific Reports</i> , 2020, 10, 4350.	1.6	5
13057	Machine Learning Supports Long Noncoding RNAs as Expression Markers for Endometrial Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	1
13058	Modular Characteristics and Mechanism of Action of Herbs for Endometriosis Treatment in Chinese Medicine: A Data Mining and Network Pharmacology-Based Identification. <i>Frontiers in Pharmacology</i> , 2020, 11, 147.	1.6	51
13059	Profiles of immune-related genes and immune cell infiltration in the tumor microenvironment of diffuse lower-grade gliomas. <i>Journal of Cellular Physiology</i> , 2020, 235, 7321-7331.	2.0	61

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13060	Network Pharmacology-based Research of Active Components of Albiziae Flos and Mechanisms of Its Antidepressant Effect. <i>Current Medical Science</i> , 2020, 40, 123-129.	0.7	17
13061	Bioinformatical Analysis of Gene Expression Omnibus Database Associates TAF7/CCNB1, TAF7/CCNA2, and GTF2E2/CDC20 Pathways with Glioblastoma Development and Prognosis. <i>World Neurosurgery</i> , 2020, 138, e492-e514.	0.7	22
13062	Quantitative Proteomics Reveals the Development of HBV-Associated Glomerulonephritis Triggered by the Downregulation of SLC7A7. <i>Journal of Proteome Research</i> , 2020, 19, 1556-1564.	1.8	7
13063	Eosinophil accumulation in postnatal lung is specific to the primary septation phase of development. <i>Scientific Reports</i> , 2020, 10, 4425.	1.6	18
13064	Identification of hub genes and pathways in adrenocortical carcinoma by integrated bioinformatic analysis. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4428-4438.	1.6	16
13065	Identification of Long Noncoding RNAs as Predictors of Survival in Triple-Negative Breast Cancer Based on Network Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	32
13066	RNA Sequencing and Bioinformatic Analysis on Retinoblastoma Revealing that Cell Cycle Dereglulation Is a Key Process in Retinoblastoma Tumorigenesis. <i>Ophthalmologica</i> , 2021, 244, 51-59.	1.0	9
13067	Identification of PTPRR and JAG1 as key genes in castration-resistant prostate cancer by integrated bioinformatics methods. <i>Journal of Zhejiang University: Science B</i> , 2020, 21, 246-255.	1.3	6
13068	A Comprehensive Analysis Identified the Key Differentially Expressed Circular Ribonucleic Acids and Methylation-Related Function in Pheochromocytomas and Paragangliomas. <i>Frontiers in Genetics</i> , 2020, 11, 15.	1.1	8
13069	Activation of the C-Type Lectin MGL by Terminal GalNAc Ligands Reduces the Glycolytic Activity of Human Dendritic Cells. <i>Frontiers in Immunology</i> , 2020, 11, 305.	2.2	22
13070	Competition Between Butyrate Fermenters and Chain-Elongating Bacteria Limits the Efficiency of Medium-Chain Carboxylate Production. <i>Frontiers in Microbiology</i> , 2020, 11, 336.	1.5	38
13071	Effects of chronic heat stress on mRNA and miRNA expressions in dairy cows. <i>Gene</i> , 2020, 742, 144550.	1.0	12
13072	Unique microbial module regulates the harmful algal bloom ( <i>Cochlodinium polykrikoides</i> ) and shifts the microbial community along the Southern Coast of Korea. <i>Science of the Total Environment</i> , 2020, 721, 137725.	3.9	25
13073	Host identity is more important in structuring bacterial epiphytes than endophytes in a tropical mangrove forest. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
13074	LncRNAs in molluscan and mammalian stages of parasitic schistosomes are developmentally-regulated and coordinately expressed with protein-coding genes. <i>RNA Biology</i> , 2020, 17, 805-815.	1.5	14
13075	The microbiome modulating activity of bile acids. <i>Gut Microbes</i> , 2020, 11, 979-996.	4.3	124
13076	Disentangling the assembly mechanisms of ant cuticular bacterial communities of two Amazonian ant species sharing a common arboreal nest. <i>Molecular Ecology</i> , 2020, 29, 1372-1385.	2.0	15
13077	Sirt2-associated transcriptome modifications in cisplatin-induced neuronal injury. <i>BMC Genomics</i> , 2020, 21, 192.	1.2	4



#	ARTICLE	IF	CITATIONS
13078	Alcohol Causes Lasting Differential Transcription in <i>Drosophila</i> Mushroom Body Neurons. <i>Genetics</i> , 2020, 215, 103-116.	1.2	20
13079	Characterization of the Gut Microbiota of the Antarctic Heart Urchin (Spatangoida) <i>Abatus agassizii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 308.	1.5	22
13080	The Prognostic Significance of Metabolic Syndrome and a Related Six-lncRNA Signature in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 61.	1.3	26
13081	Genomic and Transcriptional Analysis of Banana Ovate Family Proteins Reveals Their Relationship with Fruit Development and Ripening. <i>Biochemical Genetics</i> , 2020, 58, 412-429.	0.8	8
13082	Identification of key genes and expression profiles in osteoarthritis by co-expressed network analysis. <i>Computational Biology and Chemistry</i> , 2020, 85, 107225.	1.1	10
13083	Genome-wide discovery and functional prediction of salt-responsive lncRNAs in duckweed. <i>BMC Genomics</i> , 2020, 21, 212.	1.2	32
13084	Identification of tissue-specific and cold-responsive lncRNAs in <i>Medicago truncatula</i> by high-throughput RNA sequencing. <i>BMC Plant Biology</i> , 2020, 20, 99.	1.6	29
13085	Integrated Analysis of miRNA-mRNA Network Reveals Different Regulatory Patterns in the Endometrium of Meishan and Duroc Sows during Mid-Late Gestation. <i>Animals</i> , 2020, 10, 420.	1.0	8
13086	Integrated Seed Proteome and Phosphoproteome Analyses Reveal Interplay of Nutrient Dynamics, Carbon-Nitrogen Partitioning, and Oxidative Signaling in Chickpea. <i>Proteomics</i> , 2020, 20, 1900267.	1.3	4
13087	Understanding of Zaire ebolavirus-human protein interaction for drug repurposing. <i>VirusDisease</i> , 2020, 31, 28-37.	1.0	5
13088	Differential metabolic and hepatic transcriptome responses of two miniature pig breeds to high dietary cholesterol. <i>Life Sciences</i> , 2020, 250, 117514.	2.0	3
13089	PD-L1 engagement on T cells promotes self-tolerance and suppression of neighboring macrophages and effector T cells in cancer. <i>Nature Immunology</i> , 2020, 21, 442-454.	7.0	228
13090	Spectral analysis for gene communities in cancer cells. <i>Journal of Complex Networks</i> , 2020, 8, .	1.1	1
13091	Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. <i>GigaScience</i> , 2020, 9, .	3.3	31
13092	Rice F-bZIP transcription factors regulate the zinc deficiency response. <i>Journal of Experimental Botany</i> , 2020, 71, 3664-3677.	2.4	49
13093	Anthelmintic and metabolomic analyses of chicory ( <i>Cichorium intybus</i> ) identify an industrial by-product with potent in vitro antinematodal activity. <i>Veterinary Parasitology</i> , 2020, 280, 109088.	0.7	20
13094	Embryonic endothelial evolution towards first hematopoietic stem cells revealed by single-cell transcriptomic and functional analyses. <i>Cell Research</i> , 2020, 30, 376-392.	5.7	89
13095	Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome. <i>Scientific Reports</i> , 2020, 10, 4995.	1.6	16



#	ARTICLE	IF	CITATIONS
13096	Comparison of leaf transcriptome in response to <i>Rhizoctonia solani</i> infection between resistant and susceptible rice cultivars. <i>BMC Genomics</i> , 2020, 21, 245.	1.2	25
13097	Integrated analysis of gene expression and DNA methylation profiles in ovarian cancer. <i>Journal of Ovarian Research</i> , 2020, 13, 30.	1.3	29
13098	Specification and regulation of vascular tissue identity in the <i>Arabidopsis</i> embryo. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	24
13099	Genome-Wide Epistatic Interaction Networks Affecting Feed Efficiency in Duroc and Landrace Pigs. <i>Frontiers in Genetics</i> , 2020, 11, 121.	1.1	26
13100	Comparison of Adult Testis and Ovary MicroRNA Expression Profiles in Reevesâ€™ Pond Turtles ( <i>Mauremys reevesii</i> ) With Temperature-Dependent Sex Determination. <i>Frontiers in Genetics</i> , 2020, 11, 133.	1.1	7
13101	miRNA-Coordinated Schizophrenia Risk Network Cross-Talk With Cardiovascular Repair and Opposed Gliomagenesis. <i>Frontiers in Genetics</i> , 2020, 11, 149.	1.1	8
13102	Immune and Stroma Related Genes in Breast Cancer: A Comprehensive Analysis of Tumor Microenvironment Based on the Cancer Genome Atlas (TCGA) Database. <i>Frontiers in Medicine</i> , 2020, 7, 64.	1.2	53
13103	The Changes in the Frog Gut Microbiome and Its Putative Oxygen-Related Phenotypes Accompanying the Development of Gastrointestinal Complexity and Dietary Shift. <i>Frontiers in Microbiology</i> , 2020, 11, 162.	1.5	24
13104	Effect of Herbal Formulation on Immune Response Enhancement in RAW 264.7 Macrophages. <i>Biomolecules</i> , 2020, 10, 424.	1.8	18
13105	Comparative Molecular Analysis of Cancer Behavior Cultured In Vitro, In Vivo, and Ex Vivo. <i>Cancers</i> , 2020, 12, 690.	1.7	17
13106	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	1.7	33
13107	Deoxynivalenol Induces Inflammation in IPEC-J2 Cells by Activating P38 Mapk And Erk1/2. <i>Toxins</i> , 2020, 12, 180.	1.5	39
13108	Coxsackievirus B3 Infection of Human Neural Progenitor Cells Results in Distinct Expression Patterns of Innate Immune Genes. <i>Viruses</i> , 2020, 12, 325.	1.5	15
13109	Novel candidate biomarkers of origin recognition complex 1, 5 and 6 for survival surveillance in patients with hepatocellular carcinoma. <i>Journal of Cancer</i> , 2020, 11, 1869-1882.	1.2	15
13110	Virome: The Prodigious Little Cousin of the Family. , 2020, , 53-73.		1
13111	Frequency of stover mulching but not amount regulates the decomposition pathways of soil micro-foodwebs in a no-tillage system. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107789.	4.2	31
13112	Differential expression of AURKA/PLK4 in quiescence and senescence of osteosarcoma U2OS cells. <i>Cell Cycle</i> , 2020, 19, 884-894.	1.3	1
13113	The conserved microRNA miRâ€³p coordinates the expression of Vâ€³ATPase subunits to regulate ecdysone biosynthesis for <i>Drosophila</i> metamorphosis. <i>FASEB Journal</i> , 2020, 34, 6449-6465.	0.2	13

#	ARTICLE	IF	CITATIONS
13114	Expression of SREBP2 and cholesterol metabolism related genes in TCGA glioma cohorts. <i>Medicine (United States)</i> , 2020, 99, e18815.	0.4	7
13115	Repositioning of Hypoglycemic Drug Linagliptin for Cancer Treatment. <i>Frontiers in Pharmacology</i> , 2020, 11, 187.	1.6	11
13116	Pharmacological Mechanisms Underlying the Neuroprotective Effects of <i>Alpinia oxyphylla</i> Miq. on Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2071.	1.8	41
13117	Silencing lncRNA AGAP2-AS1 upregulates miR-195-5p to Repress Migration and Invasion of EC Cells via the Decrease of FOSL1 Expression. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 20, 331-344.	2.3	41
13118	Identification of Key Genes in Association with Progression and Prognosis in Cervical Squamous Cell Carcinoma. <i>DNA and Cell Biology</i> , 2020, 39, 848-863.	0.9	14
13119	Mammary Transcriptome Profile during Peak and Late Lactation Reveals Differentially Expression Genes Related to Inflammation and Immunity in Chinese Holstein. <i>Animals</i> , 2020, 10, 510.	1.0	9
13120	The potential drug for treatment in pancreatic adenocarcinoma: a bioinformatical study based on distinct drug databases. <i>Chinese Medicine</i> , 2020, 15, 26.	1.6	7
13121	Deep phosphoproteome analysis of <i>Schistosoma mansoni</i> leads development of a kinomic array that highlights sex-biased differences in adult worm protein phosphorylation. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008115.	1.3	11
13122	Glucocorticoid Resistant Pediatric Acute Lymphoblastic Leukemia Samples Display Altered Splicing Profile and Vulnerability to Spliceosome Modulation. <i>Cancers</i> , 2020, 12, 723.	1.7	16
13123	Slower development of lower canopy beans produces better coffee. <i>Journal of Experimental Botany</i> , 2020, 71, 4201-4214.	2.4	10
13124	Design protein-protein interaction network and protein-drug interaction network for common cancer diseases: A bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100311.	1.9	12
13125	An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. <i>Communications Biology</i> , 2020, 3, 145.	2.0	36
13126	Unraveling the iterative type I polyketide synthases hidden in <i>Streptomyces</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8449-8454.	3.3	34
13127	Genome-wide integrated analysis demonstrates widespread functions of lncRNAs in mammary gland development and lactation in dairy goats. <i>BMC Genomics</i> , 2020, 21, 254.	1.2	20
13128	Association between the cytokine storm, immune cell dynamics, and viral replicative capacity in hyperacute HIV infection. <i>BMC Medicine</i> , 2020, 18, 81.	2.3	45
13129	Transcriptomic analysis of long noncoding RNAs and mRNAs expression profiles in the spinal cord of bone cancer pain rats. <i>Molecular Brain</i> , 2020, 13, 47.	1.3	4
13130	A Computational Approach for Mapping Heme Biology in the Context of Hemolytic Disorders. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 74.	2.0	16
13131	Malignant Evaluation and Clinical Prognostic Values of m6A RNA Methylation Regulators in Glioblastoma. <i>Frontiers in Oncology</i> , 2020, 10, 208.	1.3	47

#	ARTICLE	IF	CITATIONS
13132	LncRNAs Predicted to Interfere With the Gene Regulation Activity of miR-637 and miR-196a-5p in GBM. <i>Frontiers in Oncology</i> , 2020, 10, 303.	1.3	5
13133	Integrative Analysis of Breast Cancer Cells Reveals an Epithelial-Mesenchymal Transition Role in Adaptation to Acidic Microenvironment. <i>Frontiers in Oncology</i> , 2020, 10, 304.	1.3	28
13134	Analysis of Dual Class I Histone Deacetylase and Lysine Demethylase Inhibitor Domatinostat (4SC-202) on Growth and Cellular and Genomic Landscape of Atypical Teratoid/Rhabdoid. <i>Cancers</i> , 2020, 12, 756.	1.7	25
13135	Genome-wide identification of lncRNAs during hickory ( <i>Carya cathayensis</i> ) flowering. <i>Functional and Integrative Genomics</i> , 2020, 20, 591-607.	1.4	9
13136	miR-504 expression level is increased in multiple sclerosis patients responder to interferon-beta. <i>Journal of Neuroimmunology</i> , 2020, 342, 577212.	1.1	6
13137	Oral lichen planus interactome reveals CXCR4 and CXCL12 as candidate therapeutic targets. <i>Scientific Reports</i> , 2020, 10, 5454.	1.6	6
13138	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. <i>Scientific Reports</i> , 2020, 10, 5285.	1.6	36
13139	miR-128-3p Is a Novel Regulator of Vascular Smooth Muscle Cell Phenotypic Switch and Vascular Diseases. <i>Circulation Research</i> , 2020, 126, e120-e135.	2.0	88
13140	Bioinformatics analysis of vascular RNA-seq data revealed hub genes and pathways in a novel Tibetan minipig atherosclerosis model induced by a high fat/cholesterol diet. <i>Lipids in Health and Disease</i> , 2020, 19, 54.	1.2	23
13141	Linked Data Visualization: Techniques, Tools, and Big Data. <i>Synthesis Lectures on the Semantic Web: Theory and Technology</i> , 2020, 10, 1-157.	5.0	31
13142	Regulatory Mechanism of ITGBL1 in the Metastasis of Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 259.	1.3	9
13143	Dynamic Transcriptional Responses to Injury of Regenerative and Non-regenerative Cardiomyocytes Revealed by Single-Nucleus RNA Sequencing. <i>Developmental Cell</i> , 2020, 53, 102-116.e8.	3.1	95
13144	Structural insights into the potential changes in receptor binding site found in the 1998â€“2018 influenza B/Yamagata hemagglutinin: A putative correlation between receptor binding site structural variability and seasonal infection. <i>Journal of Molecular Graphics and Modelling</i> , 2020, 97, 107580.	1.3	0
13145	Implication of the gut microbiome composition of type 2 diabetic patients from northern China. <i>Scientific Reports</i> , 2020, 10, 5450.	1.6	113
13146	Distinct physiological and transcriptional responses of leaves of paper mulberry ( <i>Broussonetia Tj</i> ETQq0 0 0 rgBT /Qverlock 10 Tf 50 18). <i>Journal of Molecular Graphics and Modelling</i> , 2020, 97, 107580.	1.4	12
13147	Genome-Scale Metabolic Modeling of Glioblastoma Reveals Promising Targets for Drug Development. <i>Frontiers in Genetics</i> , 2020, 11, 381.	1.1	22
13148	Structural Genomics of SARS-CoV-2 Indicates Evolutionary Conserved Functional Regions of Viral Proteins. <i>Viruses</i> , 2020, 12, 360.	1.5	206
13149	Inducible Antibacterial Activity in the Bacillales by Triphenyl Tetrazolium Chloride. <i>Scientific Reports</i> , 2020, 10, 5563.	1.6	3

#	ARTICLE	IF	CITATIONS
13150	Aldoxime Dehydratase Mutants as Improved Biocatalysts for a Sustainable Synthesis of Biorenewables-Based 2-Furionitrile. <i>Catalysts</i> , 2020, 10, 362.	1.6	12
13151	Systems Pharmacology-Based Strategy to Investigate Pharmacological Mechanisms of Radix Puerariae for Treatment of Hypertension. <i>Frontiers in Pharmacology</i> , 2020, 11, 345.	1.6	18
13152	Antibacterial effects of nanopillar surfaces are mediated by cell impedance, penetration and induction of oxidative stress. <i>Nature Communications</i> , 2020, 11, 1626.	5.8	235
13153	Visualizing metabolic network dynamics through time-series metabolomic data. <i>BMC Bioinformatics</i> , 2020, 21, 130.	1.2	13
13154	Dysidealactams and Dysidealactones: Sesquiterpene Glycinyl-Lactams, Imides, and Lactones from a <i>Dysidea</i> sp. Marine Sponge Collected in Southern Australia. <i>Journal of Natural Products</i> , 2020, 83, 1577-1584.	1.5	16
13155	Phenotypic Screening of Chemical Libraries Enriched by Molecular Docking to Multiple Targets Selected from Glioblastoma Genomic Data. <i>ACS Chemical Biology</i> , 2020, 15, 1424-1444.	1.6	4
13156	Sub-region-Specific Optic Nerve Head Glial Activation in Glaucoma. <i>Molecular Neurobiology</i> , 2020, 57, 2620-2638.	1.9	23
13157	Analysis of Soybean Long Non-Coding RNAs Reveals a Subset of Small Peptide-Coding Transcripts. <i>Plant Physiology</i> , 2020, 182, 1359-1374.	2.3	46
13158	Soil Water Contents Control the Responses of Dissolved Nitrogen Pools and Bacterial Communities to Freeze-Thaw in Temperate Soils. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	5
13159	Identification of Key Genes and Pathways for Enchondromas by Bioinformatics Analysis. <i>Dose-Response</i> , 2020, 18, 155932582090753.	0.7	0
13160	A Refined 3-in-1 Fused Protein Similarity Measure: Application in Threshold-Free Hub Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 192-206.	1.9	5
13161	Identification of a Plasma MicroRNA Profile Associated With Venous Thrombosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 1392-1399.	1.1	21
13162	Genes associated with inflammation may serve as biomarkers for the diagnosis of coronary artery disease and ischaemic stroke. <i>Lipids in Health and Disease</i> , 2020, 19, 37.	1.2	15
13163	Up-regulation of microRNA-335-5p reduces inflammation via negative regulation of the TPX2-mediated AKT/GSK3 $\beta$ signaling pathway in a chronic rhinosinusitis mouse model. <i>Cellular Signalling</i> , 2020, 70, 109596.	1.7	21
13164	Identification of the core ontologies and signature genes of polycystic ovary syndrome (PCOS): A bioinformatics analysis. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100304.	1.9	13
13165	Fast and Robust Proteome Screening Platform Identifies Neutrophil Extracellular Trap Formation in the Lung in Response to Cobalt Ferrite Nanoparticles. <i>ACS Nano</i> , 2020, 14, 4096-4110.	7.3	20
13166	Forecasting risk gene discovery in autism with machine learning and genome-scale data. <i>Scientific Reports</i> , 2020, 10, 4569.	1.6	32
13167	Hierarchy and levels: analysing networks to study mechanisms in molecular biology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190320.	1.8	10

#	ARTICLE	IF	CITATIONS
13168	PANOMICS meets germplasm. <i>Plant Biotechnology Journal</i> , 2020, 18, 1507-1525.	4.1	78
13169	&lt;p&gt;Weighted Gene Coexpression Network Analysis Identifies Specific Modules and Hub Genes Related to Major Depression&lt;/p&gt;. <i>Neuropsychiatric Disease and Treatment</i> , 2020, Volume 16, 703-713.	1.0	12
13170	Plasma proteomic profiling and pathway analysis of normal and overconditioned dairy cows during the transition from late pregnancy to early lactation. <i>Journal of Dairy Science</i> , 2020, 103, 4806-4821.	1.4	13
13171	Adding Appropriate Fiber in Diet Increases Diversity and Metabolic Capacity of Distal Gut Microbiota Without Altering Fiber Digestibility and Growth Rate of Finishing Pig. <i>Frontiers in Microbiology</i> , 2020, 11, 533.	1.5	39
13172	Malignancy Grade-Dependent Mapping of Metabolic Landscapes in Human Urothelial Bladder Cancer: Identification of Novel, Diagnostic, and Druggable Biomarkers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1892.	1.8	7
13173	Comparative Transcriptome-Based Mining and Expression Profiling of Transcription Factors Related to Cold Tolerance in Peanut. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1921.	1.8	29
13174	Comparative functional genomics analysis of cytochrome P450 gene superfamily in wheat and maize. <i>BMC Plant Biology</i> , 2020, 20, 93.	1.6	52
13175	The influence of hypoxia on the prostate cancer proteome. <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, 980-993.	1.4	11
13176	Fetal monocytes possess increased metabolic capacity and replace primitive macrophages in tissue macrophage development. <i>EMBO Journal</i> , 2020, 39, e103205.	3.5	28
13177	Identification of Prognostic Genes in Leiomyosarcoma by Gene Co-Expression Network Analysis. <i>Frontiers in Genetics</i> , 2020, 10, 1408.	1.1	4
13178	WGCNA Co-Expression Network Analysis Reveals ILF3-AS1 Functions as a CeRNA to Regulate PTBP1 Expression by Sponging miR-29a in Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 39.	1.1	24
13179	Ecological Differentiation in Two Major Freshwater Bacterial Taxa Along Environmental Gradients. <i>Frontiers in Microbiology</i> , 2020, 11, 154.	1.5	17
13180	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. <i>Cancers</i> , 2020, 12, 458.	1.7	5
13181	Comparative Transcriptomic Response of Two Pinus Species to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2020, 11, 204.	0.9	19
13182	A Comprehensive Transcriptomics Analysis Reveals Long Non-Coding RNA to Be Involved in the Key Metabolic Pathway in Response to Waterlogging Stress in Maize. <i>Genes</i> , 2020, 11, 267.	1.0	27
13183	Shared Molecular Genetic Mechanisms Underlie Endometriosis and Migraine Comorbidity. <i>Genes</i> , 2020, 11, 268.	1.0	53
13184	Investigation of a Novel Salt Stress-Responsive Pathway Mediated by Arabidopsis DEAD-Box RNA Helicase Gene <i>AtRH17</i> Using RNA-Seq Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1595.	1.8	15
13185	Local Phenomena Shape Backyard Soil Metabolite Composition. <i>Metabolites</i> , 2020, 10, 86.	1.3	10

#	ARTICLE	IF	CITATIONS
13186	Identification of rare variants in novel candidate genes in pulmonary atresia patients by next generation sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 381-392.	1.9	10
13187	Genetic diversity and in silico evidence of target-site mutation in the EPSPS gene in endowing glyphosate resistance in <i>Eleusine indica</i> (L.) from Malaysia. <i>Pesticide Biochemistry and Physiology</i> , 2020, 165, 104556.	1.6	11
13188	What Makes Cornea Immunologically Unique and Privileged? Mechanistic Clues from a High-Resolution Proteomic Landscape of the Human Cornea. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 129-139.	1.0	14
13189	Development and validation of hub genes for lymph node metastasis in patients with prostate cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4402-4414.	1.6	19
13190	LncRNA profile study reveals a seven-lncRNA signature predicts the prognosis of patients with colorectal cancer. <i>Biomarker Research</i> , 2020, 8, 8.	2.8	21
13191	Curcumin Enhances Radiosensitization of Nasopharyngeal Carcinoma via Mediating Regulation of Tumor Stem-like Cells by a CircRNA Network. <i>Journal of Cancer</i> , 2020, 11, 2360-2370.	1.2	31
13192	Impacts of the Zhe-Min Coastal Current on the biogeographic pattern of microbial eukaryotic communities. <i>Progress in Oceanography</i> , 2020, 183, 102309.	1.5	13
13193	Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. <i>Journal of Biological Chemistry</i> , 2020, 295, 4194-4211.	1.6	48
13194	Predicted Drosophila Interactome Resource and web tool for functional interpretation of differentially expressed genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	8
13195	KANK2 Links $\beta$ 5 Focal Adhesions to Microtubules and Regulates Sensitivity to Microtubule Poisons and Cell Migration. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 125.	1.8	22
13196	Whole Transcriptome Analysis of Mesenchyme Tissue in Sika Deer Antler Revealed the CeRNAs Regulatory Network Associated With Antler Development. <i>Frontiers in Genetics</i> , 2019, 10, 1403.	1.1	16
13197	In silico Metabolic Pathway Analysis Identifying Target Against Leishmaniasis – A Kinetic Modeling Approach. <i>Frontiers in Genetics</i> , 2020, 11, 179.	1.1	16
13198	Co-Expression Network Analysis of Spleen Transcriptome in Rock Bream ( <i>Oplegnathus fasciatus</i> ) Naturally Infected with Rock Bream Iridovirus (RBIV). <i>International Journal of Molecular Sciences</i> , 2020, 21, 1707.	1.8	17
13199	Distinct Characteristics of Bacterial Community in the Soil of Nanshazhou Island, South China Sea. <i>Current Microbiology</i> , 2020, 77, 1292-1300.	1.0	3
13200	Epitranscriptomic 5-Methylcytosine Profile in PM2.5-induced Mouse Pulmonary Fibrosis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 41-51.	3.0	41
13201	Integrative transcriptomics and proteomics analysis constructs a new molecular model for ovule abortion in the female-sterile line of <i>Pinus tabulaeformis</i> Carr.. <i>Plant Science</i> , 2020, 294, 110462.	1.7	8
13202	<i>Sonneratia apetala</i> introduction alters methane cycling microbial communities and increases methane emissions in mangrove ecosystems. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107775.	4.2	42
13203	Functionally Enigmatic Genes in Cancer: Using TCGA Data to Map the Limitations of Annotations. <i>Scientific Reports</i> , 2020, 10, 4106.	1.6	14



#	ARTICLE	IF	CITATIONS
13204	Perturbations of pathway co-expression network identify a core network in metastatic breast cancer. <i>Computational Biology and Chemistry</i> , 2020, 87, 107313.	1.1	6
13205	A circular RNA map for human induced pluripotent stem cells of foetal origin. <i>EBioMedicine</i> , 2020, 57, 102848.	2.7	9
13206	Genome-wide discovery of microsatellite markers and, population genetic diversity inferences revealed high anthropogenic pressure on endemic populations of <i>Trillium govanianum</i> . <i>Industrial Crops and Products</i> , 2020, 154, 112698.	2.5	12
13207	Exploration of gene expression profiles and immune microenvironment between high and low tumor mutation burden groups in prostate cancer. <i>International Immunopharmacology</i> , 2020, 86, 106709.	1.7	23
13208	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. <i>Molecular Cell</i> , 2020, 79, 521-534.e15.	4.5	110
13209	Uncloaking lncRNA-mediated gene expression as a potential regulator of CMS in cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.3	20
13210	Large-scale metabolic interaction network of the mouse and human gut microbiota. <i>Scientific Data</i> , 2020, 7, 204.	2.4	12
13211	Depolarization-dependent Induction of Site-specific Changes in Sialylation on N-linked Glycoproteins in Rat Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1418-1435.	2.5	18
13212	Time-resolved mRNA and miRNA expression profiling reveals crucial coregulation of molecular pathways involved in epithelial-pneumococcal interactions. <i>Immunology and Cell Biology</i> , 2020, 98, 726-742.	1.0	3
13213	Two Gene Set Variation Index as Biomarker of Bacterial and Fungal Sepsis. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	4
13214	Proteome Analysis Reveals Syndecan 1 Regulates Porcine Sapelovirus Replication. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4386.	1.8	1
13215	Molecular Pathways of Colon Inflammation Induced by Cancer Immunotherapy. <i>Cell</i> , 2020, 182, 655-671.e22.	13.5	259
13216	Network pharmacology-based prediction of the active ingredients and mechanism of Shen Gui capsule for application to coronary heart disease. <i>Computers in Biology and Medicine</i> , 2020, 122, 103825.	3.9	8
13217	Identification of epithelial-mesenchymal transition-related circRNA-miRNA-mRNA ceRNA regulatory network in breast cancer. <i>Pathology Research and Practice</i> , 2020, 216, 153088.	1.0	11
13218	Moving Pieces in a Cellular Puzzle: A Cryptic Peptide from the Scorpion Toxin Ts14 Activates AKT and ERK Signaling and Decreases Cardiac Myocyte Contractility via Dephosphorylation of Phospholamban. <i>Journal of Proteome Research</i> , 2020, 19, 3467-3477.	1.8	4
13219	The bottromycin epimerase BotH defines a group of atypical $\beta$ -hydrolase-fold enzymes. <i>Nature Chemical Biology</i> , 2020, 16, 1013-1018.	3.9	18
13220	RNA processing genes characterize RNA splicing and further stratify colorectal cancer. <i>Cell Proliferation</i> , 2020, 53, e12861.	2.4	4
13221	Identification of Immune-Related Genes Contributing to the Development of Glioblastoma Using Weighted Gene Co-expression Network Analysis. <i>Frontiers in Immunology</i> , 2020, 11, 1281.	2.2	40



#	ARTICLE	IF	CITATIONS
13222	Microbiomes of Caribbean Octocorals Vary Over Time but Are Resistant to Environmental Change. <i>Frontiers in Microbiology</i> , 2020, 11, 1272.	1.5	24
13223	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. <i>Frontiers in Physiology</i> , 2020, 11, 862.	1.3	10
13224	Multi-trait analysis for genome-wide association study of five psychiatric disorders. <i>Translational Psychiatry</i> , 2020, 10, 209.	2.4	132
13225	Genome-wide genotyping elucidates the geographical diversification and dispersal of the polyploid and clonally propagated yam ( <i>Dioscorea alata</i> ). <i>Annals of Botany</i> , 2020, 126, 1029-1038.	1.4	30
13226	Temporal Variability and Ecological Interactions of Parasitic Marine Syndiniales in Coastal Protist Communities. <i>MSphere</i> , 2020, 5, .	1.3	37
13227	CUL1-Mediated Organelle Fission Pathway Inhibits the Development of Chronic Obstructive Pulmonary Disease. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-11.	0.7	8
13228	A Comprehensive Network Pharmacology-Based Strategy to Investigate Multiple Mechanisms of HeChan Tablet on Lung Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-17.	0.5	7
13229	Genome-wide identification and comparison of differentially expressed profiles of miRNAs and lncRNAs with associated ceRNA networks in the gonads of Chinese soft-shelled turtle, <i>Pelodiscus sinensis</i> . <i>BMC Genomics</i> , 2020, 21, 443.	1.2	15
13230	Identification of Key Players Involved in CoCl <sub>2</sub> Hypoxia Induced Pulmonary Artery Hypertension in vitro. <i>Frontiers in Genetics</i> , 2020, 11, 232.	1.1	11
13231	The Construction and Comprehensive Prognostic Analysis of the lncRNA-Associated Competitive Endogenous RNAs Network in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 583.	1.1	17
13232	TP53-Deficient Angiosarcoma Expression Profiling in Rat Model. <i>Cancers</i> , 2020, 12, 1525.	1.7	3
13233	Targeted Isolation of Rubrolides from the New Zealand Marine Tunicate <i>Synoicum kuranui</i> . <i>Marine Drugs</i> , 2020, 18, 337.	2.2	9
13235	Identifying interactive biological pathways associated with reading disability. <i>Brain and Behavior</i> , 2020, 10, e01735.	1.0	7
13236	Global correlation analysis for miRNA and protein expression profiles in human peripheral blood mononuclear cells. <i>Molecular Biology Reports</i> , 2020, 47, 5295-5304.	1.0	0
13237	Health Effects of Trimellitic Anhydride Occupational Exposure: Insights from Animal Models and Immunosurveillance Programs. <i>Clinical Reviews in Allergy and Immunology</i> , 2020, 59, 61-77.	2.9	2
13238	Quantitative Proteomics of Maize Roots Treated with a Protein Hydrolysate: A Comparative Study with Transcriptomics Highlights the Molecular Mechanisms Responsive to Biostimulants. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7541-7553.	2.4	33
13239	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020, 583, 271-276.	13.7	104
13240	Mechanistic insights on the mode of action of an antiproliferative thiosemicarbazone-nickel complex revealed by an integrated chemogenomic profiling study. <i>Scientific Reports</i> , 2020, 10, 10524.	1.6	17

#	ARTICLE	IF	CITATIONS
13241	OncotRF: an online resource for exploration of tRNA-derived fragments in human cancers. <i>RNA Biology</i> , 2020, 17, 1081-1091.	1.5	39
13242	Mechanistic Modeling and Multiscale Applications for Precision Medicine: Theory and Practice. <i>Network and Systems Medicine</i> , 2020, 3, 36-56.	2.7	11
13243	The bacterial communities of <i>Tuber aestivum</i> : preliminary investigations in Molise region, Southern Italy. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	11
13244	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. <i>PLoS ONE</i> , 2020, 15, e0233311.	1.1	7
13245	Bayesian networks established functional differences between breast cancer subtypes. <i>PLoS ONE</i> , 2020, 15, e0234752.	1.1	5
13246	Transcriptomic Analysis Reveals the Involvement of lncRNA and miRNA-mRNA Networks in Hair Follicle Induction in Aohan Fine Wool Sheep Skin. <i>Frontiers in Genetics</i> , 2020, 11, 590.	1.1	16
13247	The Delivery of Multipotent Adult Progenitor Cells to Extended Criteria Human Donor Livers Using Normothermic Machine Perfusion. <i>Frontiers in Immunology</i> , 2020, 11, 1226.	2.2	40
13248	Impacts of Anthropogenic Pollutants on Benthic Prokaryotic Communities in Mediterranean Touristic Ports. <i>Frontiers in Microbiology</i> , 2020, 11, 1234.	1.5	15
13249	Ridge Tillage Improves Soil Properties, Sustains Diazotrophic Communities, and Enhances Extensively Cooperative Interactions Among Diazotrophs in a Clay Loam Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 1333.	1.5	8
13250	Human Cardiac Mesenchymal Stromal Cells From Right and Left Ventricles Display Differences in Number, Function, and Transcriptomic Profile. <i>Frontiers in Physiology</i> , 2020, 11, 604.	1.3	5
13251	Identification of Novel microRNA Profiles Dysregulated in Plasma and Tissue of Abdominal Aortic Aneurysm Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4600.	1.8	20
13252	A Metabolomics Exploration of the Sexual Phase in the Marine Diatom <i>Pseudo-nitzschia multistriata</i> . <i>Marine Drugs</i> , 2020, 18, 313.	2.2	16
13253	Corynanthean-Epicatechin Flavoalkaloids from <i>Corynanthe pachyceras</i> . <i>Molecules</i> , 2020, 25, 2654.	1.7	8
13254	IFN-I Independent Antiviral Immune Response to Vesicular Stomatitis Virus Challenge in Mouse Brain. <i>Vaccines</i> , 2020, 8, 326.	2.1	8
13255	Histone Acetyltransferase MOF Blocks Acquisition of Quiescence in Ground-State ESCs through Activating Fatty Acid Oxidation. <i>Cell Stem Cell</i> , 2020, 27, 441-458.e10.	5.2	37
13256	Molecular dissection of CRC primary tumors and their matched liver metastases reveals critical role of immune microenvironment, EMT and angiogenesis in cancer metastasis. <i>Scientific Reports</i> , 2020, 10, 10725.	1.6	21
13257	Autophagy Plays Prominent Roles in Amino Acid, Nucleotide, and Carbohydrate Metabolism during Fixed-Carbon Starvation in Maize. <i>Plant Cell</i> , 2020, 32, 2699-2724.	3.1	53
13258	Secondary Metabolism in the Gill Microbiota of Shipworms (Teredinidae) as Revealed by Comparison of Metagenomes and Nearly Complete Symbiont Genomes. <i>MSystems</i> , 2020, 5, .	1.7	15

#	ARTICLE	IF	CITATIONS
13259	Identification of Key Differentially Expressed Transcription Factors in Glioblastoma. <i>Journal of Oncology</i> , 2020, 2020, 1-9.	0.6	10
13260	&lt;p&gt;Proteomics of Sentinel Lymph Nodes in Early Breast Cancer for Identification of Thymidylate Synthase as a Potential Biomarker to Flag Metastasis: A Preliminary Study&lt;/p&gt;. <i>Cancer Management and Research</i> , 2020, Volume 12, 4841-4854.	0.9	5
13261	Circulating microRNA Signature Associated to Interstitial Lung Abnormalities in Respiratory Asymptomatic Subjects. <i>Cells</i> , 2020, 9, 1556.	1.8	14
13262	Metabolomic and Gene Expression Studies Reveal the Diversity, Distribution and Spatial Regulation of the Specialized Metabolism of YacÃ³n ( <i>Smallanthus sonchifolius</i> , Asteraceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 4555.	1.8	13
13263	Dysregulation of microRNA Modulatory Network in Abdominal Aortic Aneurysm. <i>Journal of Clinical Medicine</i> , 2020, 9, 1974.	1.0	14
13264	Neonatal Exposure to Commensal-Bacteria-Derived Antigens Directs Polysaccharide-Specific B-1 B Cell Repertoire Development. <i>Immunity</i> , 2020, 53, 172-186.e6.	6.6	50
13265	Identification of dihydroorotate dehydrogenase as a protein target of ginkgolic acid by molecular docking and dynamics. <i>Journal of Molecular Structure</i> , 2020, 1220, 128692.	1.8	5
13266	Integrated Proteomics and Metabolomics Analysis Highlights Correlative Metabolite-Protein Networks in Soybean Seeds Subjected to Warm-Water Soaking. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8057-8067.	2.4	15
13267	Linking the association between circRNAs and Alzheimerâ€™s disease progression by multi-tissue circular RNA characterization. <i>RNA Biology</i> , 2020, 17, 1789-1797.	1.5	30
13268	Multi-Habitat Radiomics Unravels Distinct Phenotypic Subtypes of Glioblastoma with Clinical and Genomic Significance. <i>Cancers</i> , 2020, 12, 1707.	1.7	18
13269	Genome-wide R-loop Landscapes during Cell Differentiation and Reprogramming. <i>Cell Reports</i> , 2020, 32, 107870.	2.9	51
13270	Bioinformatic analysis reveals that the OAS family may play an important role in lupus nephritis. <i>Journal of the National Medical Association</i> , 2020, 112, 567-577.	0.6	6
13271	Dynamics of active potential bacterial and fungal interactions in the assimilation of acidobacterial EPS in soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107916.	4.2	15
13272	Metabolite Profiling of Javanese Ginger <i>Zingiber purpureum</i> and Identification of Antiseizure Metabolites via a Low-Cost Open-Source Zebrafish Bioassay-Guided Isolation. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7904-7915.	2.4	12
13273	Positive transcriptional response on inflammation and joint remodelling influenced by physical exercise in proteoglycan-induced arthritis: An animal study. <i>Bone and Joint Research</i> , 2020, 9, 36-48.	1.3	9
13274	Expression Patterns of Immune Genes Reveal Heterogeneous Subtypes of High-Risk Neuroblastoma. <i>Cancers</i> , 2020, 12, 1739.	1.7	10
13275	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
13276	Proteomics of SARS-CoV-2-infected host cells reveals therapy targets. <i>Nature</i> , 2020, 583, 469-472.	13.7	841

#	ARTICLE	IF	CITATIONS
13277	Network of clinically-relevant lncRNAs-mRNAs associated with prognosis of hepatocellular carcinoma patients. <i>Scientific Reports</i> , 2020, 10, 11124.	1.6	10
13278	Natural-like products as potential SARS-CoV-2 M <sup>pro</sup> inhibitors: <i>in-silico</i> drug discovery. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 5722-5734.	2.0	68
13279	Subspecies Niche Specialization in the Oral Microbiome Is Associated with Nasopharyngeal Carcinoma Risk. <i>MSystems</i> , 2020, 5, .	1.7	21
13280	Bioinformatical Analysis of miRNA-mRNA Interaction Network Underlying Macrophage Aging and Cholesterol-Responsive Difference between Young and Aged Macrophages. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	2
13281	A systems biology-driven approach to construct a comprehensive protein interaction network of influenza A virus with its host. <i>BMC Infectious Diseases</i> , 2020, 20, 480.	1.3	7
13282	Microbial communities from arid environments on a global scale. A systematic review. <i>Biological Research</i> , 2020, 53, 29.	1.5	30
13283	New Insight into the Composition of Wheat Seed Microbiota. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4634.	1.8	39
13284	Integrative Proteomic Characterization of Human Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 245-261.e17.	13.5	300
13285	Proteogenomics of Non-smoking Lung Cancer in East Asia Delineates Molecular Signatures of Pathogenesis and Progression. <i>Cell</i> , 2020, 182, 226-244.e17.	13.5	178
13286	ProtExA: A tool for post-processing proteomics data providing differential expression metrics, co-expression networks and functional analytics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1695-1703.	1.9	5
13287	An integration analysis of mRNAs and miRNAs microarray data to identify key regulators for ovarian endometriosis based on competing endogenous RNAs. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2020, 252, 468-475.	0.5	3
13288	Single cell sequencing revealed the underlying pathogenesis of the development of osteoarthritis. <i>Gene</i> , 2020, 757, 144939.	1.0	21
13289	DL0410 attenuates oxidative stress and neuroinflammation via BDNF/TrkB/ERK/CREB and Nrf2/HO-1 activation. <i>International Immunopharmacology</i> , 2020, 86, 106729.	1.7	36
13290	Adaptation of plasticity to projected maximum temperatures and across climatically defined bioregions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17112-17121.	3.3	44
13291	Network pharmacology and molecular docking analysis on molecular targets and mechanisms of Huashi Baidu formula in the treatment of COVID-19. <i>Drug Development and Industrial Pharmacy</i> , 2020, 46, 1345-1353.	0.9	153
13292	Diversity and community structure of ericoid mycorrhizal fungi in European bogs and heathlands across a gradient of nitrogen deposition. <i>New Phytologist</i> , 2020, 228, 1640-1651.	3.5	26
13293	Detection and integrated analysis of lncRNA and mRNA relevant to plateau adaptation of Yak. <i>Reproduction in Domestic Animals</i> , 2020, 55, 1461-1469.	0.6	8
13294	Single-cell RNA sequencing reveals profibrotic roles of distinct epithelial and mesenchymal lineages in pulmonary fibrosis. <i>Science Advances</i> , 2020, 6, eaba1972.	4.7	571

#	ARTICLE	IF	CITATIONS
13295	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. <i>MBio</i> , 2020, 11, .	1.8	27
13296	Protein Interactions of the Mechanosensory Proteins Wsc2 and Wsc3 for Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3121-3135.	0.8	4
13297	Novel Prognostic Factor for Uveal Melanoma: Bioinformatics Analysis of Three Independent Cohorts. <i>Anticancer Research</i> , 2020, 40, 3839-3846.	0.5	7
13298	Identification of miRNA Master Regulators in Breast Cancer. <i>Cells</i> , 2020, 9, 1610.	1.8	20
13299	Resilience and technological diversity in smart homes. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2020, 11, 5825-5843.	3.3	2
13300	Rare Genetic Diseases: Nature's Experiments on Human Development. <i>IScience</i> , 2020, 23, 101123.	1.9	35
13301	Prognostic alternative mRNA splicing signatures and associated splicing factors in acute myeloid leukemia. <i>Neoplasia</i> , 2020, 22, 447-457.	2.3	12
13302	Shotgun metagenomics of dust microbiome from flight deck and cabin in civil aviation aircraft. <i>Indoor Air</i> , 2020, 30, 1199-1212.	2.0	19
13303	Systems biology of responses to simultaneous copper and iron deficiency in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 103, 2119-2138.	2.8	12
13304	A Network Pharmacology Approach to Explore the Mechanisms of Shugan Jianpi Formula in Liver Fibrosis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	8
13305	Reducing the nicotine content of tobacco by grafting with eggplant. <i>BMC Plant Biology</i> , 2020, 20, 285.	1.6	6
13306	Immune-related genes in tumor-specific CD4+ and CD8+ T cells in colon cancer. <i>BMC Cancer</i> , 2020, 20, 585.	1.1	17
13307	Low UV-C stress modulates <i>Chlamydomonas reinhardtii</i> biomass composition and oxidative stress response through proteomic and metabolomic changes involving novel signalers and effectors. <i>Biotechnology for Biofuels</i> , 2020, 13, 110.	6.2	14
13308	The benefits of smoking cessation on survival in cancer patients by integrative analysis of multi-omics data. <i>Molecular Oncology</i> , 2020, 14, 2069-2080.	2.1	9
13309	Cooperative binding of transcription factors in the human genome. <i>Genomics</i> , 2020, 112, 3427-3434.	1.3	17
13310	Morphological and metabolic profiling of a tropical-adapted potato association panel subjected to water recovery treatment reveals new insights into plant vigor. <i>Plant Journal</i> , 2020, 103, 2193-2210.	2.8	10
13311	Enhancing and Complementary Mechanisms of Synergistic Action of <i>Acori Tatarinowii</i> Rhizoma and <i>Codonopsis Radix</i> for Alzheimer's Disease Based on Systems Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-26.	0.5	4
13312	Exploring TCGA database for identification of potential prognostic genes in stomach adenocarcinoma. <i>Cancer Cell International</i> , 2020, 20, 264.	1.8	27

#	ARTICLE	IF	CITATIONS
13313	Drosophila models of pathogenic copy-number variant genes show global and non-neuronal defects during development. <i>PLoS Genetics</i> , 2020, 16, e1008792.	1.5	9
13314	Construction, analysis and validation of co-expression network to understand stress adaptation in <i>Deinococcus radiodurans</i> R1. <i>PLoS ONE</i> , 2020, 15, e0234721.	1.1	3
13315	Improving Proteoform Identifications in Complex Systems Through Integration of Bottom-Up and Top-Down Data. <i>Journal of Proteome Research</i> , 2020, 19, 3510-3517.	1.8	25
13316	Identification of Key Genes and Long Noncoding RNA-Associated Competing Endogenous RNA (ceRNA) Networks in Early-Onset Preeclampsia. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	16
13317	Redox States of Protein Cysteines in Pathways of Protein Turnover and Cytoskeleton Dynamics Are Changed with Aging and Reversed by Slc7a11 Restoration in Mouse Lung Fibroblasts. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-17.	1.9	10
13318	Integrative analyses of gene expression profile reveal potential crucial roles of mitotic cell cycle and microtubule cytoskeleton in pulmonary artery hypertension. <i>BMC Medical Genomics</i> , 2020, 13, 86.	0.7	16
13319	Identification of long noncoding RNA RP11-89K21.1 and RP11-357H14.17 as prognostic signature of endometrial carcinoma via integrated bioinformatics analysis. <i>Cancer Cell International</i> , 2020, 20, 268.	1.8	13
13320	System-wide biochemical analysis reveals ozonide antimalarials initially act by disrupting <i>Plasmodium falciparum</i> haemoglobin digestion. <i>PLoS Pathogens</i> , 2020, 16, e1008485.	2.1	24
13321	A Transcriptional Regulatory Map of Iron Homeostasis Reveals a New Control Circuit for Capsule Formation in <i>Cryptococcus neoformans</i> . <i>Genetics</i> , 2020, 215, 1171-1189.	1.2	13
13322	l-Arginine supplementation of gilts during early gestation modulates energy sensitive pathways in pig conceptuses. <i>Molecular Reproduction and Development</i> , 2020, 87, 819-834.	1.0	4
13323	Pathways involved in viral oncogenesis: New perspectives from virus-host protein interactomics. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165885.	1.8	15
13324	The Immunoglobulin Superfamily Receptome Defines Cancer-Relevant Networks Associated with Clinical Outcome. <i>Cell</i> , 2020, 182, 329-344.e19.	13.5	66
13325	Age-Induced Reduction in Human Lipolysis: A Potential Role for Adipocyte Noradrenaline Degradation. <i>Cell Metabolism</i> , 2020, 32, 1-3.	7.2	42
13326	Reservoirs of antimicrobial resistance genes in retail raw milk. <i>Microbiome</i> , 2020, 8, 99.	4.9	47
13327	Changes of the human skin microbiota upon chronic exposure to polycyclic aromatic hydrocarbon pollutants. <i>Microbiome</i> , 2020, 8, 100.	4.9	58
13328	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. <i>Scientific Reports</i> , 2020, 10, 10882.	1.6	9
13329	Identification of hub genes involved in apparent metabolizable energy of chickens. <i>Animal Biotechnology</i> , 2022, 33, 242-249.	0.7	3
13330	Association between the body weight of growing pigs and the functional capacity of their gut microbiota. <i>Animal Science Journal</i> , 2020, 91, e13418.	0.6	27



#	ARTICLE	IF	CITATIONS
13331	UFO: A tool for unifying biomedical ontology-based semantic similarity calculation, enrichment analysis and visualization. <i>PLoS ONE</i> , 2020, 15, e0235670.	1.1	9
13332	Cellular Importin- $\beta$ 3 Expression Dynamics in the Lung Regulate Antiviral Response Pathways against Influenza A Virus Infection. <i>Cell Reports</i> , 2020, 31, 107549.	2.9	11
13333	The Mammalian Crumbs Complex Defines a Distinct Polarity Domain Apical of Epithelial Tight Junctions. <i>Current Biology</i> , 2020, 30, 2791-2804.e6.	1.8	65
13334	Effects of sulforaphane on the oxidative response, apoptosis, and the transcriptional profile of human stomach mucosa cells in vitro. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2020, 854-855, 503201.	0.9	5
13335	The auxin response factor gene family in wheat ( <i>Triticum aestivum</i> L.): Genome-wide identification, characterization and expression analyses in response to leaf rust. <i>South African Journal of Botany</i> , 2021, 140, 312-325.	1.2	13
13336	Microbiome-guided evaluation of <i>Bacillus subtilis</i> BIOUFLA2 application to reduce mycotoxins in maize kernels. <i>Biological Control</i> , 2020, 150, 104370.	1.4	10
13337	Targeting hub genes and pathways of innate immune response in COVID-19: A network biology perspective. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1-8.	3.6	72
13338	UPLC-MS/MS-based molecular networking and NMR structural determination for the untargeted phytochemical characterization of the fruit of <i>Crescentia cujete</i> (Bignoniaceae). <i>Phytochemistry</i> , 2020, 177, 112438.	1.4	24
13339	Biosynthesis and tissue-specific partitioning of camphor and eugenol in <i>Ocimum kilimandscharicum</i> . <i>Phytochemistry</i> , 2020, 177, 112451.	1.4	7
13340	Feature-Based Molecular Networking Analysis of the Metabolites Produced by <i>In Vitro</i> Solid-State Fermentation Reveals Pathways for the Bioconversion of Epigallocatechin Gallate. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7995-8007.	2.4	23
13341	TMEM16K is an interorganelle regulator of endosomal sorting. <i>Nature Communications</i> , 2020, 11, 3298.	5.8	32
13342	Elongating maize root: zone-specific combinations of polysaccharides from type I and type II primary cell walls. <i>Scientific Reports</i> , 2020, 10, 10956.	1.6	42
13343	Curcuma zedoaria: Potential effect as breast cancer chemotherapeutic agents through CXCR4 inhibition. <i>AIP Conference Proceedings</i> , 2020, , .	0.3	4
13344	Bacterial protein azurin and derived peptides as potential anti-SARS-CoV-2 agents: insights from molecular docking and molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 5706-5721.	2.0	18
13345	Analysis of Medical Data Using Community Detection on Inferred Networks. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3136-3143.	3.9	9
13346	Deciphering the underlying mechanism of Xianlinggubao capsule against osteoporosis by network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 208.	1.2	17
13347	The Effect of Exercise on Gene Expression and Signaling in Mouse Melanoma Tumors. <i>Medicine and Science in Sports and Exercise</i> , 2020, 52, 1485-1494.	0.2	6
13348	Immune and Metabolic Signatures of COVID-19 Revealed by Transcriptomics Data Reuse. <i>Frontiers in Immunology</i> , 2020, 11, 1636.	2.2	104



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13349	Transcriptomic analysis identifies early cellular and molecular events by which estrogen disrupts testis differentiation and causes feminization in <i>Xenopus laevis</i> . <i>Aquatic Toxicology</i> , 2020, 226, 105557.	1.9	9
13350	Meta-analysis of gene expression profiles of lean and obese PCOS to identify differentially regulated pathways and risk of comorbidities. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1735-1745.	1.9	10
13351	Investigation of spectroscopic and proteomic alterations underlying prostate carcinogenesis. <i>Journal of Proteomics</i> , 2020, 226, 103888.	1.2	7
13352	Systems biology comprehensive analysis on breast cancer for identification of key gene modules and genes associated with TNM-based clinical stages. <i>Scientific Reports</i> , 2020, 10, 10816.	1.6	20
13353	Epithelial cadherin regulates transition between the naïve and primed pluripotent states in mouse embryonic stem cells. <i>Stem Cells</i> , 2020, 38, 1292-1306.	1.4	5
13354	Quantitative Translation of Dog-to-Human Aging by Conserved Remodeling of the DNA Methylome. <i>Cell Systems</i> , 2020, 11, 176-185.e6.	2.9	67
13355	Exploring Kawasaki disease-specific hub genes revealing a striking similarity of expression profile to bacterial infections using weighted gene co-expression network analysis (WGCNA) and co-expression modules identification tool (CEMiTool): An integrated bioinformatics and experimental study. <i>Immunobiology</i> , 2020, 225, 151980.	0.8	12
13356	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. <i>Nature Ecology and Evolution</i> , 2020, 4, 1256-1267.	3.4	98
13357	Microbiome and health implications for ethnic minorities after enforced lifestyle changes. <i>Nature Medicine</i> , 2020, 26, 1089-1095.	15.2	48
13358	Identification of genes in hepatocellular carcinoma induced by non-alcoholic fatty liver disease. <i>Cancer Biomarkers</i> , 2020, 29, 69-78.	0.8	12
13359	OASL as a Diagnostic Marker for Influenza Infection Revealed by Integrative Bioinformatics Analysis With XGBoost. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 729.	2.0	7
13360	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. <i>Genes</i> , 2020, 11, 715.	1.0	15
13361	Circular RNA Expression Profiles and the Pro-tumorigenic Function of CircRNA_10156 in Hepatitis B Virus-Related Liver Cancer. <i>International Journal of Medical Sciences</i> , 2020, 17, 1351-1365.	1.1	28
13362	Development and validation of a novel immune-related prognostic model in lung squamous cell carcinoma. <i>International Journal of Medical Sciences</i> , 2020, 17, 1393-1405.	1.1	7
13363	Transcriptome Analysis Reveals the Tolerance Mechanism of Mantis Shrimp ( <i>Oratosquilla</i> ) Tj ETQq0 0 0 rgBT /Overlock 10,7f 50 182	1.6	7
13364	Stratifying cellular metabolism during weight loss: an interplay of metabolism, metabolic flexibility and inflammation. <i>Scientific Reports</i> , 2020, 10, 1651.	1.6	8
13365	Gene expression profile and bioinformatics analysis revealed key molecular characteristics of chordoma before and after TNF- $\alpha$ treatment. <i>Medicine (United States)</i> , 2020, 99, e18790.	0.4	3
13366	SmartGraph: a network pharmacology investigation platform. <i>Journal of Cheminformatics</i> , 2020, 12, 5.	2.8	10

#	ARTICLE	IF	CITATIONS
13367	Unraveling the role of salt-sensitivity genes in obesity with integrated network biology and co-expression analysis. <i>PLoS ONE</i> , 2020, 15, e0228400.	1.1	9
13368	Germ Cell-Specific Gene 1-Like Protein Regulated by Splicing Factor CUGBP Elav-Like Family Member 5 and Primary Bile Acid Biosynthesis are Prognostic in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2019, 10, 1380.	1.1	6
13369	Aggregation of Omic Data and Secretome Prediction Enable the Discovery of Candidate Plasma Biomarkers for Beef Tenderness. <i>International Journal of Molecular Sciences</i> , 2020, 21, 664.	1.8	11
13370	Identifying the key genes and microRNAs in prostate cancer bone metastasis by bioinformatics analysis. <i>FEBS Open Bio</i> , 2020, 10, 674-688.	1.0	33
13371	Keratin 12 mRNA expression could serve as an early corneal marker for limbal explant cultures. <i>Cytotechnology</i> , 2020, 72, 239-245.	0.7	2
13372	Longitudinal metabolomic analysis of plasma enables modeling disease progression in Duchenne muscular dystrophy mouse models. <i>Human Molecular Genetics</i> , 2020, 29, 745-755.	1.4	19
13373	RNA processing machineries in Archaea: the 5'â€²-3'â€² exoribonuclease aRNase J of the Î²-CASP family is engaged specifically with the helicase ASH-Ski2 and the 3'â€²-5'â€² exoribonucleolytic RNA exosome machinery. <i>Nucleic Acids Research</i> , 2020, 48, 3832-3847.	6.5	14
13374	Genome-wide identification of cold responsive transcription factors in <i>Brassica napus</i> L. <i>BMC Plant Biology</i> , 2020, 20, 62.	1.6	24
13375	A systems biology approach for defining the potential molecular framework of idiopathic hypereosinophilic syndrome with cutaneous involvement. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 567-574.	1.0	4
13376	Transcriptome of tambaqui <i>Colossoma macropomum</i> during gonad differentiation: Different molecular signals leading to sex identity. <i>Genomics</i> , 2020, 112, 2478-2488.	1.3	29
13377	IGF1-mediated human embryonic stem cell self-renewal recapitulates the embryonic niche. <i>Nature Communications</i> , 2020, 11, 764.	5.8	41
13378	Integrative Network Analysis of Differentially Methylated and Expressed Genes for Biomarker Identification in Leukemia. <i>Scientific Reports</i> , 2020, 10, 2123.	1.6	21
13379	Transcriptome Analysis of Skeletal Muscle in Pigs with Divergent Residual Feed Intake Phenotypes. <i>DNA and Cell Biology</i> , 2020, 39, 404-416.	0.9	4
13380	Effect of Pepper-Containing Diets on the Diversity and Composition of Gut Microbiome of <i>Drosophila melanogaster</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 945.	1.8	8
13381	Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1053.	1.8	13
13382	Keystone Species and Modularity in Microbial Hydrocarbon Degradation Uncovered by Network Analysis and Association Rule Mining. <i>Microorganisms</i> , 2020, 8, 190.	1.6	5
13383	Functional expression of ZNF467 and PCBP2 supports adipogenic lineage commitment in adipose-derived mesenchymal stem cells. <i>Gene</i> , 2020, 737, 144437.	1.0	6
13384	Comprehensive Analysis of Competitive Endogenous RNAs Network, Being Associated With Esophageal Squamous Cell Carcinoma and Its Emerging Role in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 1474.	1.3	20

#	ARTICLE	IF	CITATIONS
13385	NADH-GOGAT Overexpression Does Not Improve Maize ( <i>Zea mays</i> L.) Performance Even When Pyramiding with NAD-IDH, GDH and GS. <i>Plants</i> , 2020, 9, 130.	1.6	27
13386	Comprehensive Analysis of lncRNA-Mediated ceRNA Crosstalk and Identification of Prognostic Biomarkers in Wilms's Tumor. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	20
13387	Quantitative proteomics analysis reveals important roles of N-glycosylation on ER quality control system for development and pathogenesis in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008355.	2.1	26
13388	A Connected Network of Interacting Proteins Is Involved in Human-Tau Toxicity in <i>Drosophila</i> . <i>Frontiers in Neuroscience</i> , 2020, 14, 68.	1.4	11
13389	Mining the Metabolome and the Agricultural and Pharmaceutical Potential of Sea Foam-Derived Fungi. <i>Marine Drugs</i> , 2020, 18, 128.	2.2	14
13390	Sex differences in text-mined possible adverse drug events associated with drugs for psychosis. <i>Journal of Psychopharmacology</i> , 2020, 34, 532-539.	2.0	13
13391	Chemerin contributes to in vivo adipogenesis in a location-specific manner. <i>PLoS ONE</i> , 2020, 15, e0229251.	1.1	22
13392	Identification of Specific Long Non-Coding Ribonucleic Acid Signatures and Regulatory Networks in Prostate Cancer in Fine-Needle Aspiration Biopsies. <i>Frontiers in Genetics</i> , 2020, 11, 62.	1.1	13
13393	Prognostic Value and Potential Regulatory Mechanism of Alternative Splicing in Geriatric Breast Cancer. <i>Genes</i> , 2020, 11, 200.	1.0	4
13394	RNA-Seq analysis reveals pluripotency-associated genes and their interaction networks in human embryonic stem cells. <i>Computational Biology and Chemistry</i> , 2020, 85, 107239.	1.1	17
13395	Gene interaction network studies to decipher the multi-drug resistance mechanism in <i>Salmonella enterica</i> serovar Typhi CT18 reveal potential drug targets. <i>Microbial Pathogenesis</i> , 2020, 142, 104096.	1.3	43
13396	De novo discovery of metabolic heterogeneity with immunophenotype-guided imaging mass spectrometry. <i>Molecular Metabolism</i> , 2020, 36, 100953.	3.0	32
13397	DNA-PKcs has KU-dependent function in rRNA processing and haematopoiesis. <i>Nature</i> , 2020, 579, 291-296.	13.7	57
13398	Functional omics analyses reveal only minor effects of microRNAs on human somatic stem cell differentiation. <i>Scientific Reports</i> , 2020, 10, 3284.	1.6	9
13399	Pan-cancer mapping of differential protein-protein interactions. <i>Scientific Reports</i> , 2020, 10, 3272.	1.6	36
13400	Phage protein receptors have multiple interaction partners and high expressions. <i>Bioinformatics</i> , 2020, 36, 2975-2979.	1.8	12
13401	Risk of epilepsy in rheumatoid arthritis: a meta-analysis of population based studies and bioinformatics analysis. <i>Therapeutic Advances in Chronic Disease</i> , 2020, 11, 204062231989930.	1.1	3
13402	Impact of mutations in DNA methylation modification genes on genome-wide methylation landscapes and downstream gene activations in pan-cancer. <i>BMC Medical Genomics</i> , 2020, 13, 27.	0.7	17

#	ARTICLE	IF	CITATIONS
13403	<p></p>Identification of Candidate Genes and Therapeutic Agents for Light Chain Amyloidosis Based on Bioinformatics Approach</p>. Pharmacogenomics and Personalized Medicine, 2019, Volume 12, 387-396.	0.4	3
13404	Translation-Targeting RiPPs and Where to Find Them. Frontiers in Genetics, 2020, 11, 226.	1.1	11
13405	Cross-Species Root Transcriptional Network Analysis Highlights Conserved Modules in Response to Nitrate between Maize and Sorghum. International Journal of Molecular Sciences, 2020, 21, 1445.	1.8	6
13406	Identification of Secondary Metabolites from <i>Aspergillus pachycristatus</i> by Untargeted UPLC-ESI-HRMS/MS and Genome Mining. Molecules, 2020, 25, 913.	1.7	4
13407	Genome-Wide Analysis of Gene Expression Provides New Insights into Waterlogging Responses in Barley ( <i>Hordeum vulgare</i> L.). Plants, 2020, 9, 240.	1.6	48
13408	A Clinically and Biologically Based Subclassification of the Idiopathic Inflammatory Myopathies Using Machine Learning. ACR Open Rheumatology, 2020, 2, 158-166.	0.9	12
13409	Analysis of protein missense alterations by combining sequence- and structure- based methods. Molecular Genetics & Genomic Medicine, 2020, 8, e1166.	0.6	25
13410	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. Cell, 2020, 180, 968-983.e24.	13.5	220
13411	TIFAB Regulates USP15-Mediated p53 Signaling during Stressed and Malignant Hematopoiesis. Cell Reports, 2020, 30, 2776-2790.e6.	2.9	27
13412	Gene microarray expression profile analysis of differentially expressed genes of potential alternative pathways in non- small cell lung cancer: In search of biomarkers. Gene Reports, 2020, 19, 100633.	0.4	0
13413	CIP2A Constrains Th17 Differentiation by Modulating STAT3 Signaling. IScience, 2020, 23, 100947.	1.9	12
13414	A network pharmacology approach to investigating the mechanism of Tanshinone IIA for the treatment of liver fibrosis. Journal of Ethnopharmacology, 2020, 253, 112689.	2.0	41
13415	Tridiscorhabdin and Didiscorhabdin, the First Discorhabdin Oligomers Linked with a Direct C- <sup>15</sup> N Bridge from the Sponge <i>Latrunculia biformis</i> Collected from the Deep Sea in Antarctica. Journal of Natural Products, 2020, 83, 706-713.	1.5	17
13416	The distribution and relative ecological roles of autotrophic and heterotrophic diazotrophs in the McMurdo Dry Valleys, Antarctica. FEMS Microbiology Ecology, 2020, 96, .	1.3	20
13417	Dynamic network inference and association computation discover gene modules regulating virulence, mycotoxin and sexual reproduction in <i>Fusarium graminearum</i> . BMC Genomics, 2020, 21, 179.	1.2	8
13418	Identification of microRNAs in developing wheat grain that are potentially involved in regulating grain characteristics and the response to nitrogen levels. BMC Plant Biology, 2020, 20, 87.	1.6	35
13419	Identification of molecular markers associated with the progression and prognosis of endometrial cancer: a bioinformatic study. Cancer Cell International, 2020, 20, 59.	1.8	16
13420	<p></p>Identification of the Different Roles and Potential Mechanisms of T Isoforms in the Tumor Recurrence and Cell Cycle of Chordomas</p>. OncoTargets and Therapy, 2019, Volume 12, 11777-11791.	1.0	8

#	ARTICLE	IF	CITATIONS
13421	The Distribution of Bathyarchaeota in Surface Sediments of the Pearl River Estuary Along Salinity Gradient. <i>Frontiers in Microbiology</i> , 2020, 11, 285.	1.5	30
13422	Bioinformatics Identified 17 Immune Genes as Prognostic Biomarkers for Breast Cancer: Application Study Based on Artificial Intelligence Algorithms. <i>Frontiers in Oncology</i> , 2020, 10, 330.	1.3	29
13423	Rice CaM-binding transcription factor (OsCBT) mediates defense signaling via transcriptional reprogramming. <i>Plant Biotechnology Reports</i> , 2020, 14, 309-321.	0.9	13
13424	Spatiotemporal Proteomics Reveals the Molecular Consequences of Hormone Treatment in a Mouse Model of Lower Urinary Tract Dysfunction. <i>Journal of Proteome Research</i> , 2020, 19, 1375-1382.	1.8	5
13425	Crosstalk between heterotrimeric G protein-coupled signaling pathways and WRKY transcription factors modulating plant responses to suboptimal micronutrient conditions. <i>Journal of Experimental Botany</i> , 2020, 71, 3227-3239.	2.4	19
13426	In Silico Insights into Protein-Protein Interaction Disruptive Mutations in the PCSK9-LDLR Complex. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1550.	1.8	13
13427	Fibroblast Growth Factor 2-Mediated Regulation of Neuronal Exosome Release Depends on VAMP3/Cellubrevin in Hippocampal Neurons. <i>Advanced Science</i> , 2020, 7, 1902372.	5.6	33
13428	Mitigation of Cd toxicity by Mn in young plants of cacao, evaluated by the proteomic profiles of leaves and roots. <i>Ecotoxicology</i> , 2020, 29, 340-358.	1.1	13
13429	Protein interactome of the Cancerous Inhibitor of protein phosphatase 2A (CIP2A) in Th17 cells. <i>Current Research in Immunology</i> , 2020, 1, 10-22.	1.2	6
13430	Nicotiana tabacum seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 287-295.	1.9	35
13431	Spatial transcriptional dynamics of geographically separated genotypes revealed key regulators of podophyllotoxin biosynthesis in <i>Podophyllum hexandrum</i> . <i>Industrial Crops and Products</i> , 2020, 147, 112247.	2.5	11
13432	Mechanistic insights into the deleterious roles of Nasu-Hakola disease associated TREM2 variants. <i>Scientific Reports</i> , 2020, 10, 3663.	1.6	24
13433	Disturbance in human gut microbiota networks by parasites and its implications in the incidence of depression. <i>Scientific Reports</i> , 2020, 10, 3680.	1.6	22
13434	Genetic Profile and Functional Proteomics of Anal Squamous Cell Carcinoma: Proposal for a Molecular Classification. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 690-700.	2.5	4
13435	Role of SHV-11, a Class A $\beta$ -Lactamase, Gene in Multidrug Resistance Among <i>Klebsiella pneumoniae</i> Strains and Understanding Its Mechanism by Gene Network Analysis. <i>Microbial Drug Resistance</i> , 2020, 26, 900-908.	0.9	23
13436	MetaOmGraph: a workbench for interactive exploratory data analysis of large expression datasets. <i>Nucleic Acids Research</i> , 2020, 48, e23-e23.	6.5	19
13437	Gut microbial signatures associated with moxidectin treatment efficacy of <i>Haemonchus contortus</i> in infected goats. <i>Veterinary Microbiology</i> , 2020, 242, 108607.	0.8	9
13438	A living biobank of ovarian cancer ex vivo models reveals profound mitotic heterogeneity. <i>Nature Communications</i> , 2020, 11, 822.	5.8	62

#	ARTICLE	IF	CITATIONS
13439	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8.	2.9	68
13440	Analogous wheat root rhizosphere microbial successions in field and greenhouse trials in the presence of biocontrol agents <i>Paenibacillus peoriae</i> SP9 and <i>Streptomyces fulvissimus</i> FU14. <i>Molecular Plant Pathology</i> , 2020, 21, 622-635.	2.0	29
13441	Axon microdissection and transcriptome profiling reveals the in vivo RNA content of fully differentiated myelinated motor axons. <i>Rna</i> , 2020, 26, 595-612.	1.6	13
13442	Integrative comparison of the genomic and transcriptomic landscape between prostate cancer patients of predominantly African or European genetic ancestry. <i>PLoS Genetics</i> , 2020, 16, e1008641.	1.5	78
13443	Screening of characteristic biomolecules related to bladder cancer based on construction of ceRNA regulation network. <i>World Journal of Urology</i> , 2020, 38, 2835-2847.	1.2	11
13444	Distinct Transcriptional Responses across Tissue-Resident Macrophages to Short-Term and Long-Term Metabolic Challenge. <i>Cell Reports</i> , 2020, 30, 1627-1643.e7.	2.9	38
13445	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. <i>Methods</i> , 2020, 184, 86-92.	1.9	14
13446	Spatiotemporal single-cell analysis of gene expression in the mouse suprachiasmatic nucleus. <i>Nature Neuroscience</i> , 2020, 23, 456-467.	7.1	200
13447	Surveillance-embedded genomic outbreak resolution of methicillin-susceptible <i>Staphylococcus aureus</i> in a neonatal intensive care unit. <i>Scientific Reports</i> , 2020, 10, 2619.	1.6	15
13448	Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. <i>Gut</i> , 2020, 69, 1218-1228.	6.1	465
13449	Heterogeneous Multi-Layered Network Model for Omics Data Integration and Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1381.	1.1	61
13450	Sowing Methods Influence Soil Bacterial Diversity and Community Composition in a Winter Wheat-Summer Maize Rotation System on the Loess Plateau. <i>Frontiers in Microbiology</i> , 2020, 11, 192.	1.5	10
13451	Transcript profiling reveals potential regulators for oxidative stress response of a necrotrophic chickpea pathogen <i>Ascochyta rabiei</i> . <i>3 Biotech</i> , 2020, 10, 117.	1.1	13
13452	S-adenosylmethionine synthases in plants: Structural characterization of type I and II isoenzymes from <i>Arabidopsis thaliana</i> and <i>Medicago truncatula</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 151, 554-565.	3.6	21
13453	Identification of potential candidate genes involved in the sex determination cascade in an aquatic firefly, <i>Sclerotia aquatilis</i> (Coleoptera, Lampyridae). <i>Genomics</i> , 2020, 112, 2590-2602.	1.3	9
13454	Insight into <i>Ginkgo biloba</i> L. Extract on the Improved Spatial Learning and Memory by Chemogenomics Knowledgebase, Molecular Docking, Molecular Dynamics Simulation, and Bioassay Validations. <i>ACS Omega</i> , 2020, 5, 2428-2439.	1.6	15
13455	Phytochemical and comparative transcriptome analyses reveal different regulatory mechanisms in the terpenoid biosynthesis pathways between <i>Matricaria recutita</i> L. and <i>Chamaemelum nobile</i> L.. <i>BMC Genomics</i> , 2020, 21, 169.	1.2	11
13456	Crosstalk in the darkness: bulb vernalization activates meristem transition via circadian rhythm and photoperiodic pathway. <i>BMC Plant Biology</i> , 2020, 20, 77.	1.6	14



#	ARTICLE	IF	CITATIONS
13457	Network Pharmacology-Based Strategy to Investigate the Pharmacologic Mechanisms of <i>Atractylodes macrocephala</i> Koidz. for the Treatment of Chronic Gastritis. <i>Frontiers in Pharmacology</i> , 2019, 10, 1629.	1.6	59
13458	EFMviz: A COBRA Toolbox Extension to Visualize Elementary Flux Modes in Genome-Scale Metabolic Models. <i>Metabolites</i> , 2020, 10, 66.	1.3	7
13459	Transcriptional Correlates of Tolerance and Lethality in Mice Predict Ebola Virus Disease Patient Outcomes. <i>Cell Reports</i> , 2020, 30, 1702-1713.e6.	2.9	28
13460	Genome of <i>Tripterygium wilfordii</i> and identification of cytochrome P450 involved in triptolide biosynthesis. <i>Nature Communications</i> , 2020, 11, 971.	5.8	103
13461	Transcriptome Analysis Reveals Biosynthesis of Important Bioactive Constituents and Mechanism of Stem Formation of <i>Dendrobium huoshanense</i> . <i>Scientific Reports</i> , 2020, 10, 2857.	1.6	9
13462	Disrupted Gene Networks in Subfertile Hybrid House Mice. <i>Molecular Biology and Evolution</i> , 2020, 37, 1547-1562.	3.5	22
13463	Applications of Network Pharmacology in Traditional Chinese Medicine Research. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-7.	0.5	176
13464	Candidate Genes Associated with Delayed Neuropsychomotor Development and Seizures in a Patient with Ring Chromosome 20. <i>Case Reports in Genetics</i> , 2020, 2020, 1-6.	0.1	5
13465	Bioinformatics Analysis to Screen the Key Prognostic Genes in Tumor Microenvironment of Bladder Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	9
13466	Construction and Investigation of an LINC00284-Associated Regulatory Network in Serous Ovarian Carcinoma. <i>Disease Markers</i> , 2020, 2020, 1-14.	0.6	9
13467	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. <i>PLoS Computational Biology</i> , 2020, 16, e1007652.	1.5	2
13468	Identification of Biological Pathways Contributing to Marbling in Skeletal Muscle to Improve Beef Cattle Breeding. <i>Frontiers in Genetics</i> , 2020, 10, 1370.	1.1	14
13469	A Small RNA-Mediated Regulatory Network in <i>Arabidopsis thaliana</i> Demonstrates Connectivity Between phasiRNA Regulatory Modules and Extensive Co-Regulation of Transcription by miRNAs and phasiRNAs. <i>Frontiers in Plant Science</i> , 2019, 10, 1710.	1.7	7
13470	Chaperone-Facilitated Aggregation of Thermo-Sensitive Proteins Shields Them from Degradation during Heat Stress. <i>Cell Reports</i> , 2020, 30, 2430-2443.e4.	2.9	33
13471	Label-free peptide quantification coupled with in silico mapping of proteases for identification of potential serum biomarkers in gastric adenocarcinoma patients. <i>Clinical Biochemistry</i> , 2020, 79, 61-69.	0.8	5
13472	Transcriptome analysis reveals the temporal gene expression patterns in skin of large yellow croaker ( <i>Larimichthys crocea</i> ) in response to <i>Cryptocaryon irritans</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 99, 462-472.	1.6	49
13473	Identifying heat shock response systems from the genomic assembly of <i>Ureibacillus thermophilus</i> LM102 using protein-protein interaction networks. <i>Gene</i> , 2020, 737, 144449.	1.0	0
13474	Distinct Pathological Pathways in Patients With Heart Failure and Diabetes. <i>JACC: Heart Failure</i> , 2020, 8, 234-242.	1.9	25



#	ARTICLE	IF	CITATIONS
13476	Similar drivers but different effects lead to distinct ecological patterns of soil bacterial and archaeal communities. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107759.	4.2	83
13477	Transcriptomic analysis reveals the key regulators and molecular mechanisms underlying myometrial activation during equine placentitis. <i>Biology of Reproduction</i> , 2020, 102, 1306-1325.	1.2	11
13478	The R-Loop Atlas of Arabidopsis Development and Responses to Environmental Stimuli. <i>Plant Cell</i> , 2020, 32, 888-903.	3.1	61
13479	Lipidomics reveals the dynamics of lipid profile altered by omega-3 polyunsaturated fatty acid supplementation in healthy people. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2020, 47, 1134-1144.	0.9	7
13480	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.	4.7	90
13481	Oral Microbiome Profiling in Smokers with and without Head and Neck Cancer Reveals Variations Between Health and Disease. <i>Cancer Prevention Research</i> , 2020, 13, 463-474.	0.7	18
13482	Co-expression network analysis identified atypical chemokine receptor 1 (ACKR1) association with lymph node metastasis and prognosis in cervical cancer. <i>Cancer Biomarkers</i> , 2020, 27, 213-223.	0.8	11
13483	System-Based Differential Gene Network Analysis for Characterizing a Sample-Specific Subnetwork. <i>Biomolecules</i> , 2020, 10, 306.	1.8	9
13484	Genetic variation and evolutionary history of a mycorrhizal fungus regulate the currency of exchange in symbiosis with the food security crop cassava. <i>ISME Journal</i> , 2020, 14, 1333-1344.	4.4	12
13485	Network and pathway-based analyses of genes associated with osteoporosis. <i>Medicine (United States)</i> , 2020, 99, e19120.	0.4	12
13486	Exposure of ultrafine particulate matter causes glutathione redox imbalance in the hippocampus: A neurometabolic susceptibility to Alzheimer's pathology. <i>Science of the Total Environment</i> , 2020, 718, 137267.	3.9	24
13487	Molecular Networking Reveals Serpentinine-Related Bisindole Alkaloids from <i>Picralima nitida</i> , a Previously Well-Investigated Species. <i>Journal of Natural Products</i> , 2020, 83, 1207-1216.	1.5	22
13488	Arginine in C9ORF72 Dipolypeptides Mediates Promiscuous Proteome Binding and Multiple Modes of Toxicity. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 640-654.	2.5	31
13489	Proteome of thymus and spleen reveals that 10-hydroxydec-2-enoic acid could enhance immunity in mice. <i>Expert Opinion on Therapeutic Targets</i> , 2020, 24, 267-279.	1.5	15
13490	Exploring the role of post-translational modulators of transcription factors in triple-negative breast cancer gene expression. <i>Meta Gene</i> , 2020, 24, 100681.	0.3	0
13491	Transcriptome analysis of ankylosed primary molars with infraocclusion. <i>International Journal of Oral Science</i> , 2020, 12, 7.	3.6	2
13492	BORIS/CTCFL promotes a switch from a proliferative towards an invasive phenotype in melanoma cells. <i>Cell Death Discovery</i> , 2020, 6, 1.	2.0	59
13493	CellPhoneDB: inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. <i>Nature Protocols</i> , 2020, 15, 1484-1506.	5.5	1,768

#	ARTICLE	IF	CITATIONS
13494	Construction of the gene regulatory network identifies MYC as a transcriptional regulator of SWI/SNF complex. <i>Scientific Reports</i> , 2020, 10, 158.	1.6	7
13495	The <i>Eupentacta fraudatrix</i> transcriptome provides insights into regulation of cell transdifferentiation. <i>Scientific Reports</i> , 2020, 10, 1522.	1.6	23
13496	Comparative transcriptome profiling of selected osmotic regulatory proteins in the gill during seawater acclimation of chum salmon ( <i>Oncorhynchus keta</i> ) fry. <i>Scientific Reports</i> , 2020, 10, 1987.	1.6	18
13497	Genome-wide inference of the <i>Camponotus floridanus</i> protein-protein interaction network using homologous mapping and interacting domain profile pairs. <i>Scientific Reports</i> , 2020, 10, 2334.	1.6	9
13498	New insights into cheddar cheese microbiota-metabolome relationships revealed by integrative analysis of multi-omics data. <i>Scientific Reports</i> , 2020, 10, 3164.	1.6	38
13499	An endophyte from salt-adapted Pokkali rice confers salt-tolerance to a salt-sensitive rice variety and targets a unique pattern of genes in its new host. <i>Scientific Reports</i> , 2020, 10, 3237.	1.6	58
13500	Network Pharmacology-Based Investigation of the System-Level Molecular Mechanisms of the Hematopoietic Activity of Samul-Tang, a Traditional Korean Herbal Formula. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-17.	0.5	15
13501	Adaptation to Photooxidative Stress: Common and Special Strategies of the Alphaproteobacteria <i>Rhodobacter sphaeroides</i> and <i>Rhodobacter capsulatus</i> . <i>Microorganisms</i> , 2020, 8, 283.	1.6	12
13502	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	2.6	118
13503	Caloric Restriction Reprograms the Single-Cell Transcriptional Landscape of <i>Rattus Norvegicus</i> Aging. <i>Cell</i> , 2020, 180, 984-1001.e22.	13.5	206
13504	Arsenic concentrations, diversity and co-occurrence patterns of bacterial and fungal communities in the feces of mice under sub-chronic arsenic exposure through food. <i>Environment International</i> , 2020, 138, 105600.	4.8	41
13505	High temperature induced structural changes of apo-lactoferrin and interactions with $\beta$ -lactoglobulin and $\alpha$ -lactalbumin for potential encapsulation strategies. <i>Food Hydrocolloids</i> , 2020, 105, 105817.	5.6	15
13506	Bacteroidetes can be a rich source of novel lanthipeptides: The case study of <i>Pedobacter lusitanus</i> . <i>Microbiological Research</i> , 2020, 235, 126441.	2.5	29
13507	Fungal Polyketides with Three Distinctive Ring Skeletons from the Fungus <i>Penicillium canescens</i> Uncovered by OSMAC and Molecular Networking Strategies. <i>Journal of Organic Chemistry</i> , 2020, 85, 4973-4980.	1.7	23
13508	Evolutionary insights into FYVE and PHOX effector proteins from the moss <i>Physcomitrella patens</i> . <i>Planta</i> , 2020, 251, 62.	1.6	5
13509	Biological Network Analyses of WRKY Transcription Factor Family in Soybean ( <i>Glycine max</i> ) under Low Phosphorus Treatment. <i>Journal of Crop Science and Biotechnology</i> , 2020, 23, 127-136.	0.7	5
13510	Ligands, Receptors, and Transcription Factors that Mediate Inter-Cellular and Intra-Cellular Communication during Ovarian Follicle Development. <i>Reproductive Sciences</i> , 2020, 27, 690-703.	1.1	19
13511	Cyclophosphamide in <i>Drosophila</i> promotes genes and transposable elements differential expression and mitochondrial dysfunction. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 230, 108718.	1.3	6

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13512	Growth and nitrogen metabolism are associated with nitrogen-use efficiency in cotton genotypes. <i>Plant Physiology and Biochemistry</i> , 2020, 149, 61-74.	2.8	76
13513	Integrative network modeling reveals mechanisms underlying T cell exhaustion. <i>Scientific Reports</i> , 2020, 10, 1915.	1.6	14
13514	Organ-level protein networks as a reference for the host effects of the microbiome. <i>Genome Research</i> , 2020, 30, 276-286.	2.4	6
13515	Conflicting signal in transcriptomic markers leads to a poorly resolved backbone phylogeny of chalcidoid wasps. <i>Systematic Entomology</i> , 2020, 45, 783-802.	1.7	23
13516	System Prediction and Validation of TCM for Chronic Myeloid Leukemia Treatment from the Perspective of Low-Toxicity Chemotherapy: A Stilbene $\pm$ -Viniferin Has a Proapoptotic Effect on K562 Cells via the Mitochondrial Pathway. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	5
13517	Community recovery dynamics in yellow perch microbiome after gradual and constant metallic perturbations. <i>Microbiome</i> , 2020, 8, 14.	4.9	22
13518	Computational Identification of the Proteins Associated With Quorum Sensing and Biofilm Formation in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3011.	1.5	19
13519	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. <i>Viruses</i> , 2020, 12, 105.	1.5	9
13520	Oncogene <i>PLCE1</i> may be a diagnostic biomarker and prognostic biomarker by influencing cell cycle, proliferation, migration, and invasion ability in hepatocellular carcinoma cell lines. <i>Journal of Cellular Physiology</i> , 2020, 235, 7003-7017.	2.0	9
13521	Metabolomics evaluation of repeated administration of potassium iodide on adult male rats. <i>Archives of Toxicology</i> , 2020, 94, 803-812.	1.9	7
13522	Genetic Mapping Combined with a Transcriptome Analysis to Screen for Candidate Genes Responsive to Abscisic Acid Treatment in <i>Brassica napus</i> Embryos During Seed Germination. <i>DNA and Cell Biology</i> , 2020, 39, 533-547.	0.9	4
13523	Development and validation of a novel immune-related prognostic model in hepatocellular carcinoma. <i>Journal of Translational Medicine</i> , 2020, 18, 67.	1.8	70
13524	Myxobacterial Response to Methyljasmonate Exposure Indicates Contribution to Plant Recruitment of Micropredators. <i>Frontiers in Microbiology</i> , 2020, 11, 34.	1.5	10
13525	Screening the Cancer Genome Atlas Database for Genes of Prognostic Value in Acute Myeloid Leukemia. <i>Frontiers in Oncology</i> , 2019, 9, 1509.	1.3	19
13526	IGFBP6 Is Downregulated in Unstable Carotid Atherosclerotic Plaques According to an Integrated Bioinformatics Analysis and Experimental Verification. <i>Journal of Atherosclerosis and Thrombosis</i> , 2020, 27, 1068-1085.	0.9	19
13527	Phylogenetic analysis reveals an ancient gene duplication as the origin of the MdtABC efflux pump. <i>PLoS ONE</i> , 2020, 15, e0228877.	1.1	6
13528	Identification of key genes and pathways associated with esophageal squamous cell carcinoma development based on weighted gene correlation network analysis. <i>Journal of Cancer</i> , 2020, 11, 1393-1402.	1.2	10
13529	A multi-omics investigation of the molecular characteristics and classification of six metabolic syndrome relevant diseases. <i>Theranostics</i> , 2020, 10, 2029-2046.	4.6	35

#	ARTICLE	IF	CITATIONS
13531	Comparative characterization of microbial communities that inhabit arsenic-rich and antimony-rich contaminated sites: Responses to two different contamination conditions. <i>Environmental Pollution</i> , 2020, 260, 114052.	3.7	40
13532	Transcriptome analysis of rat dorsal hippocampal CA1 after an early life seizure induced by kainic acid. <i>Epilepsy Research</i> , 2020, 161, 106283.	0.8	7
13533	Identification of Hub Genes and Analysis of Prognostic Values in Hepatocellular Carcinoma by Bioinformatics Analysis. <i>American Journal of the Medical Sciences</i> , 2020, 359, 226-234.	0.4	6
13534	20(S)-Protopanaxatriol promotes the binding of P53 and DNA to regulate the antitumor network via multiomic analysis. <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 1020-1035.	5.7	18
13535	The profile of antibiotic resistance genes in pig manure composting shaped by composting stage: Mesophilic-thermophilic and cooling-maturation stages. <i>Chemosphere</i> , 2020, 250, 126181.	4.2	65
13536	mRNA profiling reveals response regulators of decreased fungal keratitis symptoms in a tree shrew model. <i>Gene</i> , 2020, 737, 144450.	1.0	4
13537	Effect of autochthonous lactic acid bacteria on fermented Yucha quality. <i>LWT - Food Science and Technology</i> , 2020, 123, 109060.	2.5	10
13538	A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020, 21, 339-354.	7.7	72
13539	Particle Selection in Suspension-Feeding Bivalves: Does One Model Fit All?. <i>Biological Bulletin</i> , 2020, 238, 41-53.	0.7	10
13540	Identification of hub genes, key pathways, and therapeutic agents in Hutchinsonâ€“Gilford Progeria syndrome using bioinformatics analysis. <i>Medicine (United States)</i> , 2020, 99, e19022.	0.4	2
13541	Identifying potential active components of walnut leaf that action diabetes mellitus through integration of UHPLC-Q-Orbitrap HRMS and network pharmacology analysis. <i>Journal of Ethnopharmacology</i> , 2020, 253, 112659.	2.0	23
13542	Integration of proteomics and metabolomics reveals promotion of proliferation by exposure of bisphenol S in human breast epithelial MCF-10A cells. <i>Science of the Total Environment</i> , 2020, 712, 136453.	3.9	15
13543	Aromatization of natural products by a specialized detoxification enzyme. <i>Nature Chemical Biology</i> , 2020, 16, 250-256.	3.9	30
13544	Diversity spectrum analysis identifies mutation-specific effects of cancer driver genes. <i>Communications Biology</i> , 2020, 3, 6.	2.0	9
13545	Transcriptome analyses identify hub genes and potential mechanisms in adenoid cystic carcinoma. <i>Medicine (United States)</i> , 2020, 99, e18676.	0.4	4
13546	Metaboliteâ€“based genomeâ€“wide association study enables dissection of the flavonoid decoration pathway of wheat kernels. <i>Plant Biotechnology Journal</i> , 2020, 18, 1722-1735.	4.1	94
13547	Improving the organization and interactivity of metabolic pathfinding with precomputed pathways. <i>BMC Bioinformatics</i> , 2020, 21, 13.	1.2	17
13548	Identification of gene expression profiles and immune cell infiltration signatures between low and high tumor mutation burden groups in bladder cancer. <i>International Journal of Medical Sciences</i> , 2020, 17, 89-96.	1.1	37

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13549	Transcriptome analysis of tobacco root response to different concentrations of nitrate. <i>Agronomy Journal</i> , 2020, 112, 1111-1125.	0.9	1
13550	Zika Virus Targets Glioblastoma Stem Cells through a SOX2-Integrin $\beta$ 5 Axis. <i>Cell Stem Cell</i> , 2020, 26, 187-204.e10.	5.2	126
13551	A developmental landscape of 3D-cultured human pre-gastrulation embryos. <i>Nature</i> , 2020, 577, 537-542.	13.7	277
13552	B cells and tertiary lymphoid structures promote immunotherapy response. <i>Nature</i> , 2020, 577, 549-555.	13.7	1,421
13553	Unraveling Asian Soybean Rust metabolomics using mass spectrometry and Molecular Networking approach. <i>Scientific Reports</i> , 2020, 10, 138.	1.6	25
13554	Transcriptional analysis identifies potential biomarkers and molecular regulators in pneumonia and COPD exacerbation. <i>Scientific Reports</i> , 2020, 10, 241.	1.6	17
13555	Impacts of NRF2 activation in non-small cell lung cancer cell lines on extracellular metabolites. <i>Cancer Science</i> , 2020, 111, 667-678.	1.7	29
13556	A proteomic atlas of senescence-associated secretomes for aging biomarker development. <i>PLoS Biology</i> , 2020, 18, e3000599.	2.6	694
13557	Global Gene Expression Analysis Identifies Age-Related Differences in Knee Joint Transcriptome during the Development of Post-Traumatic Osteoarthritis in Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 364.	1.8	30
13558	Profiling of O-acetylated Gangliosides Expressed in Neuroectoderm Derived Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 370.	1.8	21
13559	The circular RNA aplacirc_13267 upregulates duck granulosa cell apoptosis by the apla-miR-13/THBS1 signaling pathway. <i>Journal of Cellular Physiology</i> , 2020, 235, 5750-5763.	2.0	20
13560	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	13.5	596
13561	Carbon nanomaterials affect carbon cycle-related functions of the soil microbial community and the coupling of nutrient cycles. <i>Journal of Hazardous Materials</i> , 2020, 390, 122144.	6.5	31
13562	Insights into the Effect of Lowe Syndrome-Causing Mutation p.Asn591Lys of OCRL-1 through Protein-Protein Interaction Networks and Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1019-1027.	2.5	8
13563	Cryptic Species Account for the Seemingly Idiosyncratic Secondary Metabolism of <i>Sarcophyton glaucum</i> Specimens Collected in Palau. <i>Journal of Natural Products</i> , 2020, 83, 693-705.	1.5	10
13564	Mechanisms governing the pioneering and redistribution capabilities of the non-classical pioneer PU.1. <i>Nature Communications</i> , 2020, 11, 402.	5.8	76
13565	Environmental arginine controls multinuclear giant cell metabolism and formation. <i>Nature Communications</i> , 2020, 11, 431.	5.8	37
13566	Combined proteomics/miRNomics of dendritic cell immunotherapy-treated glioblastoma patients as a screening for survival-associated factors. <i>Npj Vaccines</i> , 2020, 5, 5.	2.9	19

#	ARTICLE	IF	CITATIONS
13567	Metabolomics-Based Discovery of Molecular Signatures for Triple Negative Breast Cancer in Asian Female Population. <i>Scientific Reports</i> , 2020, 10, 370.	1.6	25
13568	Compartment and hub definitions tune metabolic networks for metabolomic interpretations. <i>GigaScience</i> , 2020, 9, .	3.3	9
13569	A Pathway for Degradation of Uracil to Acetyl Coenzyme A in <i>Bacillus megaterium</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	12
13570	Systematic Elucidation of the Potential Mechanism of Erzhi Pill against Drug-Induced Liver Injury via Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	14
13571	IL6 Induces an IL22+ CD8+ T-cell Subset with Potent Antitumor Function. <i>Cancer Immunology Research</i> , 2020, 8, 321-333.	1.6	26
13572	Co-expression network analysis predicts a key role of microRNAs in the adaptation of the porcine skeletal muscle to nutrient supply. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 10.	2.1	17
13573	Genome-Wide Investigation of Heat Shock Transcription Factor Family in Wheat ( <i>Triticum aestivum</i> L.) and Possible Roles in Anther Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 608.	1.8	23
13574	Genome based characterization of <i>Kitasatospora</i> sp. MMS16-BH015, a multiple heavy metal resistant soil actinobacterium with high antimicrobial potential. <i>Gene</i> , 2020, 733, 144379.	1.0	13
13575	Whole-genome re-sequencing and transcriptome reveal cadmium tolerance related genes and pathways in <i>Chlamydomonas reinhardtii</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 191, 110231.	2.9	15
13576	Systemic biological study for identification of miR-299-5p target genes in cancer. <i>Meta Gene</i> , 2020, 24, 100655.	0.3	3
13577	The immobilization of fibronectin- and fibroblast growth factor 2-derived peptides on a culture plate supports the attachment and proliferation of human pluripotent stem cells. <i>Stem Cell Research</i> , 2020, 43, 101700.	0.3	14
13578	p53 controls genomic stability and temporal differentiation of human neural stem cells and affects neural organization in human brain organoids. <i>Cell Death and Disease</i> , 2020, 11, 52.	2.7	33
13579	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. <i>Nature Communications</i> , 2020, 11, 499.	5.8	42
13580	The FGF, TGF $\beta$ 2 and WNT axis Modulate Self-renewal of Human SIX2+ Urine Derived Renal Progenitor Cells. <i>Scientific Reports</i> , 2020, 10, 739.	1.6	32
13581	Dipeptidyl peptidase-4 is increased in the abdominal aortic aneurysm vessel wall and is associated with aneurysm disease processes. <i>PLoS ONE</i> , 2020, 15, e0227889.	1.1	6
13582	Design of Fungal Co-Cultivation Based on Comparative Metabolomics and Bioactivity for Discovery of Marine Fungal Agrochemicals. <i>Marine Drugs</i> , 2020, 18, 73.	2.2	20
13583	Expanding the chemical diversity through microorganisms co-culture: Current status and outlook. <i>Biotechnology Advances</i> , 2020, 40, 107521.	6.0	75
13584	Biofilm formation displays intrinsic offensive and defensive features of <i>Bacillus cereus</i> . <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 3.	2.9	34



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13585	Genome-wide analysis of circular RNAs involved in Marek's disease tumourigenesis in chickens. <i>RNA Biology</i> , 2020, 17, 517-527.	1.5	18
13586	Balancing the double-edged sword effect of increased resistant starch content and its impact on rice texture: its genetics and molecular physiological mechanisms. <i>Plant Biotechnology Journal</i> , 2020, 18, 1763-1777.	4.1	36
13587	A pipeline to create predictive functional networks: application to the tumor progression of hepatocellular carcinoma. <i>BMC Bioinformatics</i> , 2020, 21, 18.	1.2	3
13588	miRNA and circRNA expression patterns in mouse brain during toxoplasmosis development. <i>BMC Genomics</i> , 2020, 21, 46.	1.2	15
13589	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. <i>Cells</i> , 2020, 9, 153.	1.8	19
13590	Uncovering the Pharmacological Mechanism of Stemazole in the Treatment of Neurodegenerative Diseases Based on a Network Pharmacology Approach. <i>International Journal of Molecular Sciences</i> , 2020, 21, 427.	1.8	16
13591	Metabolomic Profiling of Fungal Pathogens Responsible for Root Rot in American Ginseng. <i>Metabolites</i> , 2020, 10, 35.	1.3	23
13592	Genome-wide analysis and expression profiles of the StR2R3-MYB transcription factor superfamily in potato ( <i>Solanum tuberosum</i> L.). <i>International Journal of Biological Macromolecules</i> , 2020, 148, 817-832.	3.6	51
13593	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
13594	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. <i>Cancer Research</i> , 2020, 80, 1524-1537.	0.4	10
13595	Triple Mycobacterial ATP-synthase mutations impedes Bedaquiline binding: Atomistic and structural perspectives. <i>Computational Biology and Chemistry</i> , 2020, 85, 107204.	1.1	7
13596	Dynamic View of Allosteric Regulation in the Hsp70 Chaperones by J-Domain Cochaperone and Post-Translational Modifications: Computational Analysis of Hsp70 Mechanisms by Exploring Conformational Landscapes and Residue Interaction Networks. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1614-1631.	2.5	27
13597	Identification of a CDH12 potential candidate genetic variant for an autosomal dominant form of transgrediens and progrediens palmoplantar keratoderma in a Tunisian family. <i>Journal of Human Genetics</i> , 2020, 65, 397-410.	1.1	4
13598	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. <i>Translational Psychiatry</i> , 2020, 10, 4.	2.4	84
13599	Precision Medicine Informatics: Principles, Prospects, and Challenges. <i>IEEE Access</i> , 2020, 8, 13593-13612.	2.6	26
13600	Triangular correlation (TrC) between cancer aggressiveness, cell uptake capability, and cell deformability. <i>Science Advances</i> , 2020, 6, eaax2861.	4.7	24
13601	Comprehensive analysis of pseudogene HSPB1P1 and its potential roles in hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2020, 235, 6515-6527.	2.0	7
13602	Common and distinct features of potentially predictive biomarkers in small cell lung carcinoma and large cell neuroendocrine carcinoma of the lung by systematic and integrated analysis. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1126.	0.6	3



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13603	Network Analysis for Complex Neurodegenerative Diseases. <i>Current Genetic Medicine Reports</i> , 2020, 8, 17-25.	1.9	14
13604	Study on the anti-tumor mechanism related to immune microenvironment of <i>Bombyx Batryticatus</i> on viral and non-viral infections of hepatocellular carcinoma. <i>Biomedicine and Pharmacotherapy</i> , 2020, 124, 109838.	2.5	8
13605	Changes in microbial community structure during pig manure composting and its relationship to the fate of antibiotics and antibiotic resistance genes. <i>Journal of Hazardous Materials</i> , 2020, 389, 122082.	6.5	103
13606	Proneural and mesenchymal glioma stem cells display major differences in splicing and lncRNA profiles. <i>Npj Genomic Medicine</i> , 2020, 5, 2.	1.7	29
13607	MicroRNA and transcription factor co-regulatory networks and subtype classification of seminoma and non-seminoma in testicular germ cell tumors. <i>Scientific Reports</i> , 2020, 10, 852.	1.6	43
13608	Antibiotic resistome and microbial community structure during anaerobic co-digestion of food waste, paper and cardboard. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	25
13609	Disease-relevant mutations alter amino acid co-evolution networks in the second nucleotide binding domain of CFTR. <i>PLoS ONE</i> , 2020, 15, e0227668.	1.1	2
13610	Investigation of the mechanism of action of <i>Porana sinensis</i> Hemsl. against gout arthritis using network pharmacology and experimental validation. <i>Journal of Ethnopharmacology</i> , 2020, 252, 112606.	2.0	19
13611	Alterations in activin Aâ€“myostatinâ€“follistatin system associate with disease activity in inflammatory myopathies. <i>Rheumatology</i> , 2020, 59, 2491-2501.	0.9	15
13612	A long non-coding apple RNA, MSTRG.85814.11, acts as a transcriptional enhancer of <i>SAUR32</i> and contributes to the Fe-deficiency response. <i>Plant Journal</i> , 2020, 103, 53-67.	2.8	42
13613	The Active Compounds of Yixin Ningshen Tablet and Their Potential Action Mechanism in Treating Coronary Heart Disease- A Network Pharmacology and Proteomics Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-17.	0.5	2
13614	Screening and Identification of Key Biomarkers for Bladder Cancer: A Study Based on TCGA and GEO Data. <i>BioMed Research International</i> , 2020, 2020, 1-20.	0.9	32
13615	RNA proximity sequencing data and analysis pipeline from a human neuroblastoma nuclear transcriptome. <i>Scientific Data</i> , 2020, 7, 35.	2.4	2
13616	Estrogen/estrogen receptor promotes the proliferation of endometrial carcinoma cells by enhancing hMOF expression. <i>Japanese Journal of Clinical Oncology</i> , 2020, 50, 241-253.	0.6	14
13617	Differential expression of matrix metalloproteinases and miRNAs in the metastasis of oral squamous cell carcinoma. <i>BMC Oral Health</i> , 2020, 20, 24.	0.8	27
13618	Bioinformatics-based screening of key genes for transformation of liver cirrhosis to hepatocellular carcinoma. <i>Journal of Translational Medicine</i> , 2020, 18, 40.	1.8	39
13619	Integrated Bioinformatics Analysis for the Identification of Key Molecules and Pathways in the Hippocampus of Rats After Traumatic Brain Injury. <i>Neurochemical Research</i> , 2020, 45, 928-939.	1.6	9
13620	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. <i>Molecular Medicine</i> , 2020, 26, 9.	1.9	34

#	ARTICLE	IF	CITATIONS
13621	Virus Discovery in Desert Tortoise Fecal Samples: Novel Circular Single-Stranded DNA Viruses. <i>Viruses</i> , 2020, 12, 143.	1.5	26
13622	Psychological and neural responses to architectural interiors. <i>Cortex</i> , 2020, 126, 217-241.	1.1	58
13623	Whole-transcriptome analysis of the toxic effects of zearalenone exposure on ceRNA networks in porcine granulosa cells. <i>Environmental Pollution</i> , 2020, 261, 114007.	3.7	26
13624	Isolation, Genomic and Metabolomic Characterization of <i>Streptomyces tendae</i> VITAKN with Quorum Sensing Inhibitory Activity from Southern India. <i>Microorganisms</i> , 2020, 8, 121.	1.6	17
13625	Tracking the functional meaning of the human oral-microbiome protein-protein interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 199-235.	1.0	7
13626	SMAD7 and SERPINE1 as novel dynamic network biomarkers detect and regulate the tipping point of TGF-beta induced EMT. <i>Science Bulletin</i> , 2020, 65, 842-853.	4.3	19
13627	Landscape of transcriptome variations uncovering known and novel driver events in colorectal carcinoma. <i>Scientific Reports</i> , 2020, 10, 432.	1.6	16
13628	Repository of proposed pathways and protein-protein interaction networks in age-related macular degeneration. <i>Npj Aging and Mechanisms of Disease</i> , 2020, 6, 2.	4.5	24
13629	Evolutionary strategies drive a balance of the interacting gene products for the <i>CBL</i> and <i>CIPK</i> gene families. <i>New Phytologist</i> , 2020, 226, 1506-1516.	3.5	52
13630	Network Medicine Approach for Analysis of Alzheimer's Disease Gene Expression Data. <i>International Journal of Molecular Sciences</i> , 2020, 21, 332.	1.8	12
13631	Open Data for Differential Network Analysis in Glioma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 547.	1.8	9
13632	Identification of microenvironment-related genes with prognostic value in clear cell renal cell carcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3606-3615.	1.2	8
13633	Insights into the expression profiles and functions of circRNAs in a newborn hyperoxia-induced rat bronchopulmonary dysplasia model. <i>Journal of Gene Medicine</i> , 2020, 22, e3163.	1.4	8
13634	Sugars altered fungal community composition and caused high network complexity in a <i>Fusarium</i> wilt pathogen-infested soil. <i>Biology and Fertility of Soils</i> , 2020, 56, 395-409.	2.3	10
13635	Gene expression changes in arterial and venous endothelial cells exposed to gestational diabetes mellitus. <i>Gynecological Endocrinology</i> , 2020, 36, 791-795.	0.7	10
13636	Transcriptional analysis of THP-1 cells infected with <i>Leishmania infantum</i> indicates no activation of the inflammasome platform. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007949.	1.3	18
13637	Trade-off between potential phytopathogenic and non-phytopathogenic fungi in the peanut monoculture cultivation system. <i>Applied Soil Ecology</i> , 2020, 148, 103508.	2.1	11
13638	N6-methyladenosine mediates arsenite-induced human keratinocyte transformation by suppressing p53 activation. <i>Environmental Pollution</i> , 2020, 259, 113908.	3.7	51

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13639	An effective seven-CpG-based signature to predict survival in renal clear cell carcinoma by integrating DNA methylation and gene expression. <i>Life Sciences</i> , 2020, 243, 117289.	2.0	6
13640	FBA Ecological Guild: Trio of Firmicutes-Bacteroidetes Alliance against Actinobacteria in Human Oral Microbiome. <i>Scientific Reports</i> , 2020, 10, 287.	1.6	37
13641	Plasticity of <i>Phymatotrichopsis omnivora</i> infection strategies is dependent on host and nonhost plant responses. <i>Plant, Cell and Environment</i> , 2020, 43, 1084-1101.	2.8	4
13642	Construction of asthma related competing endogenous RNA network revealed novel long non-coding RNAs and potential new drugs. <i>Respiratory Research</i> , 2020, 21, 14.	1.4	18
13643	Integrating Computational Methods to Investigate the Macroecology of Microbiomes. <i>Frontiers in Genetics</i> , 2019, 10, 1344.	1.1	7
13644	The aberrant expression of rhythm genes affects the genome instability and regulates the cancer immunity in paná€cancer. <i>Cancer Medicine</i> , 2020, 9, 1818-1829.	1.3	22
13645	Gut microbiota modulation and immunity response induced by <i>Citrobacter freundii</i> strain GC01 in grass carp ( <i>Ctenopharyngodon idellus</i> ). <i>Aquaculture</i> , 2020, 521, 735015.	1.7	20
13646	Zika virus targets the human thymic epithelium. <i>Scientific Reports</i> , 2020, 10, 1378.	1.6	16
13647	Identification of genes of prognostic value in the ccRCC microenvironment from TCGA database. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1159.	0.6	17
13648	Targeted lipidomics and transcriptomics profiling reveal the heterogeneity of visceral and subcutaneous white adipose tissue. <i>Life Sciences</i> , 2020, 245, 117352.	2.0	25
13649	Discovery of a Fungal Copper Radical Oxidase with High Catalytic Efficiency toward 5-Hydroxymethylfurfural and Benzyl Alcohols for Bioprocessing. <i>ACS Catalysis</i> , 2020, 10, 3042-3058.	5.5	46
13650	Transcriptional responses of <i>Candida glabrata</i> biofilm cells to fluconazole are modulated by the carbon source. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 4.	2.9	16
13651	Structure elucidation of bacterial nonribosomal lipopeptides. <i>Organic and Biomolecular Chemistry</i> , 2020, 18, 1710-1727.	1.5	26
13652	Dysregulated FXR-FGF19 signaling and choline metabolism are associated with gut dysbiosis and hyperplasia in a novel pig model of pediatric NASH. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G582-G609.	1.6	27
13653	Perivascular Adipose Tissue Controls Insulin-Stimulated Perfusion, Mitochondrial Protein Expression, and Glucose Uptake in Muscle Through Adipomuscular Arterioles. <i>Diabetes</i> , 2020, 69, 603-613.	0.3	9
13654	Identification of Prognostic Dosage-Sensitive Genes in Colorectal Cancer Based on Multi-Omics. <i>Frontiers in Genetics</i> , 2019, 10, 1310.	1.1	7
13655	Genome-Wide Discovery of Single-Nucleotide Polymorphisms and Their Application in Population Genetic Studies in the Endangered Japanese Eel ( <i>Anguilla japonica</i> ). <i>Frontiers in Marine Science</i> , 2020, 6, .	1.2	1
13656	Genomic Features and Clinical Characteristics of Adolescents and Young Adults With Cholangiocarcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 1439.	1.3	15

#	ARTICLE	IF	CITATIONS
13657	miR-497a-5p mediates starvation-induced death in colon cancer cells by targeting acyl-CoA synthetase-5 and modulation of lipid metabolism. <i>Journal of Cellular Physiology</i> , 2020, 235, 5570-5589.	2.0	34
13658	Comprehensive molecular insights into the stress response dynamics of rice ( <i>Oryza sativa</i> L.) during rice tungro disease by RNA-seq-based comparative whole transcriptome analysis. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	5
13659	Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165714.	1.8	3
13660	Genome-wide survey and expression analysis of calcium-dependent protein kinase (CDPK) in grass <i>Brachypodium distachyon</i> . <i>BMC Genomics</i> , 2020, 21, 53.	1.2	25
13661	NetEPD: A network-based essential protein discovery platform. <i>Tsinghua Science and Technology</i> , 2020, 25, 542-552.	4.1	15
13662	A Guide to Conquer the Biological Network Era Using Graph Theory. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 34.	2.0	149
13663	Integrative analysis of highly mutated genes in hepatitis B virus-related hepatic carcinoma. <i>Cancer Medicine</i> , 2020, 9, 2462-2479.	1.3	14
13664	Identification of dysregulated genes and pathways of different brain regions in Alzheimer's disease. <i>International Journal of Neuroscience</i> , 2020, 130, 1082-1094.	0.8	8
13665	Maize ( <i>Zea mays</i> L. Sp.) varieties significantly influence bacterial and fungal community in bulk soil, rhizosphere soil and phyllosphere. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	35
13666	In Silico Analysis of the Age-Dependent Evolution of the Transcriptome of Mouse Skin Stem Cells. <i>Cells</i> , 2020, 9, 165.	1.8	4
13667	Q-Cell Glioblastoma Resource: Proteomics Analysis Reveals Unique Cell-States Are Maintained in 3D Culture. <i>Cells</i> , 2020, 9, 267.	1.8	12
13668	Identification and Characterization of circRNAs Responsive to Methyl Jasmonate in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 792.	1.8	20
13669	Comparative Transcriptome Analysis of Different <i>Dendrobium</i> Species Reveals Active Ingredients-Related Genes and Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 861.	1.8	23
13670	Mechanisms of Mixed Th1/Th2 Responses in Mice Induced by <i>Albizia julibrissin</i> Saponin Active Fraction by in Silico Analysis. <i>Vaccines</i> , 2020, 8, 48.	2.1	7
13671	MiR-3940-5p promotes granulosa cell proliferation through targeting KCNA5 in polycystic ovarian syndrome. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 791-797.	1.0	15
13672	Network pharmacology-based study on the mechanism of Yiganling capsule in hepatitis B treatment. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 37.	1.2	3
13673	Epistatic Transcription Factor Networks Differentially Modulate <i>Arabidopsis</i> Growth and Defense. <i>Genetics</i> , 2020, 214, 529-541.	1.2	12
13674	Integrated Hypothalamic Transcriptome Profiling Reveals the Reproductive Roles of mRNAs and miRNAs in Sheep. <i>Frontiers in Genetics</i> , 2019, 10, 1296.	1.1	21

#	ARTICLE	IF	CITATIONS
13675	Trophic Selective Pressures Organize the Composition of Endolithic Microbial Communities From Global Deserts. <i>Frontiers in Microbiology</i> , 2019, 10, 2952.	1.5	26
13676	The RNA-Binding Protein ATXN2 is Expressed during Megakaryopoiesis and May Control Timing of Gene Expression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 967.	1.8	8
13677	Imprinted Maternally Expressed microRNAs Antagonize Paternally Driven Gene Programs in Neurons. <i>Molecular Cell</i> , 2020, 78, 85-95.e8.	4.5	36
13678	Identification of potential miRNA-mRNA interaction network in bone marrow T cells of acquired aplastic anemia. <i>Hematology</i> , 2020, 25, 168-175.	0.7	6
13679	Cellular Identification and In Silico Characterization of Protein Phosphatase 2C (PP2C) of <i>Cryptosporidium parvum</i> . <i>Acta Parasitologica</i> , 2020, 65, 704-715.	0.4	3
13680	Proteome changes in muscles, ganglia, and gills in <i>Corbicula fluminea</i> clams exposed to crude oil: Relationship with behavioural disturbances. <i>Aquatic Toxicology</i> , 2020, 223, 105482.	1.9	6
13681	Overexpression of budding yeast protein phosphatase Ppz1 impairs translation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118727.	1.9	13
13682	Transcriptome analyses provide insights into maternal immune changes at several critical phases of giant panda reproduction. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103699.	1.0	5
13683	Mass Spectrometry Untangles Plant Membrane Protein Signaling Networks. <i>Trends in Plant Science</i> , 2020, 25, 930-944.	4.3	30
13684	MAPPS: A Web-Based Tool for Metabolic Pathway Prediction and Network Analysis in the Postgenomic Era. <i>ACS Synthetic Biology</i> , 2020, 9, 1069-1082.	1.9	14
13685	Plant 22-nt siRNAs mediate translational repression and stress adaptation. <i>Nature</i> , 2020, 581, 89-93.	13.7	112
13686	High-throughput, Label-Free Quantitative Proteomic Studies of the Anticancer Effects of Electrical Pulses with Turmeric Silver Nanoparticles: an in vitro Model Study. <i>Scientific Reports</i> , 2020, 10, 7258.	1.6	16
13687	Phylogenetics Identifies Two Eumetazoan TRPM Clades and an Eighth TRP Family, TRP Soromelastatin (TRPS). <i>Molecular Biology and Evolution</i> , 2020, 37, 2034-2044.	3.5	24
13688	Extensive Ethnolinguistic Diversity in Vietnam Reflects Multiple Sources of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2020, 37, 2503-2519.	3.5	70
13689	DDP-resistant ovarian cancer cells-derived exosomal microRNA-30a-5p reduces the resistance of ovarian cancer cells to DDP. <i>Open Biology</i> , 2020, 10, 190173.	1.5	14
13690	Gene regulatory network and its constituent transcription factors that control nitrogen-deficiency responses in rice. <i>New Phytologist</i> , 2020, 227, 1434-1452.	3.5	45
13691	Diverse types of genomic evidence converge on alcohol use disorder risk genes. <i>Journal of Medical Genetics</i> , 2020, 57, 733-743.	1.5	10
13692	ZiYinHuaTan Recipe Inhibits Cell Proliferation and Promotes Apoptosis in Gastric Cancer by Suppressing PI3K/AKT Pathway. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	11

#	ARTICLE	IF	CITATIONS
13693	Identification of Potential Biomarkers Associated with Basal Cell Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	7
13694	Mining Drug-Target Associations in Cancer: Analysis of Gene Expression and Drug Activity Correlations. <i>Biomolecules</i> , 2020, 10, 667.	1.8	9
13695	Profiling native aquifer bacteria in a uranium roll-front deposit and their role in biogeochemical cycle dynamics: Insights regarding in situ recovery mining. <i>Science of the Total Environment</i> , 2020, 721, 137758.	3.9	25
13696	The microbial abundance dynamics of the paediatric oral cavity before and after sleep. <i>Journal of Oral Microbiology</i> , 2020, 12, 1741254.	1.2	10
13697	Gene Prioritization in Parkinson's Disease Using Human Protein-Protein Interaction Network. <i>Journal of Computational Biology</i> , 2020, 27, 1610-1621.	0.8	2
13698	The Role of Overexpressed Apolipoprotein AV in Insulin-Resistant Hepatocytes. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	0
13699	The New Biomarker for Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (CESC) Based on Public Database Mining. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	19
13700	Dysregulation of Signaling Pathways Due to Differentially Expressed Genes From the B-Cell Transcriptomes of Systemic Lupus Erythematosus Patients – A Bioinformatics Approach. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 276.	2.0	57
13701	Integrative Analysis for Elucidating Transcriptomics Landscapes of Glucocorticoid-Induced Osteoporosis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 252.	1.8	3
13702	Single-Cell Transcriptomic Analysis Reveals Mitochondrial Dynamics in Oocytes of Patients With Polycystic Ovary Syndrome. <i>Frontiers in Genetics</i> , 2020, 11, 396.	1.1	39
13703	The Ratiometric Transcript Signature MX2/GPR183 Is Consistently Associated With RTS,S-Mediated Protection Against Controlled Human Malaria Infection. <i>Frontiers in Immunology</i> , 2020, 11, 669.	2.2	12
13704	Abundance, Functional, and Evolutionary Analysis of Oxalyl-Coenzyme A Decarboxylase in Human Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 672.	1.5	6
13705	A Comprehensive Proteomic and Phosphoproteomic Analysis of Retinal Pigment Epithelium Reveals Multiple Pathway Alterations in Response to the Inflammatory Stimuli. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3037.	1.8	4
13706	Dysregulations of MicroRNA and Gene Expression in Chronic Venous Disease. <i>Journal of Clinical Medicine</i> , 2020, 9, 1251.	1.0	12
13707	Prebiotic Effects of Partially Hydrolyzed Guar Gum on the Composition and Function of the Human Microbiota—Results from the PAGODA Trial. <i>Nutrients</i> , 2020, 12, 1257.	1.7	39
13708	Prediction of Transcription Factors and Their Involvement in Regulating Rifamycin Production in <i>Amycolatopsis mediterranei</i> S699. <i>Indian Journal of Microbiology</i> , 2020, 60, 310-317.	1.5	6
13709	Transcriptome analysis and metabolic profiling reveal the key role of carotenoids in the petal coloration of <i>Liriodendron tulipifera</i> . <i>Horticulture Research</i> , 2020, 7, 70.	2.9	47
13710	Comprehensive analysis of the SLC16A gene family in pancreatic cancer via integrated bioinformatics. <i>Scientific Reports</i> , 2020, 10, 7315.	1.6	37



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13711	Smad2/3 pathway ligand trap luspatercept enhances erythroid differentiation in murine $\beta$ -thalassaemia by increasing GATA-1 availability. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 6162-6177.	1.6	30
13712	Neurotransmitter networks in mouse prefrontal cortex are reconfigured by isoflurane anesthesia. <i>Journal of Neurophysiology</i> , 2020, 123, 2285-2296.	0.9	10
13713	In Silico Analysis of a Highly Mutated Gene in Cancer Provides Insight into Abnormal mRNA Splicing: Splicing Factor 3B Subunit 1K700E Mutant. <i>Biomolecules</i> , 2020, 10, 680.	1.8	6
13714	In Vitro Salivary Protein Adsorption Profile on Titanium and Ceramic Surfaces and the Corresponding Putative Immunological Implications. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3083.	1.8	8
13715	Transcriptome Analysis of Carbohydrate Metabolism Genes and Molecular Regulation of Sucrose Transport Gene LoSUT on the Flowering Process of Developing Oriental Hybrid Lily "Sorbonne" Bulb. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3092.	1.8	19
13716	Genome-wide analysis of prognostic-related lncRNAs, miRNAs and mRNAs forming a competing endogenous RNA network in lung squamous cell carcinoma. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 1711-1723.	1.2	31
13717	Prediction of circRNA-disease associations based on inductive matrix completion. <i>BMC Medical Genomics</i> , 2020, 13, 42.	0.7	42
13718	Transcriptome analysis of the response provided by <i>Lasiopodomys mandarinus</i> to severe hypoxia includes enhancing DNA repair and damage prevention. <i>Frontiers in Zoology</i> , 2020, 17, 9.	0.9	11
13719	A multidimensional systems biology analysis of cellular senescence in aging and disease. <i>Genome Biology</i> , 2020, 21, 91.	3.8	177
13720	Master Regulator Analysis of the SARS-CoV-2/Human Interactome. <i>Journal of Clinical Medicine</i> , 2020, 9, 982.	1.0	160
13721	Bioinformatic Analysis of the Flavin-Dependent Amine Oxidase Superfamily: Adaptations for Substrate Specificity and Catalytic Diversity. <i>Journal of Molecular Biology</i> , 2020, 432, 3269-3288.	2.0	21
13722	Central attacks in complex networks: A revisit with new fallback strategy. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020, 549, 124347.	1.2	17
13723	Opportunistic bacteria use quorum sensing to disturb coral symbiotic communities and mediate the occurrence of coral bleaching. <i>Environmental Microbiology</i> , 2020, 22, 1944-1962.	1.8	24
13724	GOMCL: a toolkit to cluster, evaluate, and extract non-redundant associations of Gene Ontology-based functions. <i>BMC Bioinformatics</i> , 2020, 21, 139.	1.2	37
13725	Divergent neurogenomic responses shape social learning of both personality and mate preference. <i>Journal of Experimental Biology</i> , 2020, 223, .	0.8	13
13726	Acute experimental infection of bats and ferrets with Hendra virus: Insights into the early host response of the reservoir host and susceptible model species. <i>PLoS Pathogens</i> , 2020, 16, e1008412.	2.1	22
13727	AHR Signaling Dampens Inflammatory Signature in Neonatal Skin $\gamma$ T Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2249.	1.8	11
13728	lncRNA SNHG6 plays an oncogenic role in colorectal cancer and can be used as a prognostic biomarker for solid tumors. <i>Journal of Cellular Physiology</i> , 2020, 235, 7620-7634.	2.0	27



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13729	CRISPLD1: a novel conserved target in the transition to human heart failure. <i>Basic Research in Cardiology</i> , 2020, 115, 27.	2.5	13
13730	Genome-wide identification of long non-coding RNAs and circular RNAs reveal their ceRNA networks in response to cucumber green mottle mosaic virus infection in watermelon. <i>Archives of Virology</i> , 2020, 165, 1177-1190.	0.9	41
13731	Soil pH exerts stronger impacts than vegetation type and plant diversity on soil bacterial community composition in subtropical broad-leaved forests. <i>Plant and Soil</i> , 2020, 450, 273-286.	1.8	27
13732	N-Glycoproteome Reveals That N-Glycosylation Plays Crucial Roles in Photosynthesis and Carbon Metabolism in Young Rice Leaves. <i>Journal of Plant Biology</i> , 2020, 63, 165-175.	0.9	7
13733	Corruption and complexity: a scientific framework for the analysis of corruption networks. <i>Applied Network Science</i> , 2020, 5, .	0.8	43
13734	Pan-interactomics and its applications. , 2020, , 397-435.		1
13735	ADAR1 Transcriptome editing promotes breast cancer progression through the regulation of cell cycle and DNA damage response. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118716.	1.9	17
13736	Defining and Targeting Adaptations to Oncogenic KRASG12C Inhibition Using Quantitative Temporal Proteomics. <i>Cell Reports</i> , 2020, 30, 4584-4599.e4.	2.9	53
13737	Wastewater treatment plant upgrade induces the receiving river retaining bioavailable nitrogen sources. <i>Environmental Pollution</i> , 2020, 263, 114478.	3.7	21
13738	Rapid action of mechanism investigation of Yixin Ningshen tablet in treating depression by combinatorial use of systems biology and bioinformatics tools. <i>Journal of Ethnopharmacology</i> , 2020, 257, 112827.	2.0	6
13739	The plant-growth promoting bacteria promote cadmium uptake by inducing a hormonal crosstalk and lateral root formation in a hyperaccumulator plant <i>Sedum alfredii</i> . <i>Journal of Hazardous Materials</i> , 2020, 395, 122661.	6.5	67
13740	Active constituents and mechanisms of Respiratory Detox Shot, a traditional Chinese medicine prescription, for COVID-19 control and prevention: Network-molecular docking-LC-MS/MS analysis. <i>Journal of Integrative Medicine</i> , 2020, 18, 229-241.	1.4	42
13741	The impact of rattlesnake venom on mice cerebellum proteomics points to synaptic inhibition and tissue damage. <i>Journal of Proteomics</i> , 2020, 221, 103779.	1.2	8
13742	Myeloid-specific IRE1alpha deletion reduces tumour development in a diabetic, non-alcoholic steatohepatitis-induced hepatocellular carcinoma mouse model. <i>Metabolism: Clinical and Experimental</i> , 2020, 107, 154220.	1.5	19
13743	Lack of evidence for the role of gut microbiota in PAH biodegradation by the polychaete <i>Capitella teleta</i> . <i>Science of the Total Environment</i> , 2020, 725, 138356.	3.9	4
13744	Transcriptomics in RCC. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 742-754.	0.8	6
13745	Structural Basis for the Asymmetry of a 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2020, 59, 1592-1603.	1.2	6
13746	Therapeutically actionable PAK4 is amplified, overexpressed, and involved in bladder cancer progression. <i>Oncogene</i> , 2020, 39, 4077-4091.	2.6	19

#	ARTICLE	IF	CITATIONS
13747	Al-induced proteomics changes in tomato plants over-expressing a glyoxalase I gene. Horticulture Research, 2020, 7, 43.	2.9	7
13748	An exported kinase family mediates species-specific erythrocyte remodelling and virulence in human malaria. Nature Microbiology, 2020, 5, 848-863.	5.9	44
13749	Transcriptional profiling and therapeutic targeting of oxidative stress in neuroinflammation. Nature Immunology, 2020, 21, 513-524.	7.0	118
13750	De novo transcriptome assembly and analysis of Phragmites karka, an invasive halophyte, to study the mechanism of salinity stress tolerance. Scientific Reports, 2020, 10, 5192.	1.6	24
13751	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. Scientific Reports, 2020, 10, 5753.	1.6	6
13752	Differential stromal reprogramming in benign and malignant naturally occurring canine mammary tumours identifies disease-modulating stromal components. Scientific Reports, 2020, 10, 5506.	1.6	20
13753	Skin transcriptome profiling of Changthangi goats highlights the relevance of genes involved in Pashmina production. Scientific Reports, 2020, 10, 6050.	1.6	21
13754	The regulatory and transcriptional landscape associated with carbon utilization in a filamentous fungus. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6003-6013.	3.3	75
13755	Assessment for Risk Status of Colorectal Cancer Patients: A Novel Prediction Model Based on Immune-Related Genes. DNA and Cell Biology, 2020, 39, 958-964.	0.9	7
13756	Tomato-Associated Archaea Show a Cultivar-Specific Rhizosphere Effect but an Unspecific Transmission by Seeds. Phytobiomes Journal, 2020, 4, 133-141.	1.4	31
13757	Exploring immune-related genes with prognostic value in microenvironment of breast cancer from TCGA database. Medicine (United States), 2020, 99, e19561.	0.4	9
13758	The <i>FATTY ACID DESATURASE2</i> Family in Tomato Contributes to Primary Metabolism and Stress Responses. Plant Physiology, 2020, 182, 1083-1099.	2.3	31
13759	Natural Variation in RNA m <sup>6</sup> A Methylation and Its Relationship with Translational Status. Plant Physiology, 2020, 182, 332-344.	2.3	73
13760	Integrated mRNA and microRNA transcriptome profiling during differentiation of human nasal polyp epithelium reveals an altered ciliogenesis. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2548-2561.	2.7	21
13761	Multifunctionality of biocrusts is positively predicted by network topologies consistent with interspecies facilitation. Molecular Ecology, 2020, 29, 1560-1573.	2.0	23
13762	Identification and characterization of long non-coding RNAs as competing endogenous RNAs in the cold stress response of <i>Triticum aestivum</i> . Plant Biology, 2020, 22, 635-645.	1.8	18
13763	Plausible association between drought stress tolerance of barley ( <i>Hordeum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (vulg genes. Physiologia Plantarum, 2020, 170, 46-59.	2.6	15
13764	Genetic and Chemical-Genetic Interactions Map Biogenesis and Permeability Determinants of the Outer Membrane of Escherichia coli. MBio, 2020, 11, .	1.8	20

#	ARTICLE	IF	CITATIONS
13765	Gestational Diabetes Mellitus Is Associated with Reduced Dynamics of Gut Microbiota during the First Half of Pregnancy. <i>MSystems</i> , 2020, 5, .	1.7	58
13766	Respiratory Viral Infection Alters the Gut Microbiota by Inducing Inappetence. <i>MBio</i> , 2020, 11, .	1.8	122
13767	Shotgun Metagenomics of Gut Microbiota in Humans with up to Extreme Longevity and the Increasing Role of Xenobiotic Degradation. <i>MSystems</i> , 2020, 5, .	1.7	91
13768	The Gut Microbiota in <i>Camellia</i> Weevils Are Influenced by Plant Secondary Metabolites and Contribute to Saponin Degradation. <i>MSystems</i> , 2020, 5, .	1.7	44
13769	Mining Data From Plasma Cell Differentiation Identified Novel Genes for Engineering of a Yeast Antibody Factory. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 255.	2.0	2
13770	Integrated Analysis to Evaluate the Prognostic Value of Signature mRNAs in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2020, 11, 253.	1.1	11
13771	Analysis of the Interaction Network of Hub miRNAs-Hub Genes, Being Involved in Idiopathic Pulmonary Fibers and Its Emerging Role in Non-small Cell Lung Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 302.	1.1	26
13772	Weighted Gene Co-expression Network Analysis Identifies Critical Genes for the Production of Cellulase and Xylanase in <i>Penicillium oxalicum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 520.	1.5	19
13773	The Predicted Key Molecules, Functions, and Pathways That Bridge Mild Cognitive Impairment (MCI) and Alzheimer's Disease (AD). <i>Frontiers in Neurology</i> , 2020, 11, 233.	1.1	43
13774	The Interaction Between lncRNA SNHG6 and hnRNPA1 Contributes to the Growth of Colorectal Cancer by Enhancing Aerobic Glycolysis Through the Regulation of Alternative Splicing of PKM. <i>Frontiers in Oncology</i> , 2020, 10, 363.	1.3	61
13775	Characterization of Hypoxia Signature to Evaluate the Tumor Immune Microenvironment and Predict Prognosis in Glioma Groups. <i>Frontiers in Oncology</i> , 2020, 10, 796.	1.3	118
13776	Traditional Chinese Medicine and Gut Microbiome: Their Respective and Concert Effects on Healthcare. <i>Frontiers in Pharmacology</i> , 2020, 11, 538.	1.6	32
13777	Functional Interactomes of Genes Showing Association with Type-2 Diabetes and Its Intermediate Phenotypic Traits Point towards Adipo-Centric Mechanisms in Its Pathophysiology. <i>Biomolecules</i> , 2020, 10, 601.	1.8	7
13778	Upregulation of Protein Synthesis and Proteasome Degradation Confers Sensitivity to Proteasome Inhibitor Bortezomib in Myc-Atypical Teratoid/Rhabdoid Tumors. <i>Cancers</i> , 2020, 12, 752.	1.7	6
13779	Gene Expression Profiling of Corpus luteum Reveals Important Insights about Early Pregnancy in Domestic Sheep. <i>Genes</i> , 2020, 11, 415.	1.0	15
13780	Identification of Potential Biomarkers for Anti-PD-1 Therapy in Melanoma by Weighted Correlation Network Analysis. <i>Genes</i> , 2020, 11, 435.	1.0	14
13781	Transcriptomic Profiling in Fins of Atlantic Salmon Parasitized with Sea Lice: Evidence for an Early Imbalance Between Chalimus-Induced Immunomodulation and the Host's Defense Response. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2417.	1.8	27
13782	Harvesting Mango Fruit with a Short Stem-End Altered Endophytic Microbiome and Reduce Stem-End Rot. <i>Microorganisms</i> , 2020, 8, 558.	1.6	24

#	ARTICLE	IF	CITATIONS
13783	Comparative Transcriptomics Reveals Distinct Gene Expressions of a Model Ciliated Protozoan Feeding on Bacteria-Free Medium, Digestible, and Digestion-Resistant Bacteria. <i>Microorganisms</i> , 2020, 8, 559.	1.6	12
13784	Phylogenomic Analysis of Secondary Metabolism in the Toxic Cyanobacterial Genera <i>Anabaena</i> , <i>Dolichospermum</i> and <i>Aphanizomenon</i> . <i>Toxins</i> , 2020, 12, 248.	1.5	34
13785	Systems Biology Analysis of the Antagonizing Effects of HIV-1 Tat Expression in the Brain over Transcriptional Changes Caused by Methamphetamine Sensitization. <i>Viruses</i> , 2020, 12, 426.	1.5	7
13786	Secretome-Mediated Interactions with Intestinal Epithelial Cells: A Role for Secretome Components from <i>Lactobacillus rhamnosus</i> R0011 in the Attenuation of <i>Salmonella enterica</i> Serovar Typhimurium Secretome and TNF- $\alpha$ -Induced Proinflammatory Responses. <i>Journal of Immunology</i> , 2020, 204, 2523-2534.	0.4	13
13787	Comprehensive Map of the <i>Artemisia annua</i> Proteome and Quantification of Differential Protein Expression in Chemotypes Producing High versus Low Content of Artemisinin. <i>Proteomics</i> , 2020, 20, e1900310.	1.3	6
13788	Genome-wide Profiling Identifies DNA Methylation Signatures of Aging in Rod Photoreceptors Associated with Alterations in Energy Metabolism. <i>Cell Reports</i> , 2020, 31, 107525.	2.9	20
13789	A high definition picture of somatic mutations in chronic lymphoproliferative disorder of natural killer cells. <i>Blood Cancer Journal</i> , 2020, 10, 42.	2.8	22
13790	The Flemmingsome reveals an ESCRT-to-membrane coupling via ALIX/syntenin/syndecan-4 required for completion of cytokinesis. <i>Nature Communications</i> , 2020, 11, 1941.	5.8	61
13791	Recapitulating kidney development in vitro by priming and differentiating mouse embryonic stem cells in monolayers. <i>Npj Regenerative Medicine</i> , 2020, 5, 7.	2.5	7
13792	Integrating transcriptome and metabolome reveals molecular networks involved in genetic and environmental variation in tobacco. <i>DNA Research</i> , 2020, 27, .	1.5	21
13793	Prognostic Inflammasome-Related Signature Construction in Kidney Renal Clear Cell Carcinoma Based on a Pan-Cancer Landscape. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	3
13794	<i>STAT3</i> -dependent analysis reveals <i>PDK4</i> as independent predictor of recurrence in prostate cancer. <i>Molecular Systems Biology</i> , 2020, 16, e9247.	3.2	38
13795	Transcription Factor Profiling to Predict Recurrence-Free Survival in Breast Cancer: Development and Validation of a Nomogram to Optimize Clinical Management. <i>Frontiers in Genetics</i> , 2020, 11, 333.	1.1	8
13796	A comprehensive review of computational techniques for the prediction of drug side effects. <i>Drug Development Research</i> , 2020, 81, 650-670.	1.4	27
13797	FADS1 promotes the progression of laryngeal squamous cell carcinoma through activating AKT/mTOR signaling. <i>Cell Death and Disease</i> , 2020, 11, 272.	2.7	27
13798	Metagenomic analysis of the human microbiome reveals the association between the abundance of gut bile salt hydrolases and host health. <i>Gut Microbes</i> , 2020, 11, 1300-1313.	4.3	59
13799	RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	25
13800	The TCR Repertoire Reconstitution in Multiple Sclerosis: Comparing One-Shot and Continuous Immunosuppressive Therapies. <i>Frontiers in Immunology</i> , 2020, 11, 559.	2.2	25

#	ARTICLE	IF	CITATIONS
13801	Transcriptome Analyses of lncRNAs in A2E-Stressed Retinal Epithelial Cells Unveil Advanced Links between Metabolic Impairments Related to Oxidative Stress and Retinitis Pigmentosa. <i>Antioxidants</i> , 2020, 9, 318.	2.2	49
13802	Moesin (MSN) as a Novel Proteome-Based Diagnostic Marker for Early Detection of Invasive Bladder Urothelial Carcinoma in Liquid-Based Cytology. <i>Cancers</i> , 2020, 12, 1018.	1.7	10
13803	Comprehensive Analysis of the Tumor Microenvironment in Cutaneous Melanoma associated with Immune Infiltration. <i>Journal of Cancer</i> , 2020, 11, 3858-3870.	1.2	22
13804	lincROR promotes the progression of breast cancer and decreases the sensitivity to rapamycin through miR-194 targeting MECP2. <i>Molecular Oncology</i> , 2020, 14, 2231-2250.	2.1	37
13805	Continuous cropping of soybean induced a more fluctuating fungal network and intensive pathogenic fungal interactions in a Mollisol of Northeast China. <i>Soil Science Society of America Journal</i> , 2020, 84, 775-783.	1.2	7
13806	Temporal transcriptome analysis of neuronal commitment reveals the preeminent role of the divergent lncRNA biotype and a critical candidate gene during differentiation. <i>Cell Death Discovery</i> , 2020, 6, 28.	2.0	4
13807	Conditional deletion of Nedd4-2 in lung epithelial cells causes progressive pulmonary fibrosis in adult mice. <i>Nature Communications</i> , 2020, 11, 2012.	5.8	52
13808	MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. <i>Nature Communications</i> , 2020, 11, 2025.	5.8	5
13809	Flow-induced Reorganization of Laminin-integrin Networks Within the Endothelial Basement Membrane Uncovered by Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1179-1192.	2.5	14
13810	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. <i>Plant Physiology</i> , 2020, 183, 483-500.	2.3	24
13811	Identification of gene co-expression modules and hub genes associated with the invasiveness of pituitary adenoma. <i>Endocrine</i> , 2020, 68, 377-389.	1.1	4
13812	Differential expression of nuclear genes encoding mitochondrial proteins from urban and rural populations in Morocco. <i>Cell Stress and Chaperones</i> , 2020, 25, 847-856.	1.2	5
13813	Deficiency of the onco-miRNA cluster, miR-106b <sup>1/4</sup> 25, causes oligozoospermia and the cooperative action of miR-106b <sup>1/4</sup> 25 and miR-17 <sup>1/4</sup> 92 is required to maintain male fertility. <i>Molecular Human Reproduction</i> , 2020, 1.3 26, 389-401.	1.3	10
13814	The thrombospondin module 1 domain of the matricellular protein CCN3 shows an atypical disulfide pattern and incomplete CWR layers. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 124-134.	1.1	5
13815	Structural evidence for a latch mechanism regulating access to the active site of SufS-family cysteine desulfurases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 291-301.	1.1	8
13816	Transcriptome Analysis Reveals IsiA-Regulatory Mechanisms Underlying Iron Depletion and Oxidative-Stress Acclimation in <i>Synechocystis</i> sp. Strain PCC 6803. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	7
13817	The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. <i>MSystems</i> , 2020, 5, .	1.7	11
13818	Comparative molecular networking analysis of a Rauwolfia plant powder and biological matrices in a fatal ingestion case. <i>Forensic Toxicology</i> , 2020, 38, 447-454.	1.4	12

#	ARTICLE	IF	CITATIONS
13819	Astragaloside IV acts through multi-scale mechanisms to effectively reduce diabetic nephropathy. <i>Pharmacological Research</i> , 2020, 157, 104831.	3.1	63
13820	Drug Research Meets Network Science: Where Are We?. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 8653-8666.	2.9	29
13821	Protein-protein interaction network with machine learning models and multiomics data reveal potential neurodegenerative disease-related proteins. <i>Human Molecular Genetics</i> , 2020, 29, 1378-1387.	1.4	14
13822	Insights into the Diversification and Evolution of R2R3-MYB Transcription Factors in Plants. <i>Plant Physiology</i> , 2020, 183, 637-655.	2.3	102
13823	Identifying nucleic acid-associated proteins in <i>Mycobacterium smegmatis</i> by mass spectrometry-based proteomics. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 19.	1.0	7
13824	A single cell transcriptome atlas of the developing zebrafish hindbrain. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	39
13825	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. <i>PLoS Computational Biology</i> , 2020, 16, e1007522.	1.5	8
13826	Pan-Cancer Analysis of Mitochondria Chaperone-Client Co-Expression Reveals Chaperone Functional Partitioning. <i>Cancers</i> , 2020, 12, 825.	1.7	9
13827	Exploratory Analysis of Circulating miRNA Signatures in Atrial Fibrillation Patients Determining Potential Biomarkers to Support Decision-Making in Anticoagulation and Catheter Ablation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2444.	1.8	13
13828	DNA demethylation is a driver for chick retina regeneration. <i>Epigenetics</i> , 2020, 15, 998-1019.	1.3	18
13829	Altered gut microbial profile is associated with abnormal metabolism activity of Autism Spectrum Disorder. <i>Gut Microbes</i> , 2020, 11, 1246-1267.	4.3	166
13830	SPD_1495 Contributes to Capsular Polysaccharide Synthesis and Virulence in <i>Streptococcus pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	10
13831	Integrated characterisation of cancer genes identifies key molecular biomarkers in stomach adenocarcinoma. <i>Journal of Clinical Pathology</i> , 2020, 73, 579-586.	1.0	33
13832	Molecular adaptation to salinity fluctuation in tropical intertidal environments of a mangrove tree <i>Sonneratia alba</i> . <i>BMC Plant Biology</i> , 2020, 20, 178.	1.6	24
13833	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	4.9	154
13834	Development of a Bioinformatics Framework for Identification and Validation of Genomic Biomarkers and Key Immunopathology Processes and Controllers in Infectious and Non-infectious Severe Inflammatory Response Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 380.	2.2	17
13835	CircRNA Expression Profile during Yak Adipocyte Differentiation and Screen Potential circRNAs for Adipocyte Differentiation. <i>Genes</i> , 2020, 11, 414.	1.0	25
13836	The Significance of MicroRNAs Expression in Regulation of Extracellular Matrix and Other Drug Resistant Genes in Drug Resistant Ovarian Cancer Cell Lines. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2619.	1.8	21



#	ARTICLE	IF	CITATIONS
13837	Systematic prediction of key genes for ovarian cancer by co-expression network analysis. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 6298-6307.	1.6	16
13838	Diversity of Secondary Metabolism in <i>Aspergillus nidulans</i> Clinical Isolates. <i>MSphere</i> , 2020, 5, .	1.3	32
13839	Network Pharmacology Approach to Uncover the Mechanism Governing the Effect of <i>Radix Achyranthis Bidentatae</i> on Osteoarthritis. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 121.	1.2	31
13840	Identification of the Genetic Requirements for Zinc Tolerance and Toxicity in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 479-488.	0.8	21
13841	Identification of key candidate genes and pathways revealing the protective effect of liraglutide on diabetic cardiac muscle by integrated bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 181-181.	0.7	5
13842	MicroRNA Networks in Pancreatic Islet Cells: Normal Function and Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 804-812.	0.3	35
13843	Integrative Proteome and Acetylome Analyses of Murine Responses to <i>Cryptococcus neoformans</i> Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 575.	1.5	12
13844	Identification of Key Genes and the Pathophysiology Associated With Major Depressive Disorder Patients Based on Integrated Bioinformatics Analysis. <i>Frontiers in Psychiatry</i> , 2020, 11, 192.	1.3	16
13845	Identifying Protein-metabolite Networks Associated with COPD Phenotypes. <i>Metabolites</i> , 2020, 10, 124.	1.3	25
13846	Comprehensive insights on pivotal prognostic signature involved in clear cell renal cell carcinoma microenvironment using the ESTIMATE algorithm. <i>Cancer Medicine</i> , 2020, 9, 4310-4323.	1.3	42
13847	The evolutionary and transmission characteristic of HIV-1 CRF07_BC in Nanjing, Jiangsu. <i>Journal of Medical Virology</i> , 2020, 92, 3237-3245.	2.5	4
13848	Pan-proteomics: Technologies, applications, and challenges. , 2020, , 357-369.		0
13849	Small Conformational Changes Underlie Evolution of Resistance to NNRTI in HIV Reverse Transcriptase. <i>Biophysical Journal</i> , 2020, 118, 2489-2501.	0.2	3
13850	G3BP1 Is a Tunable Switch that Triggers Phase Separation to Assemble Stress Granules. <i>Cell</i> , 2020, 181, 325-345.e28.	13.5	697
13851	Characterizing a riverine microbiome impacted by extreme disturbance caused by a mining sludge tsunami. <i>Chemosphere</i> , 2020, 253, 126584.	4.2	15
13852	Clinicopathological value and underlying molecular mechanism of annexin A2 in 992 cases of thyroid carcinoma. <i>Computational Biology and Chemistry</i> , 2020, 86, 107258.	1.1	6
13853	Characteristics of and variation in airborne ARGs among urban hospitals and adjacent urban and suburban communities: A metagenomic approach. <i>Environment International</i> , 2020, 139, 105625.	4.8	55
13854	Distributions of chlorinated paraffins and the effects on soil microbial community structure in a production plant brownfield site. <i>Environmental Pollution</i> , 2020, 262, 114328.	3.7	23



#	ARTICLE	IF	CITATIONS
13855	Screening and identification of potential prognostic biomarkers in bladder urothelial carcinoma: Evidence from bioinformatics analysis. <i>Gene Reports</i> , 2020, 20, 100658.	0.4	0
13856	Network pharmacology research of Astragali Radix in treating chronic atrophic gastritis rats based on mitochondrial metabonomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2020, 1145, 122109.	1.2	4
13857	Biogeography and emerging significance of Actinobacteria in Australia and Northern Antarctica soils. <i>Soil Biology and Biochemistry</i> , 2020, 146, 107805.	4.2	54
13858	Structure-based Identification of Endocrine Disrupting Pesticides Targeting Breast Cancer Proteins. <i>Toxicology</i> , 2020, 439, 152459.	2.0	17
13859	Functional effects of differentially expressed microRNAs in A549 cells exposed to MWCNT-7 or crocidolite. <i>Toxicology Letters</i> , 2020, 328, 7-18.	0.4	6
13860	Upregulation of TDRD1 Promotes the Sexual Maturation in Allotetraploids Hybridized from Red Crucian Carp ( <i>Carassius auratus Red var</i> ) (♀ <sup>TM</sup> ) and Common Carp ( <i>Cyprinus carpio L</i> ) (♂ <sup>TM</sup> ). <i>Journal of Proteome Research</i> , 2020, 19, 2337-2345.	1.8	2
13861	Quantitative Proteomics Reveals Docosahexaenoic Acid-Mediated Neuroprotective Effects in Lipopolysaccharide-Stimulated Microglial Cells. <i>Journal of Proteome Research</i> , 2020, 19, 2236-2246.	1.8	11
13862	Comprehensive Examination of the Mouse Lung Metabolome Following <i>Mycobacterium tuberculosis</i> Infection Using a Multiplatform Mass Spectrometry Approach. <i>Journal of Proteome Research</i> , 2020, 19, 2053-2070.	1.8	35
13863	Multiplexed Cre-dependent selection yields systemic AAVs for targeting distinct brain cell types. <i>Nature Methods</i> , 2020, 17, 541-550.	9.0	121
13864	Gene-expression profiles of abdominal perivascular adipose tissue distinguish aortic occlusive from stenotic atherosclerotic lesions and denote different pathogenetic pathways. <i>Scientific Reports</i> , 2020, 10, 6245.	1.6	8
13865	Regulatory relationship between quality variation and environment of <i>Cistanche deserticola</i> in three ecotypes based on soil microbiome analysis. <i>Scientific Reports</i> , 2020, 10, 6662.	1.6	18
13866	Phosphoproteomic characterization of the signaling network resulting from activation of the chemokine receptor CCR2. <i>Journal of Biological Chemistry</i> , 2020, 295, 6518-6531.	1.6	16
13867	Identification of Biomarkers Related to Systemic Sclerosis With or Without Pulmonary Hypertension Using Co-expression Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1519-1531.	0.8	7
13868	Alternative proteins are functional regulators in cell reprogramming by PKA activation. <i>Nucleic Acids Research</i> , 2020, 48, 7864-7882.	6.5	24
13869	<i>Camellia</i> Plant Resistance and Susceptibility to Petal Blight Disease Are Defined by the Timing of Defense Responses. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 982-995.	1.4	2
13870	Ceramide launches an acute anti-adhesion pro-migration cell signaling program in response to chemotherapy. <i>FASEB Journal</i> , 2020, 34, 7610-7630.	0.2	27
13871	Identification of potential prognostic long non-coding RNA for predicting survival in intrahepatic cholangiocarcinoma. <i>Medicine (United States)</i> , 2020, 99, e19606.	0.4	8
13872	Bioinformatic identification of hub genes and key pathways in neutrophils of patients with acute respiratory distress syndrome. <i>Medicine (United States)</i> , 2020, 99, e19820.	0.4	8

#	ARTICLE	IF	CITATIONS
13873	Suppressor mutations in <i>Mecp2</i> -null mice implicate the DNA damage response in Rett syndrome pathology. <i>Genome Research</i> , 2020, 30, 540-552.	2.4	13
13874	Putative cis-Regulatory Elements Predict Iron Deficiency Responses in Arabidopsis Roots. <i>Plant Physiology</i> , 2020, 182, 1420-1439.	2.3	26
13875	A novel landscape of nuclear human CDK2 substrates revealed by in situ phosphorylation. <i>Science Advances</i> , 2020, 6, eaaz9899.	4.7	22
13876	Cyanuric Acid Biodegradation via Biuret: Physiology, Taxonomy, and Geospatial Distribution. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
13877	Global Trends in Proteome Remodeling of the Outer Membrane Modulate Antimicrobial Permeability in <i>Klebsiella pneumoniae</i> . <i>MBio</i> , 2020, 11, .	1.8	41
13878	The Molecular Processes in the Trabecular Meshwork After Exposure to Corticosteroids and in Corticosteroid-Induced Ocular Hypertension. , 2020, 61, 24.		13
13879	Transcriptomic diversity in seedling roots of European flint maize in response to cold. <i>BMC Genomics</i> , 2020, 21, 300.	1.2	14
13880	Computational models applied to metabolomics data hints at the relevance of glutamine metabolism in breast cancer. <i>BMC Cancer</i> , 2020, 20, 307.	1.1	9
13881	Right and left-sided colon cancers - specificity of molecular mechanisms in tumorigenesis and progression. <i>BMC Cancer</i> , 2020, 20, 317.	1.1	51
13882	Microarray data analysis on gene and miRNA expression to identify biomarkers in non-small cell lung cancer. <i>BMC Cancer</i> , 2020, 20, 329.	1.1	33
13883	Investigation of cardiovascular protective effect of Shenmai injection by network pharmacology and pharmacological evaluation. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 112.	1.2	18
13884	Repeated fed-batch strategy and metabolomic analysis to achieve high docosahexaenoic acid productivity in <i>Cryptocodinium cohnii</i> . <i>Microbial Cell Factories</i> , 2020, 19, 91.	1.9	11
13885	A comprehensive overview of bull sperm-borne small non-coding RNAs and their diversity across breeds. <i>Epigenetics and Chromatin</i> , 2020, 13, 19.	1.8	31
13886	A genetic interaction map centered on cohesin reveals auxiliary factors in sister chromatid cohesion. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	5
13887	Primary myeloid cell proteomics and transcriptomics: importance of $\beta$ tubulin isotypes for osteoclast function. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	11
13888	Blood co-expression modules identify potential modifier genes of diabetes and lung function in cystic fibrosis. <i>PLoS ONE</i> , 2020, 15, e0231285.	1.1	6
13889	<i>ZGRF1</i> Is Associated with Poor Prognosis in Triple-Negative Breast Cancer and Promotes Cancer Stemness Based on Bioinformatics. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 2843-2854.	1.0	7
13890	An Investigation of the Mechanism of Rapid Relief of Ulcerative Colitis Induced by Five-flavor <i>Sophora Flavescens</i> Enteric-coated Capsules Based on Network Pharmacology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 239-252.	0.6	9

#	ARTICLE	IF	CITATIONS
13891	A novel mechanism of intervertebral disc degeneration: imbalance between autophagy and apoptosis. <i>Epigenomics</i> , 2020, 12, 1095-1108.	1.0	16
13892	Knowledge-Based Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 23-41.	2.8	34
13893	The Construction and Analysis of the Aberrant lncRNA-miRNA-mRNA Network in Adipose Tissue from Type 2 Diabetes Individuals with Obesity. <i>Journal of Diabetes Research</i> , 2020, 2020, 1-14.	1.0	24
13894	The <i>miR-582/CD1B</i> Axis Is Involved in Regulation of Dendritic Cells and Is Associated with Clinical Outcomes in Advanced Lung Adenocarcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	8
13895	Single-Cell-Derived Primary Rectal Carcinoma Cell Lines Reflect Intratumor Heterogeneity Associated with Treatment Response. <i>Clinical Cancer Research</i> , 2020, 26, 3468-3480.	3.2	9
13896	Induced Tumor Heterogeneity Reveals Factors Informing Radiation and Immunotherapy Combinations. <i>Clinical Cancer Research</i> , 2020, 26, 2972-2985.	3.2	9
13897	Blood Gene Expression Profile Study Revealed the Activation of Apoptosis and p53 Signaling Pathway May Be the Potential Molecular Mechanisms of Ionizing Radiation Damage and Radiation-Induced Bystander Effects. <i>Dose-Response</i> , 2020, 18, 155932582091418.	0.7	7
13898	Identification of novel biomarkers in ischemic stroke: a genome-wide integrated analysis. <i>BMC Medical Genetics</i> , 2020, 21, 66.	2.1	22
13899	A key genomic signature associated with lymphovascular invasion in head and neck squamous cell carcinoma. <i>BMC Cancer</i> , 2020, 20, 266.	1.1	12
13900	An integrative, genomic, transcriptomic and network-assisted study to identify genes associated with human cleft lip with or without cleft palate. <i>BMC Medical Genomics</i> , 2020, 13, 39.	0.7	16
13901	MicroRNA-1202 plays a vital role in osteoarthritis via KCNQ1OT1 has-miR-1202-ETS1 regulatory pathway. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 130.	0.9	10
13902	Probing lasting cryoinjuries to oocyte-embryo transcriptome. <i>PLoS ONE</i> , 2020, 15, e0231108.	1.1	10
13903	piRNAs Regulated by Mitochondria Variation Linked With Reproduction and Aging in <i>Caenorhabditis elegans</i> . <i>Frontiers in Genetics</i> , 2020, 11, 190.	1.1	3
13904	Cell Type-Specific Gene Network-Based Analysis Depicts the Heterogeneity of Autism Spectrum Disorder. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 59.	1.8	9
13905	A Systematic Bioinformatics Workflow With Meta-Analytics Identified Potential Pathogenic Factors of Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2020, 14, 209.	1.4	7
13906	A Genome-Wide Integrative Association Study of DNA Methylation and Gene Expression Data and Later Life Cognitive Functioning in Monozygotic Twins. <i>Frontiers in Neuroscience</i> , 2020, 14, 233.	1.4	5
13907	Cleavage of the APE1 N-Terminal Domain in Acute Myeloid Leukemia Cells Is Associated with Proteasomal Activity. <i>Biomolecules</i> , 2020, 10, 531.	1.8	6
13908	Deciphering Master Gene Regulators and Associated Networks of Human Mesenchymal Stromal Cells. <i>Biomolecules</i> , 2020, 10, 557.	1.8	8

#	ARTICLE	IF	CITATIONS
13909	Nucleolin-Sle A Glycoforms as E-Selectin Ligands and Potentially Targetable Biomarkers at the Cell Surface of Gastric Cancer Cells. <i>Cancers</i> , 2020, 12, 861.	1.7	20
13910	Male sterile 305 Mutation Leads the Misregulation of Anther Cuticle Formation by Disrupting Lipid Metabolism in Maize. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2500.	1.8	4
13911	â€œNotameâ€ Workflow for Non-Targeted LCâ€MS Metabolic Profiling. <i>Metabolites</i> , 2020, 10, 135.	1.3	71
13912	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. <i>Viruses</i> , 2020, 12, 398.	1.5	10
13913	Proximity mapping of the microtubule plus-end tracking protein SLAIN2 using the BioID approach. <i>Turkish Journal of Biology</i> , 2020, 44, 61-72.	2.1	4
13914	Decreased Expression of NUSAP1 Predicts Poor Overall Survival in Cervical Cancer. <i>Journal of Cancer</i> , 2020, 11, 2852-2863.	1.2	19
13915	EphB2 represents an independent prognostic marker in patients with gastric cancer and promotes tumour cell aggressiveness. <i>Journal of Cancer</i> , 2020, 11, 2778-2787.	1.2	10
13916	Identification of Key Gene and Pathways for the Prediction of Peritoneal Metastasis of Gastric Cancer by Co-expression Analysis. <i>Journal of Cancer</i> , 2020, 11, 3041-3051.	1.2	13
13917	The secretome of skin cancer cells activates the mTOR/MYC pathway in healthy keratinocytes and induces tumorigenic properties. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118717.	1.9	6
13918	Lumbar intervertebral disc mRNA sequencing identifies the regulatory pathway in patients with disc herniation and spondylolisthesis. <i>Gene</i> , 2020, 750, 144634.	1.0	15
13919	A comprehensive analysis of the lysine acetylome reveals diverse functions of acetylated proteins during de-etiolation in <i>Zea mays</i> . <i>Journal of Plant Physiology</i> , 2020, 248, 153158.	1.6	9
13920	Pro-opiomelanocortin (POMC) neuron translome signatures underlying obesogenic gestational malprogramming in mice. <i>Molecular Metabolism</i> , 2020, 36, 100963.	3.0	12
13921	Quantitative Proteomics of Human Heart Samples Collected In Vivo Reveal the Remodeled Protein Landscape of Dilated Left Atrium Without Atrial Fibrillation. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1132-1144.	2.5	24
13922	Geneâ€based association analysis reveals involvement of LAMA5 and cell adhesion pathways in nicotine dependence in Africanâ€and Europeanâ€American samples. <i>Addiction Biology</i> , 2021, 26, e12898.	1.4	2
13923	Fucosidases from the human gut symbiont <i>Ruminococcus gnavus</i> . <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 675-693.	2.4	52
13924	Autophagy is responsible for the accumulation of proteogenic dipeptides in response to heat stress in <i>Arabidopsis thaliana</i> . <i>FEBS Journal</i> , 2021, 288, 281-292.	2.2	26
13925	Potential target identification for breast cancer and screening of small molecule inhibitors: A bioinformatics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1975-1989.	2.0	2
13926	In silico evaluation of the antidiabetic activity of natural compounds from <i>Hovenia dulcis</i> Thunberg. <i>Journal of Herbal Medicine</i> , 2021, 28, 100349.	1.0	3

#	ARTICLE	IF	CITATIONS
13927	RNA-seq Transcriptome Profiling of the Halophyte <i>Salicornia persica</i> in Response to Salinity. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 707-721.	2.8	11
13928	Protection against peripheral artery disease injury by Ruan Jian Qing Mai formula via metabolic programming. <i>Biotechnology and Applied Biochemistry</i> , 2021, 68, 366-380.	1.4	5
13929	tax2vec: Constructing Interpretable Features from Taxonomies for Short Text Classification. <i>Computer Speech and Language</i> , 2021, 65, 101104.	2.9	27
13930	Prevention of age-associated neuronal hyperexcitability with improved learning and attention upon knockout or antagonism of LPAR2. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1029-1050.	2.4	15
13931	Forecasting Flight Delays Using Clustered Models Based on Airport Networks. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2021, 22, 3179-3189.	4.7	12
13932	The circRNA-miRNA-mRNA regulatory network in systemic lupus erythematosus. <i>Clinical Rheumatology</i> , 2021, 40, 331-339.	1.0	28
13933	Novel FMRP interaction networks linked to cellular stress. <i>FEBS Journal</i> , 2021, 288, 837-860.	2.2	31
13934	Analysis of carcinogenic signaling networks in endometrial cancer identifies RAB17 as a potential target. <i>Journal of Cellular Physiology</i> , 2021, 236, 328-339.	2.0	4
13935	Identification of novel genes in testicular cancer microenvironment based on ESTIMATE algorithm-derived immune scores. <i>Journal of Cellular Physiology</i> , 2021, 236, 706-713.	2.0	35
13936	Dietary supplementation with <i>Bacillus subtilis</i> DSM 32315 alters the intestinal microbiota and metabolites in weaned piglets. <i>Journal of Applied Microbiology</i> , 2021, 130, 217-232.	1.4	19
13937	Cold adaptation in drylands: transcriptomic insights into cold-stressed <i>Nostoc flagelliforme</i> and characterization of a hypothetical gene with cold and nitrogen stress tolerance. <i>Environmental Microbiology</i> , 2021, 23, 713-727.	1.8	11
13938	Insights into gene expression responses to infections in teleosts using microarray data: a systematic review. <i>Reviews in Aquaculture</i> , 2021, 13, 18-42.	4.6	2
13939	Transcriptomic analysis reveals the role of a peptide derived from CRYAB on the CoCl <sub>2</sub> -induced hypoxic HL-1 cardiomyocytes. <i>Journal of Thrombosis and Thrombolysis</i> , 2021, 51, 265-276.	1.0	2
13940	Dynamics of the antibiotic resistome in agricultural soils amended with different sources of animal manures over three consecutive years. <i>Journal of Hazardous Materials</i> , 2021, 401, 123399.	6.5	57
13941	Proteome-wide data analysis reveals tissue-specific network associated with SARS-CoV-2 infection. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 946-957.	1.5	30
13942	Obesity Drives Delayed Infarct Expansion, Inflammation, and Distinct Gene Networks in a Mouse Stroke Model. <i>Translational Stroke Research</i> , 2021, 12, 331-346.	2.3	7
13943	Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms. , 2021, , 490-506.		0
13944	Inhibition of cathepsin S attenuates myocardial ischemia/reperfusion injury by suppressing inflammation and apoptosis. <i>Journal of Cellular Physiology</i> , 2021, 236, 1309-1320.	2.0	21

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13945	Dramatic changes in bacterial co-occurrence patterns and keystone taxa responses to cropping systems in Mollisols of Northeast China. <i>Archives of Agronomy and Soil Science</i> , 2021, 67, 426-434.	1.3	5
13946	A novel immune-related prognostic index for predicting breast cancer overall survival. <i>Breast Cancer</i> , 2021, 28, 434-447.	1.3	7
13947	Indicator species and co-occurrence pattern of sediment bacterial community in relation to alkaline copper mine drainage contamination. <i>Ecological Indicators</i> , 2021, 120, 106884.	2.6	19
13948	<i>Candida albicans</i> promotes tooth decay by inducing oral microbial dysbiosis. <i>ISME Journal</i> , 2021, 15, 894-908.	4.4	67
13949	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021, 6, 123-135.	5.9	47
13950	Bacterial-fungal interactions revealed by genome-wide analysis of bacterial mutant fitness. <i>Nature Microbiology</i> , 2021, 6, 87-102.	5.9	49
13951	PathExt: a general framework for path-based mining of omics-integrated biological networks. <i>Bioinformatics</i> , 2021, 37, 1254-1262.	1.8	11
13952	The risk of COVID-19 for pregnant women: Evidences of molecular alterations associated with preeclampsia in SARS-CoV-2 infection. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 165999.	1.8	18
13953	Population dynamics and interactions of <i>Noctiluca scintillans</i> and <i>Mesodinium rubrum</i> during their successive blooms in a subtropical coastal water. <i>Science of the Total Environment</i> , 2021, 755, 142349.	3.9	10
13954	Bioinformatics Gene Analysis of Potential Biomarkers and Therapeutic Targets for Unstable Atherosclerotic Plaque-Related Stroke. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 1031-1045.	1.1	18
13955	Biogeographic patterns and co-occurrence networks of diazotrophic and arbuscular mycorrhizal fungal communities in the acidic soil ecosystem of southern China. <i>Applied Soil Ecology</i> , 2021, 158, 103798.	2.1	21
13956	Untangling the fibre ball: Proteomic characterization of South American camelid hair fibres by untargeted multivariate analysis and molecular networking. <i>Journal of Proteomics</i> , 2021, 231, 104040.	1.2	8
13957	Interacting effects of the MAM model of schizophrenia and antipsychotic treatment: Untargeted proteomics approach in adipose tissue. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 108, 110165.	2.5	10
13958	Dissecting Herpes Simplex Virus 1-Induced Host Shutoff at the RNA Level. <i>Journal of Virology</i> , 2021, 95, .	1.5	25
13959	Role of the methionine cycle in the temperature-sensitive responses of potato plants to potato virus Y. <i>Molecular Plant Pathology</i> , 2021, 22, 77-91.	2.0	22
13960	Metabolomics reveal dynamic changes in eicosanoid profile in patients with ST-elevation myocardial infarction after percutaneous coronary intervention. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2021, 48, 463-470.	0.9	4
13961	Sitagliptin: a potential drug for the treatment of COVID-19?. <i>Acta Pharmaceutica</i> , 2021, 71, 175-184.	0.9	35
13962	A transcriptional response atlas of <i>Chrysanthemum morifolium</i> to dodder invasion. <i>Environmental and Experimental Botany</i> , 2021, 181, 104272.	2.0	3



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13963	Pharmacology-informed prediction of the risk posed to fish by mixtures of non-steroidal anti-inflammatory drugs (NSAIDs) in the environment. <i>Environment International</i> , 2021, 146, 106222.	4.8	23
13964	Comprehensive analysis of polygalacturonase genes offers new insights into their origin and functional evolution in land plants. <i>Genomics</i> , 2021, 113, 1096-1108.	1.3	8
13965	Connecting the dots on vertical transmission of SARS-CoV-2 using protein-protein interaction network analysis – Potential roles of placental ACE2 and ENDOU. <i>Placenta</i> , 2021, 104, 16-19.	0.7	10
13966	Cell-Free Exploration of the Natural Product Chemical Space. <i>ChemBioChem</i> , 2021, 22, 84-91.	1.3	32
13967	Systems pharmacology reveals the multi-level synergetic mechanism of action of Ginkgo biloba L. leaves for cardiomyopathy treatment. <i>Journal of Ethnopharmacology</i> , 2021, 264, 113279.	2.0	17
13968	Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. <i>Science of the Total Environment</i> , 2021, 751, 141687.	3.9	37
13969	Amoeba Genome Reveals Dominant Host Contribution to Plastid Endosymbiosis. <i>Molecular Biology and Evolution</i> , 2021, 38, 344-357.	3.5	23
13970	Biochar affects taxonomic and functional community composition of protists. <i>Biology and Fertility of Soils</i> , 2021, 57, 15-29.	2.3	26
13971	Integrative Analysis of Gene Expression and Regulatory Network Interaction Data Reveals the Protein Kinase C Family of Serine/Threonine Receptors as a Significant Druggable Target for Parkinson's Disease. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 466-480.	1.1	7
13972	Reprogramming of m <sup>6</sup> A epitranscriptome is crucial for shaping of transcriptome and proteome in response to hypoxia. <i>RNA Biology</i> , 2021, 18, 131-143.	1.5	26
13973	Recent advances in user-friendly computational tools to engineer protein function. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	41
13974	Identification of epigenetic interactions between microRNA and DNA methylation associated with polycystic ovarian syndrome. <i>Journal of Human Genetics</i> , 2021, 66, 123-137.	1.1	36
13975	Deregulation of desmosomal proteins and extracellular matrix proteases in odontogenic keratocyst. <i>Oral Diseases</i> , 2021, 27, 952-961.	1.5	5
13976	Pathogenetic profiling of COVID-19 and SARS-like viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1175-1196.	3.2	42
13977	Proteomic Characterization of Circulating Molecular Perturbations Associated With Pancreatic Adenocarcinoma Following Intravenous 1% Fatty Acid and Gemcitabine Administration: A Pilot Study. <i>Journal of Parenteral and Enteral Nutrition</i> , 2021, 45, 738-750.	1.3	1
13978	A chemical biology approach to identifying molecular pathways associated with aging. <i>GeroScience</i> , 2021, 43, 353-365.	2.1	6
13979	Integrated Systems Analysis Explores Dysfunctional Molecular Modules and Regulatory Factors in Children with Autism Spectrum Disorder. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 358-368.	1.1	9
13980	Network Biology Approaches in Ophthalmological Diseases: A Case Study of Glaucoma. , 2021, , 190-202.		5

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13981	Community succession of the grapevine fungal microbiome in the annual growth cycle. <i>Environmental Microbiology</i> , 2021, 23, 1842-1857.	1.8	69
13982	Flows of information and meaning: a vocabulary approach to integrated thinking and reporting. <i>Meditari Accountancy Research</i> , 2021, 29, 740-774.	2.4	7
13983	Turning chemistry into information for heterogeneous catalysis. <i>International Journal of Quantum Chemistry</i> , 2021, 121, e26382.	1.0	9
13984	Identification of KHSRP-Regulated RNAs in Esophageal Cancer by Integrated Bioinformatics Analysis. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2021, 36, 412-424.	0.7	1
13985	Sarcaglarols Aâ€”D, Lindenaneâ”Monoterpene Heterodimers from <i>Sarcandra glabra</i> Based on Molecular Networks. <i>Chinese Journal of Chemistry</i> , 2021, 39, 129-136.	2.6	22
13986	Changes in Bacterial Diversity, Composition and Interactions During the Development of the Seabird Tick <i>Ornithodoros maritimus</i> (Argasidae). <i>Microbial Ecology</i> , 2021, 81, 770-783.	1.4	10
13987	Transcriptome differential expression analysis reveals the activated genes in <i>Litopenaeus vannamei</i> shrimp families of superior growth performance. <i>Aquaculture</i> , 2021, 531, 735871.	1.7	22
13988	Cross-disease analysis of depression, ataxia and dystonia highlights a role for synaptic plasticity and the cerebellum in the pathophysiology of these comorbid diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 165976.	1.8	13
13989	Identification of a survival-related signature for sarcoma patients through integrated transcriptomic and proteomic profiling analyses. <i>Gene</i> , 2021, 764, 145105.	1.0	8
13990	Computed tomography-based deep-learning prediction of neoadjuvant chemoradiotherapy treatment response in esophageal squamous cell carcinoma. <i>Radiotherapy and Oncology</i> , 2021, 154, 6-13.	0.3	78
13991	Identification of genes and miRNAs in paclitaxel treatment for breast cancer. <i>Gynecological Endocrinology</i> , 2021, 37, 65-71.	0.7	4
13992	The Coming of Age for Big Data in Systems Radiobiology, an Engineering Perspective. <i>Big Data</i> , 2021, 9, 63-71.	2.1	2
13993	Network-based identification genetic effect of SARS-CoV-2 infections to Idiopathic pulmonary fibrosis (IPF) patients. <i>Briefings in Bioinformatics</i> , 2021, 22, 1254-1266.	3.2	64
13994	Molecular Regulatory Mechanism and Toxicology of Neurodegenerative Processes in MPTP/Probenecid-Induced Progressive Parkinsonâ”s Disease Mice Model Revealed by Transcriptome. <i>Molecular Neurobiology</i> , 2021, 58, 603-616.	1.9	13
13995	Comparative gene expression profiling of milk somatic cells of Sahiwal cattle and Murrah buffaloes. <i>Gene</i> , 2021, 764, 145101.	1.0	10
13996	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. <i>Gastroenterology</i> , 2021, 160, 362-377.e13.	0.6	90
13997	Exploring Protein Space: From Hydrolase to Ligase by Substitution. <i>Molecular Biology and Evolution</i> , 2021, 38, 761-776.	3.5	5
13998	Diversity, novelty, antimicrobial activity, and new antibiotics of cultivable endophytic actinobacteria isolated from psammophytes collected from Taklamakan Desert. <i>Journal of Pharmaceutical Analysis</i> , 2021, 11, 241-250.	2.4	20

#	ARTICLE	IF	CITATIONS
13999	Antagonistic cytoprotective effects of C60 fullerene nanoparticles in simultaneous exposure to benzo[a]pyrene in a molluscan animal model. <i>Science of the Total Environment</i> , 2021, 755, 142355.	3.9	11
14000	Genome-wide DNA methylation analysis using MethylCap-seq in canine high-grade B-cell lymphoma. <i>Journal of Leukocyte Biology</i> , 2021, 109, 1089-1103.	1.5	4
14001	Sea cucumbers in a high temperature and low dissolved oxygen world: Roles of miRNAs in the regulation of environmental stresses. <i>Environmental Pollution</i> , 2021, 268, 115509.	3.7	11
14002	Protein anabolism is key to long-term survival in high-grade serous ovarian cancer. <i>Translational Oncology</i> , 2021, 14, 100885.	1.7	6
14003	Protein signatures from blood plasma and urine suggest changes in vascular function and IL-12 signaling in elderly with a history of chronic diseases compared with an age-matched healthy cohort. <i>GeroScience</i> , 2021, 43, 593-606.	2.1	9
14004	Bacterial community composition and assembly along a natural sodicity/salinity gradient in surface and subsurface soils. <i>Applied Soil Ecology</i> , 2021, 157, 103731.	2.1	26
14005	From classical to new generation approaches: An excursus of -omics methods for investigation of protein-protein interaction networks. <i>Journal of Proteomics</i> , 2021, 230, 103990.	1.2	31
14006	The crosstalk between bone metabolism, lncRNAs, microRNAs and mRNAs in coronary artery calcification. <i>Genomics</i> , 2021, 113, 503-513.	1.3	11
14007	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2-related Disease. <i>Gastroenterology</i> , 2021, 160, 287-301.e20.	0.6	98
14008	Population-Level Configurations of Gut Mycobiome Across 6 Ethnicities in Urban and Rural China. <i>Gastroenterology</i> , 2021, 160, 272-286.e11.	0.6	63
14009	Genome-wide association study identified genomic regions and putative candidate genes affecting meat color traits in Nellore cattle. <i>Meat Science</i> , 2021, 171, 108288.	2.7	19
14010	Self-regulating microbiome networks ensure functional resilience of biofilms in sand biofilters during manganese load fluctuations. <i>Water Research</i> , 2021, 188, 116473.	5.3	22
14011	Rare taxa maintain the stability of crop mycobiomes and ecosystem functions. <i>Environmental Microbiology</i> , 2021, 23, 1907-1924.	1.8	132
14012	Comparative proteomics of <i>Mesembryanthemum crystallinum</i> guard cells and mesophyll cells in transition from C3 to CAM. <i>Journal of Proteomics</i> , 2021, 231, 104019.	1.2	10
14013	Expression profile of proinflammatory mediators in the placenta of mares during physiological detachment and retention of fetal membranes. <i>Cytokine</i> , 2021, 137, 155307.	1.4	4
14014	Integration of network and experimental pharmacology to decipher the antidiabetic action of <i>Duranta repens</i> L.. <i>Journal of Integrative Medicine</i> , 2021, 19, 66-77.	1.4	22
14015	Artificial intelligence based identification of the functional role of hirudin in diabetic erectile dysfunction treatment. <i>Pharmacological Research</i> , 2021, 163, 105244.	3.1	4
14016	Occurrence and quantification of culturable and viable but non-culturable (VBNC) pathogens in biofilm on different pipes from a metropolitan drinking water distribution system. <i>Science of the Total Environment</i> , 2021, 764, 142851.	3.9	33

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14017	Coronavirus: proteomics analysis of chicken kidney tissue infected with variant 2 (IS-1494)-like avian infectious bronchitis virus. <i>Archives of Virology</i> , 2021, 166, 101-113.	0.9	4
14018	PLncDB V2.0: a comprehensive encyclopedia of plant long noncoding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D1489-D1495.	6.5	83
14019	Speaking across boundaries to explore the potential for interdisciplinarity in ecosystem services knowledge production. <i>Conservation Biology</i> , 2021, 35, 1198-1209.	2.4	3
14020	Fluoride exposure during pregnancy and lactation triggers oxidative stress and molecular changes in hippocampus of offspring rats. <i>Ecotoxicology and Environmental Safety</i> , 2021, 208, 111437.	2.9	37
14021	Identification of potential key genes and miRNAs involved in Hepatoblastoma pathogenesis and prognosis. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 131-142.	1.8	8
14022	Identification of microRNAs involved in crosstalk between nitrogen, phosphorus and potassium under multiple nutrient deficiency in sorghum. <i>Crop Journal</i> , 2021, 9, 465-475.	2.3	16
14023	A genome-wide association study identifies a gene network associated with paranoid schizophrenia and antipsychotics-induced tardive dyskinesia. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 105, 110134.	2.5	4
14024	Bioaccumulation and reproductive toxicity of bisphenol A in male-pregnant seahorse ( <i>Hippocampus</i> ) Tj ETQq1 1 0.784314 rgBT /Over 141805.	3.9	17
14025	Identification of differentially expressed long non-coding RNAs and mRNAs in orbital adipose/connective tissue of thyroid-associated ophthalmopathy. <i>Genomics</i> , 2021, 113, 440-449.	1.3	13
14026	Micro RNA Targets in HIV Latency: Insights into Novel Layers of Latency Control. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 109-121.	0.5	11
14027	Culturing novel and abundant pelagiphages in the ocean. <i>Environmental Microbiology</i> , 2021, 23, 1145-1161.	1.8	27
14028	Salinity controls soil microbial community structure and function in coastal estuarine wetlands. <i>Environmental Microbiology</i> , 2021, 23, 1020-1037.	1.8	109
14029	Leaf Transcriptome and Weight Gene Co-expression Network Analysis Uncovers Genes Associated with Photosynthetic Efficiency in <i>Camellia oleifera</i> . <i>Biochemical Genetics</i> , 2021, 59, 398-421.	0.8	8
14030	Quantitative proteomics of cerebrospinal fluid using tandem mass tags in dogs with recurrent epileptic seizures. <i>Journal of Proteomics</i> , 2021, 231, 103997.	1.2	12
14031	Analysis of aroma-related volatile compounds affected by "Ginsen Makuwa"™ genomic regions introgressed in "Vedrantais"™ melon background. <i>Scientia Horticulturae</i> , 2021, 276, 109664.	1.7	5
14032	Stable-isotopic and metagenomic analyses reveal metabolic and microbial link of aerobic methane oxidation coupled to denitrification at different O <sub>2</sub> levels. <i>Science of the Total Environment</i> , 2021, 764, 142901.	3.9	20
14033	Analysis of the circRNAs expression profile in mouse lung with H7N9 influenza A virus infection. <i>Genomics</i> , 2021, 113, 716-727.	1.3	9
14034	Therapeutic Opportunities for Intestinal Angioectasia—Targeting PPAR <sup>δ</sup> and Oxidative Stress. <i>Clinical and Translational Science</i> , 2021, 14, 518-528.	1.5	6

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14035	The stronger impact of inorganic nitrogen fertilization on soil bacterial community than organic fertilization in short-term condition. <i>Geoderma</i> , 2021, 382, 114752.	2.3	61
14036	miR-130a-3p, a Preclinical Therapeutic Target for Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 647-664.	0.6	10
14037	Data mining combined with experiments to validate CEP55 as a prognostic biomarker in colorectal cancer. <i>Immunity, Inflammation and Disease</i> , 2021, 9, 167-182.	1.3	8
14038	Long non-coding RNAs associate with jasmonate-mediated plant defence against herbivores. <i>Plant, Cell and Environment</i> , 2021, 44, 982-994.	2.8	27
14039	Metabolomic analysis of the hippocampus in a rat model of chronic mild unpredictable stress-induced depression based on a pathway crosstalk and network module approach. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 193, 113755.	1.4	13
14040	Influence of the cold bottom water on taxonomic and functional composition and complexity of microbial communities in the southern Yellow Sea during the summer. <i>Science of the Total Environment</i> , 2021, 759, 143496.	3.9	12
14041	The communities and functional profiles of virioplankton along a salinity gradient in a subtropical estuary. <i>Science of the Total Environment</i> , 2021, 759, 143499.	3.9	16
14042	Ultrasensitive single-cell proteomics workflow identifies >1000 protein groups per mammalian cell. <i>Chemical Science</i> , 2021, 12, 1001-1006.	3.7	165
14043	Selection and validation of differentially expressed metabolic and immune genes in weaned Ghurrah versus crossbred piglets. <i>Tropical Animal Health and Production</i> , 2021, 53, 14.	0.5	3
14044	Regulation of circular RNAs act as ceRNA in a hypoxic pulmonary hypertension rat model. <i>Genomics</i> , 2021, 113, 11-19.	1.3	14
14045	Exploring the Potential Mechanism of Guchang Zhixie Wan for Treating Ulcerative Colitis by Comprehensive Network Pharmacological Approaches and Molecular Docking Validation as Well as Cell Experiments. <i>Chemistry and Biodiversity</i> , 2021, 18, e2000810.	1.0	13
14046	Genome-wide characterization and expression analyses of the auxin/indole-3-acetic acid (Aux/IAA) gene family in apple ( <i>Malus domestica</i> ). <i>Gene</i> , 2021, 768, 145302.	1.0	11
14047	A case-control study to identify molecular risk factors for local recurrence in young breast cancer patients. <i>Radiotherapy and Oncology</i> , 2021, 156, 127-135.	0.3	8
14048	Expression of genes and pathways associated with the B7-CD28 superfamily in response to irradiation of blood cells using <sup>137</sup> Cs. <i>International Journal of Radiation Biology</i> , 2021, 97, 149-155.	1.0	2
14049	Statistical methods with exhaustive search in the identification of gene-gene interactions for colorectal cancer. <i>Genetic Epidemiology</i> , 2021, 45, 222-234.	0.6	5
14050	Combining quantitative trait locus and co-expression analysis allowed identification of new candidates for oil accumulation in rapeseed. <i>Journal of Experimental Botany</i> , 2021, 72, 1649-1660.	2.4	12
14051	Dietary supplementation of glycyrrhetic acid benefit growth performance and lipid metabolism in blunt snout bream ( <i>Megalobrama amblycephala</i> ) juveniles. <i>Aquaculture Nutrition</i> , 2021, 27, 407-416.	1.1	1
14052	Proteomic investigation of Zn-challenged rice roots reveals adverse effects and root physiological adaptation. <i>Plant and Soil</i> , 2021, 460, 69-88.	1.8	9

#	ARTICLE	IF	CITATIONS
14053	Mechanism of Chinese yam for the treatment of aging-related diseases based on network pharmacology. <i>European Journal of Integrative Medicine</i> , 2021, 41, 101254.	0.8	7
14054	Characterizing microRNAs and their targets in different organs of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Genomics</i> , 2021, 113, 159-170.	1.3	10
14055	Identification of genuine and novel miRNAs in <i>Amaranthus hypochondriacus</i> from high-throughput sequencing data. <i>Genomics</i> , 2021, 113, 88-103.	1.3	2
14056	Chaetolactam A, an Azaphilone Derivative from the Endophytic Fungus <i>Chaetomium</i> sp. g1. <i>Journal of Organic Chemistry</i> , 2021, 86, 475-483.	1.7	13
14057	A Proteomic Approach to Understand the Clinical Significance of Acute Myeloid Leukemiaâ€Derived Extracellular Vesicles Reflecting Essential Characteristics of Leukemia. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100017.	2.5	8
14058	Investigating the gut microbial community and genes in children with differing levels of change in serum asparaginase activity during pegaspargase treatment for acute lymphoblastic leukemia and Lymphoma, 2021, 62, 927-936.	0.6	4
14059	Establishment and characterization of a cold-sensitive neural cell line from the brain of tilapia ( <i>Oreochromis niloticus</i> ). <i>Journal of Fish Biology</i> , 2021, 98, 842-854.	0.7	5
14060	Targeted inhibition of ER signaling and PIP5K1/Akt pathways in castration-resistant prostate cancer. <i>Molecular Oncology</i> , 2021, 15, 968-986.	2.1	14
14061	Discovery of anti-flu substances and mechanism of Shuang-Huang-Lian water extract based on serum pharmaco-chemistry and network pharmacology. <i>Journal of Ethnopharmacology</i> , 2021, 268, 113660.	2.0	22
14062	Human gene expression profiling identifies key therapeutic targets in tuberculosis infection: A systematic network meta-analysis. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104649.	1.0	10
14063	Nature's therapy for COVID-19: Targeting the vital non-structural proteins (NSP) from SARS-CoV-2 with phytochemicals from Indian medicinal plants. <i>Phytomedicine Plus</i> , 2021, 1, 100002.	0.9	12
14064	Genome-wide identification of novel long non-coding RNAs and their possible roles in hypoxic zebrafish brain. <i>Genomics</i> , 2021, 113, 29-43.	1.3	9
14065	Associating chitosan and microemulsion as a topical vehicle for the administration of herbal medicines. <i>Carbohydrate Polymers</i> , 2021, 255, 117482.	5.1	17
14066	Transcriptional network modulated by the prognostic signature transcription factors and their long noncoding RNA partners in primary prostate cancer. <i>EBioMedicine</i> , 2021, 63, 103150.	2.7	10
14067	Comprehensive analysis of lncRNAs, miRNAs and mRNAs related to thymic development and involution in goose. <i>Genomics</i> , 2021, 113, 1176-1188.	1.3	7
14068	Intratumoral immunosuppression profiles in 11q-deleted neuroblastomas provide new potential therapeutic targets. <i>Molecular Oncology</i> , 2021, 15, 364-380.	2.1	4
14069	Prognostic value of lipid metabolism-related genes in head and neck squamous cell carcinoma. <i>Immunity, Inflammation and Disease</i> , 2021, 9, 196-209.	1.3	17
14070	A circRNA-miRNA-mRNA regulatory network associated with the treatment response to tuberculosis. <i>Microbial Pathogenesis</i> , 2021, 150, 104672.	1.3	4



#	ARTICLE	IF	CITATIONS
14071	Applying an association weight matrix in weighted genomic prediction of boar taint compounds. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 442-453.	0.8	4
14072	Network analyses identify a transcriptomic proximodistal prepattern in the maize leaf primordium. <i>New Phytologist</i> , 2021, 230, 218-227.	3.5	10
14073	Manipulation of Saliva-Derived Microcosm Biofilms To Resemble Dysbiotic Subgingival Microbiota. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	6
14074	A strategy for identifying effective and risk compounds of botanical drugs with LC-QTOF-MS and network analysis: A case study of Ginkgo biloba preparation. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 193, 113759.	1.4	7
14075	Multimodularity of a GH10 Xylanase Found in the Termite Gut Metagenome. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
14076	Characterization of Small-Molecule-Induced Changes in Parkinson's-Related Trafficking via the Nedd4 Ubiquitin Signaling Cascade. <i>Cell Chemical Biology</i> , 2021, 28, 14-25.e9.	2.5	15
14077	Application of a microbial consortium improves the growth of <i>Camellia sinensis</i> and influences the indigenous rhizosphere bacterial communities. <i>Journal of Applied Microbiology</i> , 2021, 130, 2029-2040.	1.4	25
14078	Comprehensive analysis of partial epithelial mesenchymal transition-related genes in hepatocellular carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 448-462.	1.6	23
14079	Reduced growth capacity of preimplantation mouse embryos in chronic unpredictable stress model. <i>Molecular Reproduction and Development</i> , 2021, 88, 80-95.	1.0	1
14080	Comprehensive Analysis of the Proteome and PTMomes of C2C12 Myoblasts Reveals that Sialylation Plays a Role in the Differentiation of Skeletal Muscle Cells. <i>Journal of Proteome Research</i> , 2021, 20, 222-235.	1.8	3
14081	Genome-wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. <i>Plant Biotechnology Journal</i> , 2021, 19, 910-925.	4.1	26
14082	Phenotypic, Transcriptomic, and Metabolomic Signatures of Root-Specifically Overexpressed OsCKX2 in Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 575304.	1.7	3
14083	A photo-crosslinkable cartilage-derived extracellular matrix bioink for auricular cartilage tissue engineering. <i>Acta Biomaterialia</i> , 2021, 121, 193-203.	4.1	81
14084	Determinants of bacterioplankton structures in the typically turbid Weihe River and its clear tributaries from the northern foot of the Qinling Mountains. <i>Ecological Indicators</i> , 2021, 121, 107168.	2.6	10
14085	Systems toxicogenomics of prenatal low-dose BPA exposure on liver metabolic pathways, gut microbiota, and metabolic health in mice. <i>Environment International</i> , 2021, 146, 106260.	4.8	42
14086	Systematic classification of unknown metabolites using high-resolution fragmentation mass spectra. <i>Nature Biotechnology</i> , 2021, 39, 462-471.	9.4	317
14087	Exome Sequencing Identifies Abnormalities in Glycosylation and ANKRD36C in Patients with Immune-Mediated Thrombotic Thrombocytopenic Purpura. <i>Thrombosis and Haemostasis</i> , 2021, 121, 506-517.	1.8	4
14088	A Single-Cell Transcriptomic Atlas of Human Skin Aging. <i>Developmental Cell</i> , 2021, 56, 383-397.e8.	3.1	145

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14089	Evaluating the impact of methionine-enriched diets in the liver of European seabass through label-free shotgun proteomics. <i>Journal of Proteomics</i> , 2021, 232, 104047.	1.2	10
14090	How to Make a Rodent Giant: Genomic Basis and Tradeoffs of Gigantism in the Capybara, the World's Largest Rodent. <i>Molecular Biology and Evolution</i> , 2021, 38, 1715-1730.	3.5	16
14091	Comparable Plasma Lipid Changes in Patients with High-Grade Cervical Intraepithelial Neoplasia and Patients with Cervical Cancer. <i>Journal of Proteome Research</i> , 2021, 20, 740-750.	1.8	13
14092	A comprehensive meta-analysis to identify transcriptional signatures of abiotic stress responses in barley ( <i>Hordeum vulgare</i> ). <i>Cereal Research Communications</i> , 2021, 49, 385-391.	0.8	4
14093	A computational framework for identifying the transcription factors involved in enhancer-promoter loop formation. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 23, 347-354.	2.3	9
14094	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. <i>ISME Journal</i> , 2021, 15, 921-937.	4.4	33
14095	Elevated CO <sub>2</sub> and nitrate levels increase wheat root-associated bacterial abundance and impact rhizosphere microbial community composition and function. <i>ISME Journal</i> , 2021, 15, 1073-1084.	4.4	30
14096	Manure application increases microbiome complexity in soil aggregate fractions: Results of an 18-year field experiment. <i>Agriculture, Ecosystems and Environment</i> , 2021, 307, 107249.	2.5	54
14097	Network-based analysis of Jinfukang in the treatment of lung cancer. <i>European Journal of Integrative Medicine</i> , 2021, 41, 101232.	0.8	0
14098	Regio- and stereoselective intermolecular phenol coupling enzymes in secondary metabolite biosynthesis. <i>Natural Product Reports</i> , 2021, 38, 1011-1043.	5.2	44
14099	Engulfment and cell motility 1 (ELMO1) and apolipoprotein A1 (APOA1) as candidate genes for sickle cell nephropathy. <i>British Journal of Haematology</i> , 2021, 193, 628-632.	1.2	4
14100	TENET: gene network reconstruction using transfer entropy reveals key regulatory factors from single cell transcriptomic data. <i>Nucleic Acids Research</i> , 2021, 49, e1-e1.	6.5	26
14101	Transcriptomic analysis of tea plant ( <i>Camellia sinensis</i> ) revealed the co-expression network of 4111 paralogous genes and biosynthesis of quality-related key metabolites under multiple stresses. <i>Genomics</i> , 2021, 113, 908-918.	1.3	6
14102	High-throughput proteomics of breast cancer interstitial fluid: identification of tumor subtype-specific serologically relevant biomarkers. <i>Molecular Oncology</i> , 2021, 15, 429-461.	2.1	19
14103	Immunoprotective potential of Ayurvedic herb Kalmegh ( <i>Andrographis paniculata</i> ) against respiratory viral infections – LC-MS/MS and network pharmacology analysis. <i>Phytochemical Analysis</i> , 2021, 32, 629-639.	1.2	42
14104	Transcriptomic analysis of equine placenta reveals key regulators and pathways involved in ascending placentitis. <i>Biology of Reproduction</i> , 2021, 104, 638-656.	1.2	9
14105	Evolutionary expansion and functional divergence of sugar transporters in <i>Saccharum</i> ( <i>S.</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	20
14106	Overexpressed miR-335-5p reduces atherosclerotic vulnerable plaque formation in acute coronary syndrome. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23608.	0.9	19

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14107	Comprehensive genomic and immunophenotypic analysis of CD4 T cell infiltrating human triple-negative breast cancer. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 1649-1665.	2.0	11
14108	A balanced reduction in mineral fertilizers benefits P reserve and inorganic P-solubilizing bacterial communities under residue input. <i>Applied Soil Ecology</i> , 2021, 159, 103833.	2.1	14
14109	Discovery, development, chemical diversity and design of isoxazoline-based insecticides. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 30, 115934.	1.4	22
14110	An integrated green methodology for the continuous biological removal and fixation of arsenic from acid wastewater through the GAC-catalyzed As(III) oxidation. <i>Chemical Engineering Journal</i> , 2021, 421, 127758.	6.6	11
14111	Identification of key genes of hesperidin in inhibition of breast cancer stem cells by functional network analysis. <i>Computational Biology and Chemistry</i> , 2021, 90, 107427.	1.1	11
14112	SciKGraph: A knowledge graph approach to structure a scientific field. <i>Journal of Informetrics</i> , 2021, 15, 101109.	1.4	15
14113	Species and tissue specific analysis based on quantitative proteomics from allotetraploid and the parents. <i>Journal of Proteomics</i> , 2021, 232, 104073.	1.2	4
14114	Multiple-genotypes transcriptional analysis revealed candidate genes and nucleotide variants for improvement of quality characteristics in tea ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Genomics</i> , 2021, 113, 305-316.	1.3	10
14115	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate <i>Mesodinium rubrum</i> . <i>ISME Journal</i> , 2021, 15, 1056-1072.	4.4	15
14116	Brain Transcriptome Analysis Reveals Potential Transcription Factors and Biological Pathways Associated with Feed Efficiency in Commercial DLY Pigs. <i>DNA and Cell Biology</i> , 2021, 40, 272-282.	0.9	7
14117	Serum MicroRNA Differences Between Fracture in Postmenopausal Women with and without Diabetes. <i>Orthopaedic Surgery</i> , 2021, 13, 285-295.	0.7	1
14118	Soil bacterial and eukaryotic co-occurrence networks across a desert climate gradient in northern China. <i>Land Degradation and Development</i> , 2021, 32, 1938-1950.	1.8	17
14119	Genetic variants in glutamate-, A $\beta$ , and tau-related pathways determine polygenic risk for Alzheimer's disease. <i>Neurobiology of Aging</i> , 2021, 101, 299.e13-299.e21.	1.5	7
14120	Flowering time regulation model revisited by pooled sequencing of mass selection populations. <i>Plant Science</i> , 2021, 304, 110797.	1.7	5
14121	Modification of the <i>Pseudomonas aeruginosa</i> toxin 2a heptyl-1-hydroxyquinolin-4(1H)-one and other secondary metabolites by methyltransferases from mycobacteria. <i>FEBS Journal</i> , 2021, 288, 2360-2376.	2.2	3
14122	Identification of potential <i>circRNAs</i> and <i>circRNA-miRNA-mRNA</i> regulatory network in the development of diabetic foot ulcers by integrated bioinformatics analysis. <i>International Wound Journal</i> , 2021, 18, 323-331.	1.3	20
14123	Epidemiological and ES cell-based functional evaluation of BRCA2 variants identified in families with breast cancer. <i>Human Mutation</i> , 2021, 42, 200-212.	1.1	4
14124	Bisphenol A promotes breast cancer cell proliferation by driving miR-381-3p-PTTG1-dependent cell cycle progression. <i>Chemosphere</i> , 2021, 268, 129221.	4.2	25

#	ARTICLE	IF	CITATIONS
14125	Hypoxia-reoxygenation stress modulates the hepatopancreas transcriptome of Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Gene</i> , 2021, 771, 145361.	1.0	10
14126	The comparative genomic landscape of adaptive radiation in crater lake cichlid fishes. <i>Molecular Ecology</i> , 2021, 30, 955-972.	2.0	12
14127	Genome-wide alternative splicing profiling in the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> during the colonization of diverse host families. <i>Molecular Plant Pathology</i> , 2021, 22, 31-47.	2.0	25
14128	Hearing impairment due to <i>Mir183/96/182</i> mutations suggests both loss-of-function and gain-of-function effects. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	14
14129	Decoding Human Megakaryocyte Development. <i>Cell Stem Cell</i> , 2021, 28, 535-549.e8.	5.2	79
14130	In-depth study to decipher mechanisms underlying <i>Arabidopsis thaliana</i> tolerance to metal(loid) soil contamination in association with biochar and/or bacteria. <i>Environmental and Experimental Botany</i> , 2021, 182, 104335.	2.0	23
14131	Environmental Conditions Modulate the Protein Content and Immunomodulatory Activity of Extracellular Vesicles Produced by the Probiotic <i>Propionibacterium freudenreichii</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
14132	Different responses of soil carbon chemistry to fertilization regimes in the paddy soil and upland soil were mainly reflected by the opposite shifts of OCH and alkyl C. <i>Geoderma</i> , 2021, 385, 114876.	2.3	3
14133	Effects of wastewater treatment and manure application on the dissemination of antimicrobial resistance around swine feedlots. <i>Journal of Cleaner Production</i> , 2021, 280, 123794.	4.6	28
14134	Expression analysis of microRNAs and their target mRNAs of testes with high and low sperm motility in domestic pigeons ( <i>Columba livia</i> ). <i>Genomics</i> , 2021, 113, 257-264.	1.3	10
14135	Inhaled multi-walled carbon nanotubes differently modulate global gene and protein expression in rat lungs. <i>Nanotoxicology</i> , 2021, 15, 238-256.	1.6	14
14136	Cobalamin and microbial plankton dynamics along a coastal to offshore transect in the Eastern North Atlantic Ocean. <i>Environmental Microbiology</i> , 2021, 23, 1559-1583.	1.8	19
14137	Deciphering key regulators involved in epilepsy-induced cardiac damage through whole transcriptome and proteome analysis in a rat model. <i>Epilepsia</i> , 2021, 62, 504-516.	2.6	17
14138	Genome-wide identification, classification and expression analysis of the Hsf and Hsp70 gene families in maize. <i>Gene</i> , 2021, 770, 145348.	1.0	28
14139	Effect of the acute and chronic administration of <i>Lupinus albus</i> $\beta$ -conglutin on glycaemia, circulating cholesterol, and genes potentially involved. <i>Biomedicine and Pharmacotherapy</i> , 2021, 133, 110969.	2.5	4
14140	Comparative microRNAs expression profiles analysis during embryonic development of common carp, <i>Cyprinus carpio</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 37, 100754.	0.4	5
14141	Coevolving Plasmids Drive Gene Flow and Genome Plasticity in Host-Associated Intracellular Bacteria. <i>Current Biology</i> , 2021, 31, 346-357.e3.	1.8	21
14142	<i>Penicillium oxalicum</i> S-adenosylmethionine synthetase is essential for the viability of fungal cells and the expression of genes encoding cellulytic enzymes. <i>Fungal Biology</i> , 2021, 125, 1-11.	1.1	5

#	ARTICLE	IF	CITATIONS
14143	IL-4â€“BATF signaling directly modulates IL-9 producing mucosal mast cell (MMC9) function in experimental food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 280-295.	1.5	23
14144	Identifying biomolecules and constructing a prognostic risk prediction model for recurrence in osteosarcoma. <i>Journal of Bone Oncology</i> , 2021, 26, 100331.	1.0	11
14145	The inflammatory response of the supraspinatus muscle in rotator cuff tear conditions. <i>Journal of Shoulder and Elbow Surgery</i> , 2021, 30, e261-e275.	1.2	18
14146	Maternal obesity persistently alters cardiac progenitor gene expression and programs adult-onset heart disease susceptibility. <i>Molecular Metabolism</i> , 2021, 43, 101116.	3.0	8
14147	Expression and functionality of allergenic genes regulated by simulated gastric juice in <i>Anisakis pegreffii</i> . <i>Parasitology International</i> , 2021, 80, 102223.	0.6	3
14148	Immunological Role and Prognostic Value of APBB1IP in Pan-Cancer Analysis. <i>Journal of Cancer</i> , 2021, 12, 595-610.	1.2	24
14149	FBXO44 promotes DNA replication-coupled repetitive element silencing in cancer cells. <i>Cell</i> , 2021, 184, 352-369.e23.	13.5	50
14150	Rapid Structure-Based Annotation and Profiling of Dihydrochalcones in Star Fruit ( <i>Averrhoa</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Food Chemistry, 2021, 69, 555-567.	2.4	13
14151	Genome-Scale Identification of SARS-CoV-2 and Pan-coronavirus Host Factor Networks. <i>Cell</i> , 2021, 184, 120-132.e14.	13.5	328
14152	Community diversity metrics, interactions, and metabolic functions of bacteria associated with municipal solid waste landfills at different maturation stages. <i>MicrobiologyOpen</i> , 2021, 10, e1118.	1.2	14
14153	A multifactorial model of pathology for age of onset heterogeneity in familial Alzheimerâ€™s disease. <i>Acta Neuropathologica</i> , 2021, 141, 217-233.	3.9	33
14154	Using Interactome Big Data to Crack Genetic Mysteries and Enhance Future Crop Breeding. <i>Molecular Plant</i> , 2021, 14, 77-94.	3.9	34
14155	Possible immune regulation mechanisms for the progression of chronic thromboembolic pulmonary hypertension. <i>Thrombosis Research</i> , 2021, 198, 122-131.	0.8	11
14156	Peptide Correlation Analysis (PeCorA) Reveals Differential Proteoform Regulation. <i>Journal of Proteome Research</i> , 2021, 20, 1972-1980.	1.8	22
14157	The allosteric interplay between Sâ€“nitrosylation and glycine binding controls the activity of human serine racemase. <i>FEBS Journal</i> , 2021, 288, 3034-3054.	2.2	8
14158	Identification of key genes associated with overwintering in <i>Anoplophora glabripennis</i> larva using gene coâ€“expression network analysis. <i>Pest Management Science</i> , 2021, 77, 805-816.	1.7	11
14159	Effects of Plants on Metacommunities and Correlation Networks of Soil Microbial Groups in an Ecologically Restored Wetland. <i>Microbial Ecology</i> , 2021, 81, 657-672.	1.4	3
14160	Ruby chocolate: A study of its phytochemical composition and quantitative comparison with dark, milk and white chocolate. <i>Food Chemistry</i> , 2021, 343, 128446.	4.2	10

#	ARTICLE	IF	CITATIONS
14161	Temporal variation and sharing of antibiotic resistance genes between water and wild fish gut in a peri-urban river. <i>Journal of Environmental Sciences</i> , 2021, 103, 12-19.	3.2	30
14162	Coordinated regulation of starch synthesis in maize endosperm by microRNAs and DNA methylation. <i>Plant Journal</i> , 2021, 105, 108-123.	2.8	17
14163	Network pharmacology, molecular docking integrated surface plasmon resonance technology reveals the mechanism of Toujie Quwen Granules against coronavirus disease 2019 pneumonia. <i>Phytomedicine</i> , 2021, 85, 153401.	2.3	65
14164	CNS genomic profiling in the mouse chronic social stress model implicates a novel category of candidate genes integrating affective pathogenesis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 105, 110086.	2.5	6
14165	Alternative splicing and duplication of PI-like genes in maize. <i>Gene</i> , 2021, 769, 145064.	1.0	0
14166	Bioturbation by the marine polychaete <i>Capitella teleta</i> alters the sediment microbial community by ingestion and defecation of sediment particles. <i>Science of the Total Environment</i> , 2021, 752, 142239.	3.9	4
14167	MASI: microbiota- active substance interactions database. <i>Nucleic Acids Research</i> , 2021, 49, D776-D782.	6.5	28
14168	Identification of a stool long non-coding RNAs panel as a potential biomarker for early detection of colorectal cancer. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23601.	0.9	21
14169	Physiological and transcription analyses reveal the regulatory mechanism of melatonin in inducing drought resistance in loquat ( <i>Eriobotrya japonica</i> Lindl.) seedlings. <i>Environmental and Experimental Botany</i> , 2021, 181, 104291.	2.0	54
14170	A chromosome-level genome assembly provides insights into ascorbic acid accumulation and fruit softening in guava ( <i>Psidium guajava</i> ). <i>Plant Biotechnology Journal</i> , 2021, 19, 717-730.	4.1	52
14171	A temporal hierarchy underpins the transcription factor-DNA interactome of the maize UPR. <i>Plant Journal</i> , 2021, 105, 254-270.	2.8	7
14172	Diagnostic potential of a gradient boosting-based model for detecting pediatric sepsis. <i>Genomics</i> , 2021, 113, 874-883.	1.3	8
14173	Differences in biomarkers of inflammation and immune responses in chronic smokers and moist snuff users. <i>Cytokine</i> , 2021, 137, 155299.	1.4	2
14174	Structural and dynamical effects of targeted mutations on <sup>14</sup> O-Conotoxin MfVIA: Molecular simulation studies. <i>Journal of Molecular Graphics and Modelling</i> , 2021, 102, 107777.	1.3	3
14175	Mg deficiency interacts with the circadian clock and phytochromes pathways in <i>Arabidopsis</i> . <i>Annals of Applied Biology</i> , 2021, 178, 387-399.	1.3	5
14176	Zooming on dynamics of marine microbial communities in the phycosphere of <i>Akashiwo sanguinea</i> (Dinophyta) blooms. <i>Molecular Ecology</i> , 2021, 30, 207-221.	2.0	19
14177	Multi-omics integration in biomedical research - A metabolomics-centric review. <i>Analytica Chimica Acta</i> , 2021, 1141, 144-162.	2.6	125
14178	Human Histone Interaction Networks: An Old Concept, New Trends. <i>Journal of Molecular Biology</i> , 2021, 433, 166684.	2.0	4



#	ARTICLE	IF	CITATIONS
14179	Dissection of the potential anti-influenza materials and mechanism of <i>Lonicerae japonicae</i> flos based on in vivo substances profiling and network pharmacology. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 193, 113721.	1.4	19
14180	Genome-wide analysis of long non-coding RNAs responsive to multiple nutrient stresses in <i>Arabidopsis thaliana</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 17-30.	1.4	14
14181	Insect egg-induced physiological changes and transcriptional reprogramming leading to gall formation. <i>Plant, Cell and Environment</i> , 2021, 44, 535-547.	2.8	9
14182	Plant genome-scale metabolic networks. <i>Advances in Botanical Research</i> , 2021, , 237-270.	0.5	1
14183	Compositional diversity and evolutionary pattern of coronavirus accessory proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, 1267-1278.	3.2	26
14184	Mechanistic insights into SARS-CoV-2 epidemic via revealing the features of SARS-CoV-2 coding proteins and host responses upon its infection. <i>Bioinformatics</i> , 2021, 36, 5133-5138.	1.8	4
14185	Transcriptome differential co-expression reveals distinct molecular response of fall armyworm strains to DIMBOA. <i>Pest Management Science</i> , 2021, 77, 518-526.	1.7	9
14186	Independent replications and integrative analyses confirm TRANK1 as a susceptibility gene for bipolar disorder. <i>Neuropsychopharmacology</i> , 2021, 46, 1103-1112.	2.8	20
14187	Mucosal Inflammatory and Wound Healing Gene Programmes Reveal Targets for Structuring Behaviour in Paediatric Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 273-286.	0.6	20
14188	Polyphenism of a Novel Trait Integrated Rapidly Evolving Genes into Ancestrally Plastic Networks. <i>Molecular Biology and Evolution</i> , 2021, 38, 331-343.	3.5	19
14189	NetSets.js: a JavaScript framework for compositional assessment and comparison of biological networks through Venn-integrated network diagrams. <i>Bioinformatics</i> , 2021, 37, 580-582.	1.8	2
14190	Computational Analysis of Phosphoproteomics Data in Multi-Omics Cancer Studies. <i>Proteomics</i> , 2021, 21, e1900312.	1.3	20
14191	Expansin Engineering Database: A navigation and classification tool for expansins and homologues. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 149-162.	1.5	9
14192	Proteometabolomic characterization of apical bud maturation in <i>Pinus pinaster</i> . <i>Tree Physiology</i> , 2021, 41, 508-521.	1.4	12
14193	Analysis of insect nuclear small heat shock proteins and interacting proteins. <i>Cell Stress and Chaperones</i> , 2021, 26, 265-274.	1.2	5
14194	A phylogenetic view and functional annotation of the animal Î²1,3-glycosyltransferases of the GT31 CAZy family. <i>Glycobiology</i> , 2021, 31, 243-259.	1.3	9
14195	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 545-556.	3.5	5
14196	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. <i>Human Genetics</i> , 2021, 140, 529-552.	1.8	36

#	ARTICLE	IF	CITATIONS
14197	Seasonal Dynamics of Core Fungi in the Switchgrass Phyllosphere, and Co-Occurrence with Leaf Bacteria. <i>Phytobiomes Journal</i> , 2021, 5, 60-68.	1.4	29
14198	CD73 contributes to anti-inflammatory properties of afferent lymphatic endothelial cells in humans and mice. <i>European Journal of Immunology</i> , 2021, 51, 231-246.	1.6	12
14199	Blunted nutrient-response pathways in adipose tissue following high fat meals in men with metabolic syndrome: A randomized postprandial transcriptomic study. <i>Clinical Nutrition</i> , 2021, 40, 1355-1366.	2.3	2
14200	Disruption of protein phosphatase 1 complexes with the use of biopeptides as a novel approach to target sperm motility. <i>Fertility and Sterility</i> , 2021, 115, 348-362.	0.5	10
14201	Potential compound from herbal food of <i>Rhizoma Polygonati</i> for treatment of COVID-19 analyzed by network pharmacology: Viral and cancer signaling mechanisms. <i>Journal of Functional Foods</i> , 2021, 77, 104149.	1.6	97
14202	Systems pharmacological study illustrates the immune regulation, anti-infection, anti-inflammation, and multi-organ protection mechanism of Qing-Fei-Pai-Du decoction in the treatment of COVID-19. <i>Phytomedicine</i> , 2021, 85, 153315.	2.3	100
14203	Genomic adaptations to cereal-based diets contribute to mitigate metabolic risk in some human populations of East Asian ancestry. <i>Evolutionary Applications</i> , 2021, 14, 297-313.	1.5	9
14204	Single-cell transcriptomic atlas of primate cardiopulmonary aging. <i>Cell Research</i> , 2021, 31, 415-432.	5.7	88
14205	Overexpression of $\beta$ -Synuclein Reorganises Growth Factor Profile of Human Astrocytes. <i>Molecular Neurobiology</i> , 2021, 58, 184-203.	1.9	17
14206	A network analysis framework of genetic and nongenetic risks for type 2 diabetes. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2021, 22, 461-469.	2.6	4
14207	Intestinal Receptor of SARS-CoV-2 in Inflamed IBD Tissue Seems Downregulated by HNF4A in Ileum and Upregulated by Interferon Regulating Factors in Colon. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 485-498.	0.6	34
14208	Molecular characteristics associated with ferroptosis in hepatocellular carcinoma progression. <i>Human Cell</i> , 2021, 34, 177-186.	1.2	20
14209	Archaeal roots of intramembrane aspartyl protease siblings signal peptide peptidase and presenilin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 232-241.	1.5	7
14210	Mechanomics analysis of hESCs under combined mechanical shear, stretch, and compression. <i>Biomechanics and Modeling in Mechanobiology</i> , 2021, 20, 205-222.	1.4	4
14211	Transcriptome analysis and association mapping reveal the genetic regulatory network response to cadmium stress in <i>Populus tomentosa</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 576-591.	2.4	21
14212	Weighted gene co-expression analysis for identification of key genes regulating heat stress in wheat. <i>Cereal Research Communications</i> , 2021, 49, 73-81.	0.8	7
14213	Host selection shapes crop microbiome assembly and network complexity. <i>New Phytologist</i> , 2021, 229, 1091-1104.	3.5	349
14214	A novel prognostic index of hepatocellular carcinoma based on immunogenomic landscape analysis. <i>Journal of Cellular Physiology</i> , 2021, 236, 2572-2591.	2.0	26

#	ARTICLE	IF	CITATIONS
14215	Cut Microbiota of Five Sympatrically Farmed Marine Fish Species in the Aegean Sea. <i>Microbial Ecology</i> , 2021, 81, 460-470.	1.4	27
14216	Object Weighting: A New Clustering Approach to Deal with Outliers and Cluster Overlap in Computational Biology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 633-643.	1.9	8
14217	Probing the Relation Between Community Evolution in Dynamic Residue Interaction Networks and Xylanase Thermostability. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 686-696.	1.9	1
14218	Preparing students for the data-driven life science era through a real-world viral infection case. <i>Journal of Biological Education</i> , 2021, 55, 178-187.	0.8	2
14219	Karyon: A scalable and easy to integrate ontology summarisation framework. <i>Journal of Information Science</i> , 2021, 47, 255-268.	2.0	2
14220	Identification of the potential dual inhibitor of protein tyrosine phosphatase sigma and leukocyte common antigen-related phosphatase by virtual screen, molecular dynamic simulations and post-analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 45-62.	2.0	6
14222	Molecular pathology associated with altered synaptic transcriptome in the dorsolateral prefrontal cortex of depressed subjects. <i>Translational Psychiatry</i> , 2021, 11, 73.	2.4	16
14223	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. <i>ISME Journal</i> , 2021, 15, 1569-1584.	4.4	16
14224	Integrated Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
14225	Comparative RNA-Seq analysis unfolds a complex regulatory network imparting yellow mosaic disease resistance in mungbean [ <i>Vigna radiata</i> (L.) R. Wilczek]. <i>PLoS ONE</i> , 2021, 16, e0244593.	1.1	31
14226	Molecular subgroup of periodontitis revealed by integrated analysis of the microbiome and metabolome in a cross-sectional observational study. <i>Journal of Oral Microbiology</i> , 2021, 13, 1902707.	1.2	15
14227	Discovery of a novel HDACi structure that inhibits the proliferation of ovarian cancer cells <i>in vivo</i> and <i>in vitro</i> . <i>International Journal of Biological Sciences</i> , 2021, 17, 3493-3507.	2.6	8
14228	Sinbase 2.0: An Updated Database to Study Multi-Omics in <i>Sesamum indicum</i> . <i>Plants</i> , 2021, 10, 272.	1.6	6
14229	Systems pharmacology investigation of mechanism of action of nutraceuticals. , 2021, , 345-361.		2
14230	Whole-exome Sequencing of Prostate Cancer in Sardinian Identify Recurrent UDP-glucuronosyltransferase Amplifications. <i>Journal of Cancer</i> , 2021, 12, 438-450.	1.2	5
14231	Role of Transportome in the Gills of Chinese Mitten Crabs in Response to Salinity Change: A Meta-Analysis of RNA-Seq Datasets. <i>Biology</i> , 2021, 10, 39.	1.3	13
14234	NLRC4 gene silencing-dependent blockade of NOD-like receptor pathway inhibits inflammation, reduces proliferation and increases apoptosis of dendritic cells in mice with septic shock. <i>Aging</i> , 2021, 13, 1440-1457.	1.4	5
14235	Identification of a PLCE1-regulated competing endogenous RNA regulatory network for esophageal squamous cell carcinoma. <i>Oncology Reports</i> , 2021, 45, 857-868.	1.2	5

#	ARTICLE	IF	CITATIONS
14236	Temporal Bibliometry Networks of SARS, MERS and COVID19 Reveal Dynamics of the Pandemic. <i>Studies in Computational Intelligence</i> , 2021, , 700-711.	0.7	0
14237	Identification of dysregulated pathways underlying HTLV-1-associated myelopathy/tropical spastic paraparesis through co-expression network analysis. <i>Journal of NeuroVirology</i> , 2021, 27, 820-830.	1.0	8
14238	Danhong Injection and Trimetazidine Protect Cardiomyocytes and Enhance Calcium Handling after Myocardial Infarction. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	5
14239	The Roles of Chromatin Accessibility in Regulating the <i>Candida albicans</i> White-Opaque Phenotypic Switch. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 37.	1.5	5
14240	The Roles of the miRNAome and Transcriptome in the Ovine Ovary Reveal Poor Efficiency in Juvenile Superovulation. <i>Animals</i> , 2021, 11, 239.	1.0	7
14242	Enhanced Metabolic Potentials and Functional Gene Interactions of Microbial Stress Responses to a 4,100-m Elevational Increase in Freshwater Lakes. <i>Frontiers in Microbiology</i> , 2020, 11, 595967.	1.5	5
14243	Analysis of Herbal Mechanisms and Prescriptions for Chronic Cerebral Circulatory Insufficiency Based on Data Mining and Network Pharmacology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 1239-1253.	0.6	4
14244	Diabetes Induces a Transcriptional Signature in Bone Marrowâ€Derived CD34+ Hematopoietic Stem Cells Predictive of Their Progeny Dysfunction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1423.	1.8	5
14247	Identifying <i>FBLN1</i> (Gene ID: 2192) as a Potential Melanoma Biomarker for Melanoma based on an Analysis of microRNA Expression Profiles in the GEO and TCGA Databases. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 68-78.	0.3	2
14249	Single-Cell Analysis Reveals Characterization of Infiltrating T Cells in Moderately Differentiated Colorectal Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 620196.	2.2	14
14250	Identification of downstream signaling cascades of ACK1 and prognostic classifiers in non-small cell lung cancer. <i>Aging</i> , 2021, 13, 4482-4502.	1.4	11
14253	The human GPCR signal transduction network. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2021, 10, 1.	1.2	1
14256	Identification of key genes associated with lung adenocarcinoma by bioinformatics analysis. <i>Science Progress</i> , 2021, 104, 003685042199727.	1.0	5
14257	The Methods and Tools for Molecular Network Construction. , 2021, , 14-28.		0
14258	Overview: Standards for Modeling in Systems Medicine. , 2021, , 345-353.		4
14259	Mitochondria-related core genes and TF-miRNA-hub mrDEGs network in breast cancer. <i>Bioscience Reports</i> , 2021, 41, .	1.1	14
14260	Identification of a Five-Gene Prognostic Model and Its Potential Drug Repurposing in Colorectal Cancer Based on TCGA, GTEx and GEO Databases. <i>Frontiers in Genetics</i> , 2020, 11, 622659.	1.1	10
14261	Transcriptomic analysis reveals that mTOR pathway can be modulated in macrophage cells by the presence of cryptococcal cells. <i>Genetics and Molecular Biology</i> , 2021, 44, e20200390.	0.6	2

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14262	A ferroptosis-related gene signature for graft loss prediction following renal allograft. <i>Bioengineered</i> , 2021, 12, 4217-4232.	1.4	10
14263	Integrated analysis reveals the alterations that LMNA interacts with euchromatin in LMNA mutation-associated dilated cardiomyopathy. <i>Clinical Epigenetics</i> , 2021, 13, 3.	1.8	11
14264	Identification of potential key genes and pathways associated with the Pashmina fiber initiation using RNA-Seq and integrated bioinformatics analysis. <i>Scientific Reports</i> , 2021, 11, 1766.	1.6	14
14265	Identification of Functional Microbial Modules Through Network-Based Analysis of Meta-Microbial Features Using Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2851-2862.	1.9	3
14266	Impaired Activated/Memory Regulatory T Cell Clonal Expansion Instigates Diabetes in NOD Mice. <i>Diabetes</i> , 2021, 70, 976-985.	0.3	12
14267	Identification of prognostic biomarkers associated with metastasis and immune infiltration in osteosarcoma. <i>Oncology Letters</i> , 2021, 21, 180.	0.8	21
14268	Deciphering the architecture and interactome of hnRNP proteins and enigmRBPs. <i>Molecular Omics</i> , 2021, 17, 503-516.	1.4	1
14269	Dynamic changes of transcriptome of fifth-instar <i>spodoptera litura</i> larvae in response to insecticide. <i>3 Biotech</i> , 2021, 11, 98.	1.1	9
14270	Prediction, Analysis, Visualization, and Storage of Protein-Protein Interactions Using Computational Approaches. , 2021, , 265-346.		1
14271	Linking Economic Complexity, Diversification, and Industrial Policy with Sustainable Development: A Structured Literature Review. <i>Sustainability</i> , 2021, 13, 1265.	1.6	31
14272	Dietary Indole-3-Carbinol Activates AhR in the Gut, Alters Th17-Microbe Interactions, and Exacerbates Insulinitis in NOD Mice. <i>Frontiers in Immunology</i> , 2020, 11, 606441.	2.2	19
14273	Malonyl-proteome profiles of <i>Staphylococcus aureus</i> reveal lysine malonylation modification in enzymes involved in energy metabolism. <i>Proteome Science</i> , 2021, 19, 1.	0.7	15
14274	Identification of mast cells as a candidate significant target of immunotherapy for acute myeloid leukemia. <i>Hematology</i> , 2021, 26, 284-294.	0.7	7
14275	Berberine alters gut microbial function through modulation of bile acids. <i>BMC Microbiology</i> , 2021, 21, 24.	1.3	13
14276	A Comprehensive Analysis Identified Hub Genes and Associated Drugs in Alzheimer's Disease. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	9
14277	Study of the active ingredients and mechanism of <i>Sparganii rhizoma</i> in gastric cancer based on HPLC-Q-TOF-MS/MS and network pharmacology. <i>Scientific Reports</i> , 2021, 11, 1905.	1.6	20
14278	CCT6A, a novel prognostic biomarker for Ewing sarcoma. <i>Medicine (United States)</i> , 2021, 100, e24484.	0.4	16
14279	Beneficial effects of an endogenous enrichment in n3-PUFAs on Wnt signaling are associated with attenuation of alcohol-mediated liver disease in mice. <i>FASEB Journal</i> , 2021, 35, e21377.	0.2	14

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14280	Profiling of MicroRNAs and Their Targets in Roots and Shoots Reveals a Potential miRNA-Mediated Interaction Network in Response to Phosphate Deficiency in the Forestry Tree <i>Betula luminifera</i> . <i>Frontiers in Genetics</i> , 2021, 12, 552454.	1.1	10
14281	Intestinal SIRT1 Deficiency-Related Intestinal Inflammation and Dysbiosis Aggravate TNF $\alpha$ -Mediated Renal Dysfunction in Cirrhotic Ascitic Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1233.	1.8	6
14282	SRGAP1 Controls Small Rho GTPases To Regulate Podocyte Foot Process Maintenance. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 563-579.	3.0	18
14283	Advances in decomposing complex metabolite mixtures using substructure- and network-based computational metabolomics approaches. <i>Natural Product Reports</i> , 2021, 38, 1967-1993.	5.2	78
14284	Differential profiles of HDAC1 substrates and associated proteins in breast cancer cells revealed by trapping. <i>Molecular Omics</i> , 2021, 17, 544-553.	1.4	7
14285	Gene Ontology and Pathway Enrichment Analysis. , 2021, , 257-279.		1
14286	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. <i>Cell Reports</i> , 2021, 34, 108670.	2.9	22
14287	Gene Expression Profiling Reveals the Shared and Distinct Transcriptional Signatures in Human Lung Epithelial Cells Infected With SARS-CoV-2, MERS-CoV, or SARS-CoV: Potential Implications in Cardiovascular Complications of COVID-19. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 623012.	1.1	31
14288	Genomic Footprinting Analyses from DNase-seq Data to Construct Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2021, 2328, 25-46.	0.4	1
14290	Identification of 37 Heterogeneous Drug Candidates for Treatment of COVID-19 via a Rational Transcriptomics-Based Drug Repurposing Approach. <i>Pharmaceuticals</i> , 2021, 14, 87.	1.7	5
14291	Induced organoids derived from patients with ulcerative colitis recapitulate colitic reactivity. <i>Nature Communications</i> , 2021, 12, 262.	5.8	51
14292	The underlying molecular mechanism and identification of transcription factor markers for laryngeal squamous cell carcinoma. <i>Bioengineered</i> , 2021, 12, 208-224.	1.4	9
14293	lncRNA expression profiles and associated ceRNA network analyses in epicardial adipose tissue of patients with coronary artery disease. <i>Scientific Reports</i> , 2021, 11, 1567.	1.6	16
14294	Identification of hub lncRNA ceRNAs in multiple sclerosis based on ceRNA mechanisms. <i>Molecular Genetics and Genomics</i> , 2021, 296, 423-435.	1.0	12
14295	Integrated analyses of miRNA and mRNA profiles in leukocytes and serums in traditional Chinese medicine (TCM)-defined Pi-qi-deficiency syndrome and Pi-wei damp-heat syndrome resulting from chronic atrophic gastritis. <i>Chinese Medicine</i> , 2021, 16, 4.	1.6	9
14296	Gene regulatory network analysis identifies key genes and regulatory mechanisms involved in acute myocardial infarction using bulk and single cell RNA-seq data. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 7774-7789.	1.0	2
14297	Huntington Disease Mice Exhibit a TCF7L2-Responsive Suppression of Both Homeostatic and Compensatory Remyelination. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
14298	Identification of the genetic basis of sporadic polydactyly in China by targeted sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3482-3490.	1.9	0



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14299	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021, 93, 1912-1923.	3.2	30
14300	The Expression of NTAL and Its Protein Interactors Is Associated With Clinical Outcomes in Acute Myeloid Leukemia. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100091.	2.5	1
14301	Diarylheptanoid analogues from the rhizomes of <i>Zingiber officinale</i> and their anti-tumour activity. <i>RSC Advances</i> , 2021, 11, 29376-29384.	1.7	4
14303	Identifying of biomarkers associated with gastric cancer based on 11 topological analysis methods of CytoHubba. <i>Scientific Reports</i> , 2021, 11, 1331.	1.6	36
14304	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100069.	2.5	21
14305	Expression and affinity purification of recombinant mammalian mitochondrial ribosomal small subunit (MRPS) proteins and protein-protein interaction analysis indicate putative role in tumourigenic cellular processes. <i>Journal of Biochemistry</i> , 2021, 169, 675-692.	0.9	6
14306	Increased Expression of TICRR Predicts Poor Clinical Outcomes: A Potential Therapeutic Target for Papillary Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 605378.	1.1	10
14307	Multiple screening approaches reveal HDAC6 as a novel regulator of glycolytic metabolism in triple-negative breast cancer. <i>Science Advances</i> , 2021, 7, .	4.7	38
14308	Transcriptome and degradome sequencing reveals changes in <i>Populus trichocarpa</i> caused by its allelopathic response to p-hydroxybenzoic acid. <i>Journal of Forestry Research</i> , 2021, 32, 2155-2168.	1.7	3
14309	Enrichment of Circular RNA Expression Dereglulation at the Transition to Recurrent Spontaneous Seizures in Experimental Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , 2021, 12, 627907.	1.1	13
14310	CREBBP/EP300 mutations promoted tumor progression in diffuse large B-cell lymphoma through altering tumor-associated macrophage polarization via FBXW7-NOTCH-CCL2/CSF1 axis. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 10.	7.1	93
14311	Enrichment and description of novel bacteria performing syntrophic propionate oxidation at high ammonia level. <i>Environmental Microbiology</i> , 2021, 23, 1620-1637.	1.8	21
14312	Integrative network analysis of N6-methyladenosine methylation-related genes reveal potential therapeutic targets for spinal cord injury. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 8174-8187.	1.0	3
14313	Genome-Wide Expression and Alternative Splicing in Domesticated Sunflowers ( <i>Helianthus annuus</i> L.) under Flooding Stress. <i>Agronomy</i> , 2021, 11, 92.	1.3	7
14314	Potential prognostic markers and significant lncRNA-mRNA co-expression pairs in laryngeal squamous cell carcinoma. <i>Open Life Sciences</i> , 2021, 16, 544-557.	0.6	6
14315	Mass spectrometry-based protein-protein interaction networks for the study of human diseases. <i>Molecular Systems Biology</i> , 2021, 17, e8792.	3.2	96
14316	HBFP: a new repository for human body fluid proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	17
14317	Dietary, Cultural, and Pathogens-Related Selective Pressures Shaped Differential Adaptive Evolution among Native Mexican Populations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	6

#	ARTICLE	IF	CITATIONS
14318	Common Network Pharmacology Software. , 2021, , 127-173.		0
14319	High-Density, Targeted Monitoring of Tyrosine Phosphorylation Reveals Activated Signaling Networks in Human Tumors. <i>Cancer Research</i> , 2021, 81, 2495-2509.	0.4	41
14320	miR-128-3p reduced acute lung injury induced by sepsis via targeting PEL12. <i>Open Medicine (Poland)</i> , 2021, 16, 1109-1120.	0.6	7
14321	Identification of the key target profiles underlying the drugs of narrow therapeutic index for treating cancer and cardiovascular disease. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2318-2328.	1.9	7
14322	Genome-scale mechanistic modeling of signaling pathways made easy: A bioconductor/cytoscape/web server framework for the analysis of omic data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2968-2978.	1.9	9
14323	Active phase prebiotic feeding alters gut microbiota, induces weight-independent alleviation of hepatic steatosis and serum cholesterol in high-fat diet-fed mice. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 448-458.	1.9	16
14324	Stress-Induced Detoxification Enzymes in Rice Have Broad Substrate Affinity. <i>ACS Omega</i> , 2021, 6, 3399-3410.	1.6	9
14325	Nonalcoholic Steatohepatitis and HCC in a Hyperphagic Mouse Accelerated by Western Diet. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 891-920.	2.3	17
14326	Elevated CDK5R1 predicts worse prognosis in hepatocellular carcinoma based on TCGA data. <i>Bioscience Reports</i> , 2021, 41, .	1.1	9
14327	A network pharmacology based approach for predicting active ingredients and potential mechanism of Lianhuaqingwen capsule in treating COVID-19. <i>International Journal of Medical Sciences</i> , 2021, 18, 1866-1876.	1.1	34
14328	Nitrogen Use Efficiency Phenotype and Associated Genes: Roles of Germination, Flowering, Root/Shoot Length and Biomass. <i>Frontiers in Plant Science</i> , 2020, 11, 587464.	1.7	23
14329	Use of bioinformatic database analysis and specimen verification to identify novel biomarkers predicting gastric cancer metastasis. <i>Journal of Cancer</i> , 2021, 12, 5967-5976.	1.2	6
14330	Identification of biomarkers and construction of a microRNA-mRNA regulatory network for clear cell renal cell carcinoma using integrated bioinformatics analysis. <i>PLoS ONE</i> , 2021, 16, e0244394.	1.1	8
14331	ORA, FCS, and PT Strategies in Functional Enrichment Analysis. <i>Methods in Molecular Biology</i> , 2021, 2361, 163-178.	0.4	1
14332	Tools for time-course simulation in systems biology: a brief overview. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
14333	Human Cardiac Transcription Factor Networks. , 2021, , 429-453.		5
14334	Stem girdling affects the onset of autumn senescence in aspen in interaction with metabolic signals. <i>Physiologia Plantarum</i> , 2021, 172, 201-217.	2.6	12
14335	Multiple microarray analyses identify key genes associated with the development of Non-Small Cell Lung Cancer from Chronic Obstructive Pulmonary Disease. <i>Journal of Cancer</i> , 2021, 12, 996-1010.	1.2	11

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14336	<i>Planomonospora</i> : A Metabolomics Perspective on an Underexplored Actinobacteria Genus. <i>Journal of Natural Products</i> , 2021, 84, 204-219.	1.5	23
14337	Low-dose <i>Drosera rotundifolia</i> induces gene expression changes in 16HBE human bronchial epithelial cells. <i>Scientific Reports</i> , 2021, 11, 2356.	1.6	5
14338	Coexistence of atypical adenomatous hyperplasia, minimally invasive adenocarcinoma and invasive adenocarcinoma: Gene mutation analysis. <i>Thoracic Cancer</i> , 2021, 12, 693-698.	0.8	1
14339	Synaptic Scaling—An Artificial Neural Network Regularization Inspired by Nature. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2022, 33, 3094-3108.	7.2	5
14341	A Mechanism of Action Study on Danggui Sini Decoction to Discover Its Therapeutic Effect on Gastric Cancer. <i>Frontiers in Pharmacology</i> , 2020, 11, 592903.	1.6	10
14342	Ī,-SGA: synthetic genetic array analysis for systematically screening and quantifying trigenic interactions in yeast. <i>Nature Protocols</i> , 2021, 16, 1219-1250.	5.5	6
14343	High expression of MAPK-14 promoting the death of chondrocytes is an important signal of osteoarthritis process. <i>PeerJ</i> , 2021, 9, e10656.	0.9	9
14344	Distinct transcriptional profile of blood mononuclear cells in Behçet's disease: insights into the central role of neutrophil chemotaxis. <i>Rheumatology</i> , 2021, 60, 4910-4919.	0.9	16
14345	Effect of Yinlai Decoction on the metabolic pathways in the lung of high-calorie diet-induced pneumonia rats. <i>Journal of Traditional Chinese Medical Sciences</i> , 2021, 8, 4-16.	0.1	0
14346	Four hub genes regulate tumor infiltration by immune cells, antitumor immunity in the tumor microenvironment, and survival outcomes in lung squamous cell carcinoma patients. <i>Aging</i> , 2021, 13, 3819-3842.	1.4	6
14347	Systematic analysis of enhancer regulatory circuit perturbation driven by copy number variations in malignant glioma. <i>Theranostics</i> , 2021, 11, 3060-3073.	4.6	6
14348	Dissecting the Invasion-Associated Long Non-coding RNAs Using Single-Cell RNA-Seq Data of Glioblastoma. <i>Frontiers in Genetics</i> , 2020, 11, 633455.	1.1	4
14349	Biotin Proximity Labeling for Protein-Protein Interaction Discovery: The BioID Method. <i>Methods in Molecular Biology</i> , 2021, 2261, 357-379.	0.4	3
14350	Serum proteome profiling provides a deep understanding of the 'gut-liver axis' in relation to liver injury and regeneration. <i>Acta Biochimica Et Biophysica Sinica</i> , 2021, 53, 372-380.	0.9	5
14354	MMP9 and IGFBP1 Regulate Tumor Immune and Drive Tumor Progression in Clear Cell Renal Cell Carcinoma. <i>Journal of Cancer</i> , 2021, 12, 2243-2257.	1.2	15
14355	Immune-related prognostic genes signatures in the tumor microenvironment of sarcoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 2243-2257.	1.0	6
14356	Short loop functional commonality identified in leukaemia proteome highlights crucial protein sub-networks. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab010.	1.5	0
14357	Computational intelligence for genomic data. , 2021, , 247-260.		0

#	ARTICLE	IF	CITATIONS
14358	Gene fusion of IL7 involved in the regulation of idiopathic pulmonary fibrosis. <i>Therapeutic Advances in Respiratory Disease</i> , 2021, 15, 175346662199504.	1.0	2
14359	Obesogenic Diets Cause Alterations on Proteins and Theirs Post-Translational Modifications in Mouse Brains. <i>Nutrition and Metabolic Insights</i> , 2021, 14, 117863882110124.	0.8	5
14360	In Silico Metagenomics Analysis. The Microbiomes of Humans, Animals, Plants, and the Environment, 2021, , 29-39.	0.2	0
14361	Effect of HPV 16 E6 Oncoprotein Variants on the Alterations of the Proteome of C33A Cells. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 273-283.	1.0	4
14362	Exploring Networks in the STRING and Reactome Database. , 2021, , 507-520.		6
14363	Complement Activation Induces Excessive T Cell Cytotoxicity in Severe COVID-19. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
14364	Pecan kinome: classification and expression analysis of all protein kinases in &lt;i>&lt;i>Carya illinoensis&lt;/i&lt;/i>. <i>Forestry Research</i> , 2021, 1, 1-12.	0.5	3
14365	Revealing the potential pharmacological mechanism of traditional Chinese medicine by integrating metabolite profiling of a Q-marker and network pharmacology, prim-O-glucosylcimifugin as an example. <i>New Journal of Chemistry</i> , 2021, 45, 15571-15581.	1.4	2
14366	Identifying the miRNA Signature Association with Aging-Related Senescence in Glioblastoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 517.	1.8	5
14367	Effects of Three-Month Feeding High Fat Diets with Different Fatty Acid Composition on Myocardial Proteome in Mice. <i>Nutrients</i> , 2021, 13, 330.	1.7	9
14368	Co-expression Networks in Predicting Transcriptional Gene Regulation. <i>Methods in Molecular Biology</i> , 2021, 2328, 1-11.	0.4	5
14369	An immune-based risk-stratification system for predicting prognosis in pulmonary sarcomatoid carcinoma (PSC). <i>Oncolmmunology</i> , 2021, 10, 1947665.	2.1	6
14370	Brain Disease Network Analysis to Elucidate the Neurological Manifestations of COVID-19. <i>Molecular Neurobiology</i> , 2021, 58, 1875-1893.	1.9	37
14372	Common bean SNP alleles and candidate genes affecting photosynthesis under contrasting water regimes. <i>Horticulture Research</i> , 2021, 8, 4.	2.9	13
14373	Mapping Genetic Interactions in Human Cancer Cells Using a One-Step tRNA-CRISPR System. <i>Methods in Molecular Biology</i> , 2021, 2381, 175-187.	0.4	1
14374	Î²-Arrestin2 Inhibits the Apoptosis and Facilitates the Proliferation of Fibroblast-like Synoviocytes in Diffuse-type Tenosynovial Giant Cell Tumor. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 461-470.	1.0	4
14375	The expression and clinical prognostic value of protein phosphatase 1 catalytic subunit beta in pancreatic cancer. <i>Bioengineered</i> , 2021, 12, 2763-2778.	1.4	1
14376	Quasispecies of SARS-CoV-2 revealed by single nucleotide polymorphisms (SNPs) analysis. <i>Virulence</i> , 2021, 12, 1209-1226.	1.8	16

#	ARTICLE	IF	CITATIONS
14377	Single Cell Clonal Analysis Identifies an AID-Dependent Pathway of Plasma Cell Differentiation. SSRN Electronic Journal, 0, , .	0.4	0
14378	System Biology-Guided Chemical Proteomics to Discover Protein Targets of Monoethylhexyl Phthalate in Regulating Cell Cycle. Environmental Science & Technology, 2021, 55, 1842-1851.	4.6	16
14379	The cytoprotective protein MANF promotes neuronal survival independently from its role as a GRP78 cofactor. Journal of Biological Chemistry, 2021, 296, 100295.	1.6	31
14380	Network pharmacology of Withania somnifera against stress associated neurodegenerative diseases. Advances in Traditional Medicine, 2021, 21, 565-578.	1.0	7
14381	Identification of potential genes associated with immune cell infiltration in atherosclerosis. Mathematical Biosciences and Engineering, 2021, 18, 2230-2242.	1.0	6
14382	Fungal sporocarps house diverse and host-specific communities of fungicolous fungi. ISME Journal, 2021, 15, 1445-1457.	4.4	24
14383	PROMISed: A novel web-based tool to facilitate analysis and visualization of the molecular interaction networks from co-fractionation mass spectrometry (CF-MS) experiments. Computational and Structural Biotechnology Journal, 2021, 19, 5117-5125.	1.9	9
14384	Transcriptomic analysis reveals essential microRNAs after peripheral nerve injury. Neural Regeneration Research, 2021, 16, 1865.	1.6	13
14385	Bioinformaticsâ€™computer programming. , 2021, , 125-148.		0
14386	DNA methylation perturbations may link altered development and aging in the lung. Aging, 2021, 13, 1742-1764.	1.4	6
14387	GVES: machine learning model for identification of prognostic genes with a small dataset. Scientific Reports, 2021, 11, 439.	1.6	12
14388	Elucidation of the Mechanism of Action of Ginseng Against Acute Lung Injury/Acute Respiratory Distress Syndrome by a Network Pharmacology-Based Strategy. Frontiers in Pharmacology, 2020, 11, 611794.	1.6	19
14389	Five Circular RNAs in Metabolism Pathways Related to Prostate Cancer. Frontiers in Genetics, 2021, 12, 636419.	1.1	7
14390	The First Report for the Presence of Spiroplasma and Rickettsia in Red Palm Weevil Rhynchophorus ferrugineus (Coleoptera: Curculionidae) in Egypt. Acta Parasitologica, 2021, 66, 593-604.	0.4	2
14391	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0
14392	Overexpression of microRNA-29b inhibits epithelial-mesenchymal transition and angiogenesis of colorectal cancer through the ETV4/ERK/EGFR axis. Cancer Cell International, 2021, 21, 17.	1.8	17
14393	Identification of core gene in obese type 2 diabetes patients using bioinformatics analysis. Adipocyte, 2021, 10, 310-321.	1.3	8
14394	Structurally diverse diterpenoid alkaloids from the lateral roots of <i>Aconitum carmichaelii</i> Debx. and their anti-tumor activities based on <i>in vitro</i> systematic evaluation and network pharmacology analysis. RSC Advances, 2021, 11, 26594-26606.	1.7	6

#	ARTICLE	IF	CITATIONS
14395	A novel strategy for exploring food originated anti-adipogenesis substances and mechanism by structural similarity evaluation, ADME prediction, network pharmacology and experimental validation. Food and Function, 2021, 12, 7081-7091.	2.1	8
14396	The micro-RNA content of unsorted cryopreserved bovine sperm and its relation to the fertility of sperm after sex-sorting. BMC Genomics, 2021, 22, 30.	1.2	21
14397	Transcriptomic analysis of human brains with Alzheimer's disease reveals the altered expression of synaptic genes linked to cognitive deficits. Brain Communications, 2021, 3, fcab123.	1.5	25
14398	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. Eurosurveillance, 2021, 26, .	3.9	9
14399	Expression levels of chemokine (C-X-C motif) ligands CXCL1 and CXCL3 as prognostic biomarkers in rectal adenocarcinoma: evidence from Gene Expression Omnibus (GEO) analyses. Bioengineered, 2021, 12, 3711-3725.	1.4	8
14400	MYC regulates ribosome biogenesis and mitochondrial gene expression programs through its interaction with host cell factor 1. ELife, 2021, 10, .	2.8	45
14401	NGS Methodologies and Computational Algorithms for the Prediction and Analysis of. Methods in Molecular Biology, 2021, 2362, 119-145.	0.4	2
14402	Integrated weighted gene co-expression network analysis uncovers STAT1 (signal transducer and activator of transcription 1) overexpression in arterial hypertension. Bioengineered, 2021, 12, 6021-6034.	1.4	7
14403	Unlocking the Diversity of Pyrroloiminoquinones Produced by Latrunculid Sponge Species. Marine Drugs, 2021, 19, 68.	2.2	8
14404	Proteomic and Functional Studies Reveal Detyrosinated Tubulin as Treatment Target in Sarcomere Mutation-Induced Hypertrophic Cardiomyopathy. Circulation: Heart Failure, 2021, 14, e007022.	1.6	58
14405	Mash-based analyses of Escherichia coli genomes reveal 14 distinct phylogroups. Communications Biology, 2021, 4, 117.	2.0	52
14406	Proteome-wide identification of NEDD8 modification sites reveals distinct proteomes for canonical and atypical NEDDylation. Cell Reports, 2021, 34, 108635.	2.9	35
14407	Distribution and comparison of bacterial communities in HVAC systems of two university buildings: Implications for indoor air quality and public health. Environmental Monitoring and Assessment, 2021, 193, 47.	1.3	11
14408	Glycoconjugate pathway connections revealed by sequence similarity network analysis of the monotopic phosphoglycosyl transferases. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	17
14409	Comparative Analysis of Core and Accessory Genes in Coexpression Network. Methods in Molecular Biology, 2021, 2242, 45-58.	0.4	2
14410	Pyrovobasine, hybrid alkylated pyrrolidine monoterpene indole alkaloid pseudodimer discovered using a combination of mass spectral and NMR-based machine learning annotations. Organic and Biomolecular Chemistry, 2021, 20, 98-105.	1.5	4
14411	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	3.2	4
14412	Transfer RNA-derived non-coding RNAs (tncRNAs): Hidden regulation of plants' transcriptional regulatory circuits. Computational and Structural Biotechnology Journal, 2021, 19, 5278-5291.	1.9	9



#	ARTICLE	IF	CITATIONS
14413	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	9.4	377
14414	Coupling the endophytic microbiome with the host transcriptome in olive roots. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4777-4789.	1.9	8
14415	Virus systems biology: Proteomics profiling of dynamic protein networks during infection. <i>Advances in Virus Research</i> , 2021, 109, 1-29.	0.9	5
14416	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
14417	Exploring the mechanism of Shenqisherong pill against cervical spondylotic myelopathy by network pharmacology and molecular docking. <i>Annals of Palliative Medicine</i> , 2021, 10, 10253-10275.	0.5	2
14418	Fertilization alters protistan consumers and parasites in crop-associated microbiomes. <i>Environmental Microbiology</i> , 2021, 23, 2169-2183.	1.8	52
14419	Prognostic value of LRRC4C in Colon and Gastric Cancers correlates with Tumour Microenvironment Immunity. <i>International Journal of Biological Sciences</i> , 2021, 17, 1413-1427.	2.6	6
14420	Gene expression evaluation of antioxidant enzymes in patients with hepatocellular carcinoma: RT-qPCR and bioinformatic analyses. <i>Genetics and Molecular Biology</i> , 2021, 44, e20190373.	0.6	9
14421	Toward Identifying Key Gene Group in the Occurrence and Development of Lung Adenocarcinoma. <i>IEEE Access</i> , 2021, 9, 26156-26167.	2.6	0
14422	Screening of disease-related biomarkers related to neuropathic pain (NP) after spinal cord injury (SCI). <i>Human Genomics</i> , 2021, 15, 5.	1.4	12
14423	Cognitive Maps Across Multiple Social Sectors: Shared and Unique Perceptions on the Quality of Agricultural Soils in Mexico. <i>Frontiers in Sustainable Food Systems</i> , 2021, 4, .	1.8	7
14424	Dysregulated LncRNAs Act as Competitive Endogenous RNAs and Are Associated With Cervical Cancer Development in UYGHUR Women. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382198971.	0.8	4
14425	G-Protein-coupled Estrogen Receptor 1 Agonist G-1 Perturbs Sunitinib Resistance-related Phosphoproteomic Signatures in Renal Cell Carcinoma. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 207-220.	1.0	5
14426	Biomolecular condensation of NUP98 fusion proteins drives leukemogenic gene expression. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 190-201.	3.6	56
14427	Integrative Bioinformatics Analysis Identified Hub Genes in Association with Development of Lung Adenocarcinoma. <i>Advances in Clinical Medicine</i> , 2021, 11, 2970-2977.	0.0	0
14428	Study on mechanism of matrine in treatment of COVID-19 combined with liver injury by network pharmacology and molecular docking technology. <i>Drug Delivery</i> , 2021, 28, 325-342.	2.5	28
14429	Transcriptomic characterization reveals prognostic molecular signatures of sorafenib resistance in hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 3969-3993.	1.4	7
14430	Bioinformatics analysis identifies biomarkers associated with poor prognosis in diffuse-type gastric cancer. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	4

#	ARTICLE	IF	CITATIONS
14431	Future Climate Alters Pathogens-Microbiome Co-occurrence Networks in Wheat Straw Residues during Decomposition. <i>Proceedings (mdpi)</i> , 2020, 66, 22.	0.2	2
14432	The Fecal and Serum Metabolomics of Giant Pandas Based on Untargeted Metabolomics. <i>Zoological Science</i> , 2021, 38, 179-186.	0.3	2
14433	Identification of small proline-rich protein <scp>1B</scp> (<scp>SPRR1B</scp>) as a prognostically predictive biomarker for lung adenocarcinoma by integrative bioinformatic analysis. <i>Thoracic Cancer</i> , 2021, 12, 796-806.	0.8	16
14434	An Integrative Transcriptomic Analysis of Systemic Juvenile Idiopathic Arthritis for Identifying Potential Genetic Markers and Drug Candidates. <i>International Journal of Molecular Sciences</i> , 2021, 22, 712.	1.8	6
14436	Genome-Wide Association Study of Maize Aboveground Dry Matter Accumulation at Seedling Stage. <i>Frontiers in Genetics</i> , 2020, 11, 571236.	1.1	9
14437	Transcriptomic markers in pediatric septic shock prognosis: an integrative analysis of gene expression profiles. <i>Brazilian Journal of Medical and Biological Research</i> , 2021, 54, e10152.	0.7	2
14438	Synergism of Proneurogenic miRNAs Provides a More Effective Strategy to Target Glioma Stem Cells. <i>Cancers</i> , 2021, 13, 289.	1.7	7
14439	Rosetta design with co-evolutionary information retains protein function. <i>PLoS Computational Biology</i> , 2021, 17, e1008568.	1.5	12
14440	Constructing a ceRNA-immunoregulatory network associated with the development and prognosis of human atherosclerosis through weighted gene co-expression network analysis. <i>Aging</i> , 2021, 13, 3080-3100.	1.4	14
14443	Identification of Key Modules and Hub Genes of Annulus Fibrosus in Intervertebral Disc Degeneration. <i>Frontiers in Genetics</i> , 2020, 11, 596174.	1.1	4
14445	Full-Length Transcriptome Analysis of Four Different Tissues of <i>Cephalotaxus oliveri</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 787.	1.8	16
14446	Extracellular Vesicles From Liver Progenitor Cells Downregulates Fibroblast Metabolic Activity and Increase the Expression of Immune-Response Related Molecules. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 613583.	1.8	0
14447	Protein-Protein Interaction Analysis through Network Topology (Oral Cancer). <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-9.	1.1	5
14449	Transfer of oral bacteria to the fetus during late gestation. <i>Scientific Reports</i> , 2021, 11, 708.	1.6	4
14451	Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. <i>Nature Communications</i> , 2021, 12, 350.	5.8	13
14452	Bioinformatic analysis of dysregulated proteins in prostate cancer patients reveals putative urinary biomarkers and key biological pathways. <i>Medical Oncology</i> , 2021, 38, 9.	1.2	6
14455	Functional Prediction of Long Noncoding RNAs in Cutaneous Melanoma Using a Systems Biology Approach. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222098850.	1.0	0
14457	CHRNA5 belongs to the secondary estrogen signaling network exhibiting prognostic significance in breast cancer. <i>Cellular Oncology (Dordrecht)</i> , 2021, 44, 453-472.	2.1	6

#	ARTICLE	IF	CITATIONS
14458	Construction and validation of a three-microRNA signature as prognostic biomarker in patients with hepatocellular carcinoma. <i>International Journal of Medical Sciences</i> , 2021, 18, 984-999.	1.1	11
14459	Clinical Proteomics for the Analysis of Circulating Extracellular Vesicles. <i>Methods in Molecular Biology</i> , 2021, 2259, 13-23.	0.4	5
14462	Structure of cyanobacterial phycobilisome core revealed by structural modeling and chemical cross-linking. <i>Science Advances</i> , 2021, 7, .	4.7	20
14463	An overview of graph databases and their applications in the biomedical domain. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	19
14464	Loss of tRNA-modifying enzyme Etp3 activates a p53-dependent antitumor checkpoint in hematopoiesis. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	14
14465	Genome-wide identification, characterization and expression analysis of the expansin gene family under drought stress in tea ( <i>Camellia sinensis</i> L.). <i>Plant Science Today</i> , 2021, 8, 32-44.	0.4	9
14466	Broad Kinase Inhibition Mitigates Early Neuronal Dysfunction in Tauopathy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1186.	1.8	6
14467	Identification of Key Pathways and Genes Related to the Development of Hair Follicle Cycle in Cashmere Goats. <i>Genes</i> , 2021, 12, 180.	1.0	23
14468	Predicting and understanding synergistic pairwise compound combinations of Shexian Baoxin Pill (SBP) using network biology. <i>Synergy</i> , 2021, 11, 100073.	1.1	1
14469	Conserved regulatory logic at accessible and inaccessible chromatin during the acute inflammatory response in mammals. <i>Nature Communications</i> , 2021, 12, 567.	5.8	15
14470	Network- and systems-based re-engineering of dendritic cells with non-coding RNAs for cancer immunotherapy. <i>Theranostics</i> , 2021, 11, 1412-1428.	4.6	8
14471	Dermatomyositis: immunological landscape, biomarkers, and potential candidate drugs. <i>Clinical Rheumatology</i> , 2021, 40, 2301-2310.	1.0	4
14472	An efficient and effective method to identify significantly perturbed subnetworks in cancer. <i>Nature Computational Science</i> , 2021, 1, 79-88.	3.8	10
14473	New novel non-MHC genes were identified for cervical cancer with an integrative analysis approach of transcriptome-wide association study. <i>Journal of Cancer</i> , 2021, 12, 840-848.	1.2	7
14474	Microbial dynamics of elevated carbon flux in the open ocean's abyss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	65
14475	Dietary spinach reshapes the gut microbiome in an Apc-mutant genetic background: mechanistic insights from integrated multi-omics. <i>Gut Microbes</i> , 2021, 13, 1972756.	4.3	15
14476	Association of Baseline Luminal Narrowing With Ileal Microbial Shifts and Gene Expression Programs and Subsequent Transmural Healing in Pediatric Crohn Disease. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 1707-1718.	0.9	9
14477	Proteomic analysis reveals differentially abundant proteins probably involved in the virulence of amastigote and promastigote forms of <i>Leishmania infantum</i> . <i>Parasitology Research</i> , 2021, 120, 679-692.	0.6	9

#	ARTICLE	IF	CITATIONS
14478	Mdfi Promotes C2C12 Cell Differentiation and Positively Modulates Fast-to-Slow-Twitch Muscle Fiber Transformation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 605875.	1.8	14
14479	Repression of barley cathepsins, HvPap-19 and HvPap-1, differentially alters grain composition and delays germination. <i>Journal of Experimental Botany</i> , 2021, 72, 3474-3485.	2.4	4
14480	An empirical meta-analysis of the life sciences linked open data on the web. <i>Scientific Data</i> , 2021, 8, 24.	2.4	10
14481	Screening differentially expressed proteins of coronary heart disease with congenital cold syndrome based on tandem mass tag (TMT) technology. <i>Bioengineered</i> , 2021, 12, 1338-1350.	1.4	7
14482	Identification and immunoprofiling of key prognostic genes in the tumor microenvironment of hepatocellular carcinoma. <i>Bioengineered</i> , 2021, 12, 1555-1575.	1.4	12
14483	Prognostic score model-based signature genes for predicting the prognosis of metastatic skin cutaneous melanoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 5125-5145.	1.0	1
14484	Molecular mechanism of Wutou Decoction in the treatment of osteoarthritis: a bioinformatics and molecular docking study. <i>Annals of Palliative Medicine</i> , 2021, 10, 7706-7720.	0.5	7
14485	Meta-analysis identifying epithelial-derived transcriptomes predicts poor clinical outcome and immune infiltrations in ovarian cancer. <i>Quantitative Finance and Economics</i> , 2021, 18, 6527-6551.	1.4	2
14486	Estrogen-induced circRNA, circPGR, functions as a ceRNA to promote estrogen receptor-positive breast cancer cell growth by regulating cell cycle-related genes. <i>Theranostics</i> , 2021, 11, 1732-1752.	4.6	42
14487	Proteomic Analysis Reveals the Importance of Exudates on Sclerotial Development in <i>Sclerotinia sclerotiorum</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 1430-1440.	2.4	12
14488	Glycolysis-Related Genes Serve as Potential Prognostic Biomarkers in Clear Cell Renal Cell Carcinoma. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-20.	1.9	29
14489	Comparative Host Interactomes of the SARS-CoV-2 Nonstructural Protein 3 and Human Coronavirus Homologs. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100120.	2.5	15
14491	Bioinformatic Approaches for Identification of Potential Repurposable Drugs in COVID-19. <i>Journal of Drug Delivery and Therapeutics</i> , 2021, 11, 13-22.	0.2	1
14492	Sequential fate-switches in stem-like cells drive the tumorigenic trajectory from human neural stem cells to malignant glioma. <i>Cell Research</i> , 2021, 31, 684-702.	5.7	41
14493	Co-expression for Genotype-Phenotype Function Annotation in Potato Research. <i>Methods in Molecular Biology</i> , 2021, 2354, 261-272.	0.4	0
14494	RNA Sequencing Analyses for Deciphering Potato Molecular Responses. <i>Methods in Molecular Biology</i> , 2021, 2354, 57-94.	0.4	2
14496	Heterogeneity Analysis of Esophageal Squamous Cell Carcinoma in Cell Lines, Tumor Tissues and Patient-Derived Xenografts. <i>Journal of Cancer</i> , 2021, 12, 3930-3944.	1.2	13
14497	A network pharmacology perspective for deciphering potential mechanisms of action of <i>Solanum nigrum</i> L. in bladder cancer. <i>BMC Complementary Medicine and Therapies</i> , 2021, 21, 45.	1.2	19

#	ARTICLE	IF	CITATIONS
14498	Identifying the molecular targets and mechanisms of xuebijing injection for the treatment of COVID-19 via network pharmacology and molecular docking. <i>Bioengineered</i> , 2021, 12, 2274-2287.	1.4	17
14499	Integrating Network Pharmacology and Experimental Validation to Investigate the Effects and Mechanism of Astragalus Flavonoids Against Hepatic Fibrosis. <i>Frontiers in Pharmacology</i> , 2020, 11, 618262.	1.6	32
14500	Computational Identification of ceRNA and Reconstruction of ceRNA Regulatory Network Based on RNA-seq and Small RNA-seq Data in Plants. <i>Methods in Molecular Biology</i> , 2021, 2328, 261-275.	0.4	2
14501	Integration of network pharmacology and molecular docking technology reveals the mechanism of the herbal pairing of <i>Codonopsis Pilosula</i> (Franch.) Nannf and <i>Astragalus Membranaceus</i> (Fisch.) Bge on chronic heart failure. <i>Annals of Palliative Medicine</i> , 2021, 10, 7942-7959.	0.5	9
14502	Identification novel prognostic signatures for Head and Neck Squamous Cell Carcinoma based on ceRNA network construction and immune infiltration analysis. <i>International Journal of Medical Sciences</i> , 2021, 18, 1297-1311.	1.1	18
14503	Interspecific Variation in the Unsaturation Level of Seed Oils Were Associated With the Expression Pattern Shifts of Duplicated Desaturase Genes and the Potential Role of Other Regulatory Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 616338.	1.7	3
14504	Molecular characterization of selectively vulnerable neurons in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 276-287.	7.1	238
14505	Transcriptomic and Network Analysis of Minor Salivary Glands of Patients With Primary Sjögren's Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 606268.	2.2	21
14506	IBDDDB: a manually curated and text-mining-enhanced database of genes involved in inflammatory bowel disease. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	8
14507	Iscador – Pharmazeutische Grundlagen und spirituelles Verständnis für die Verarbeitung der Mistel zum Krebspräparat. <i>Der Merkur</i> , 2021, 74, 219-226.	0.0	0
14508	Identification of the correlations between interleukin-27 (IL-27) and immune-inflammatory imbalance in preterm birth. <i>Bioengineered</i> , 2021, 12, 3201-3218.	1.4	5
14509	Bioinformatics Technologies in Autophagy Research. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1208, 387-453.	0.8	3
14510	Identification of the Relationships between Tumor Mutation Burden with Immune Infiltrates in Liver Hepatocellular Carcinoma. <i>Advances in Clinical Medicine</i> , 2021, 11, 2880-2890.	0.0	0
14511	Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector <i>Rhodnius prolixus</i> . <i>Scientific Reports</i> , 2021, 11, 1918.	1.6	18
14512	MyoData: An expression knowledgebase at single cell/nucleus level for the discovery of coding-noncoding RNA functional interactions in skeletal muscle. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4142-4155.	1.9	4
14513	The DisGeNET cytoscape app: Exploring and visualizing disease genomics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2960-2967.	1.9	221
14514	Comprehensive Analysis of ceRNA Regulation Network Involved in the Development of Coronary Artery Disease. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	6
14515	Gene signature of children with severe respiratory syncytial virus infection. <i>Pediatric Research</i> , 2021, 89, 1664-1672.	1.1	13

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14516	The inhibition of Mpro, the primary protease of COVID-19, by <i>Poria cocos</i> and its active compounds: a network pharmacology and molecular docking study. <i>RSC Advances</i> , 2021, 11, 11821-11843.	1.7	13
14517	An integrative analysis to distinguish between emphysema (EML) and alpha-1 antitrypsin deficiency-related emphysema (ADL)â€™A systems biology approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 315-342.	1.0	16
14518	Transcriptome analysis of cepharanthine against a SARS-CoV-2-related coronavirus. <i>Briefings in Bioinformatics</i> , 2021, 22, 1378-1386.	3.2	39
14519	An integrated network analysis approach to identify potential key genes, transcription factors, and microRNAs regulating human hematopoietic stem cell aging. <i>Molecular Omics</i> , 2021, 17, 967-984.	1.4	2
14520	Equine synovial fluid small non-coding RNA signatures in early osteoarthritis. <i>BMC Veterinary Research</i> , 2021, 17, 26.	0.7	19
14521	A hybrid model connecting regulatory interactions with stem cell divisions in the root. <i>Quantitative Plant Biology</i> , 2021, 2, .	0.8	25
14522	Zinc finger C3H1 domain-containing protein (ZFC3H1) evaluates the prognosis and treatment of prostate adenocarcinoma (PRAD): A study based on TCGA data. <i>Bioengineered</i> , 2021, 12, 5504-5515.	1.4	3
14523	Coupled Biotic-Abiotic Processes Control Biogeochemical Cycling of Dissolved Organic Matter in the Columbia River Hyporheic Zone. <i>Frontiers in Water</i> , 2021, 2, .	1.0	18
14524	Systematic Identification and Analysis of Circular RNAs of Japanese Flounder ( <i>Paralichthys olivaceus</i> ) in Response to <i>Vibrio anguillarum</i> Infection. <i>Genes</i> , 2021, 12, 100.	1.0	7
14525	Investigation on the active ingredient and mechanism of <i>Cannabis sativa</i> L. for treating epilepsy based on network pharmacology. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 994-1009.	0.5	7
14526	IBD Systems Biology Is Here to Stay. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 760-770.	0.9	14
14527	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	13.7	228
14528	An Ebola, Neisseria and Trypanosoma human protein interaction census reveals a conserved human protein cluster targeted by various human pathogens. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5292-5308.	1.9	4
14529	Preventing Alzheimer's disease within reach by 2025: Targetedâ€™riskâ€™ADâ€™prevention (TRAP) strategy. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2021, 7, e12190.	1.8	4
14530	Determination of the two-component systems regulatory network reveals core and accessory regulations across <i>Pseudomonas aeruginosa</i> lineages. <i>Nucleic Acids Research</i> , 2021, 49, 11476-11490.	6.5	28
14531	Identification of cancer related genes using feature selection and association rule mining. <i>Informatics in Medicine Unlocked</i> , 2021, 24, 100595.	1.9	15
14533	Weighted gene co-expression network analysis identifies modules and functionally enriched pathways in the lactation process. <i>Scientific Reports</i> , 2021, 11, 2367.	1.6	36
14534	GutBalance: a server for the human gut microbiome-based disease prediction and biomarker discovery with compositionality addressed. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12



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14535	Clinical Proteomics of Metastatic Melanoma Reveals Profiles of Organ Specificity and Treatment Resistance. <i>Clinical Cancer Research</i> , 2021, 27, 2074-2086.	3.2	12
14536	Introduction to Data Analysis in Omics Sciences. , 2021, , 226-240.		0
14537	Modeling of Pneumonia and Acute Lung Injury: Bioinformatics, Systems Medicine, and Artificial Intelligence. , 2021, , 573-580.		1
14538	Network and Systems Biology Approaches in Glial Cells. , 2021, , 71-80.		0
14539	Adaptor Protein ShcD/ <i>SHC4</i> Interacts with Tie2 Receptor to Synergistically Promote Glioma Cell Invasion. <i>Molecular Cancer Research</i> , 2021, 19, 757-770.	1.5	6
14540	Single-cell transcriptome analysis revealed the heterogeneity and microenvironment of gastrointestinal stromal tumors. <i>Cancer Science</i> , 2021, 112, 1262-1274.	1.7	18
14541	Effects of Immunization With the Soil-Derived Bacterium <i>Mycobacterium vaccae</i> on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. <i>Frontiers in Physiology</i> , 2020, 11, 524833.	1.3	9
14543	Trigenic Synthetic Genetic Array (T <sub>3</sub> -SGA) Technique for Complex Interaction Analysis. <i>Methods in Molecular Biology</i> , 2021, 2212, 377-400.	0.4	2
14544	Identification of Prognosis-related Hub RNA Binding Proteins Function through Regulating Metabolic Processes in Tongue Cancer. <i>Journal of Cancer</i> , 2021, 12, 2230-2242.	1.2	5
14546	Deep Proteome Profiling of Human Mammary Epithelia at Lineage and Age Resolution. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
14547	Bioinformatics Investigation and Contribution of Other Chromosomes Besides Chromosome 21 in the Risk of Down Syndrome Development. <i>Basic and Clinical Neuroscience</i> , 2021, 12, 79-88.	0.3	1
14548	BULKED SEGREGANT RNA SEQUENCING (BSR-SEQ) IDENTIFIES A NOVEL ALLELE ASSOCIATED WITH WEEPING TRAITS IN PRUNUS MUME. <i>Frontiers of Agricultural Science and Engineering</i> , 2021, , .	0.9	2
14549	Systems Pharmacology-Based Strategy to Explore the Pharmacological Mechanisms of <i>Citrus</i> Peel (Chenpi) for Treating Complicated Diseases. <i>The American Journal of Chinese Medicine</i> , 2021, 49, 391-411.	1.5	11
14550	MTFR2, A Potential Biomarker for Prognosis and Immune Infiltrates, Promotes Progression of Gastric Cancer Based on Bioinformatics Analysis and Experiments. <i>Journal of Cancer</i> , 2021, 12, 3611-3625.	1.2	8
14551	Square root stress-sum index for graphs. <i>Proyecciones</i> , 0, , .	0.1	0
14552	Exploiting the molecular basis of age and gender differences in outcomes of SARS-CoV-2 infections. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4092-4100.	1.9	23
14554	A Seven-Long Non-coding RNA Signature Improves Prognosis Prediction of Lung Adenocarcinoma: An Integrated Competing Endogenous RNA Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 625977.	1.1	5
14556	Identification of predictors based on drug targets highlights accurate treatment of goserelin in breast and prostate cancer. <i>Cell and Bioscience</i> , 2021, 11, 5.	2.1	8

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14557	Identification of RNA-binding protein SNRPA1 for prognosis in prostate cancer. <i>Aging</i> , 2021, 13, 2895-2911.	1.4	3
14558	Identification and Downstream Analyses of Domains Amplified in Plant Genomes: The Case of StAR-Related Lipid Transfer (START) Domains in Rice. <i>Methods in Molecular Biology</i> , 2021, 2238, 325-338.	0.4	1
14559	Fungal and Bacterial Diversity Patterns of Two Diversity Levels Retrieved From a Late Decaying <i>Fagus sylvatica</i> Under Two Temperature Regimes. <i>Frontiers in Microbiology</i> , 2020, 11, 548793.	1.5	4
14560	Mucosal microbiome dysbiosis associated with duodenum bulb inflammation. <i>Microbial Pathogenesis</i> , 2021, 150, 104711.	1.3	4
14561	Identification of candidate genes encoding tumor-specific neoantigens in early- and late-stage colon adenocarcinoma. <i>Aging</i> , 2021, 13, 4024-4044.	1.4	3
14562	Bioinformatics analysis of common key genes and pathways of intracranial, abdominal, and thoracic aneurysms. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 14.	0.7	4
14563	The prognostic value of circular RNA regulatory genes in competitive endogenous RNA network in gastric cancer. <i>Cancer Gene Therapy</i> , 2021, 28, 1175-1187.	2.2	6
14564	&lt;i>&lt;i>BIRC5&lt;/i>, &lt;i>GAJ5&lt;/i> and lncRNA NPHP3-AS1 Are Correlated with the Development of Atrial Fibrillation-Valvular Heart Disease. <i>International Heart Journal</i> , 2021, 62, 153-161.	0.5	13
14566	Expression and gene regulatory network of SNHG1 in hepatocellular carcinoma. <i>BMC Medical Genomics</i> , 2021, 14, 28.	0.7	4
14567	System Pharmacology-Based Strategy to Decode the Synergistic Mechanism of GanDouLing for Wilson's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-11.	0.5	2
14568	HIR V2: a human interactome resource for the biological interpretation of differentially expressed genes via gene set linkage analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, .	1.4	3
14569	Fifteen-MiRNA-Based Signature Is a Reliable Prognosis-Predicting Tool for Prostate Cancer Patients. <i>International Journal of Medical Sciences</i> , 2021, 18, 284-294.	1.1	5
14570	Cryptotanshinone Is a Intervention for ER-Positive Breast Cancer: An Integrated Approach to the Study of Natural Product Intervention Mechanisms. <i>Frontiers in Pharmacology</i> , 2020, 11, 592109.	1.6	3
14571	Conserved paradoxical relationships among the evolutionary, structural and expressional features of KRAB zinc-finger proteins reveal their special functional characteristics. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 7.	1.0	7
14572	Î±2-3 Sialic acid binding and uptake by human monocyte-derived dendritic cells alters metabolism and cytokine release and initiates tolerizing T cell programming. <i>Immunotherapy Advances</i> , 2021, 1, .	1.2	7
14574	Screening of key biomarkers and immune infiltration in Pulmonary Arterial Hypertension via integrated bioinformatics analysis. <i>Bioengineered</i> , 2021, 12, 2576-2591.	1.4	11
14575	Suppressed inflammation in obese children induced by a high-fiber diet is associated with the attenuation of gut microbial virulence factor genes. <i>Virulence</i> , 2021, 12, 1754-1770.	1.8	6
14576	Exploring the molecular subclasses and stage-specific genes of oral cancer: A bioinformatics analysis. <i>Cancer Treatment and Research Communications</i> , 2021, 27, 100320.	0.7	3

#	ARTICLE	IF	CITATIONS
14578	Uncovering potential novel biomarkers and immune infiltration characteristics in persistent atrial fibrillation using integrated bioinformatics analysis. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 4696-4712.	1.0	20
14579	Poor Personâ€™s pH Simulation of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2021, 2315, 197-217.	0.4	1
14580	EpiMOGA: An Epistasis Detection Method Based on a Multi-Objective Genetic Algorithm. <i>Genes</i> , 2021, 12, 191.	1.0	12
14581	A loss of function mutation in the filaggrin gene associated with ichthyosis vulgaris and rheumatoid arthritis. <i>European Journal of Inflammation</i> , 2021, 19, 205873922110328.	0.2	0
14582	Integrative analyses of TEDDY Omics data reveal lipid metabolism abnormalities, increased intracellular ROS and heightened inflammation prior to autoimmunity for type 1 diabetes. <i>Genome Biology</i> , 2021, 22, 39.	3.8	22
14583	Exosomal hsa-miR-129-2 and hsa-miR-889 from a 6-microRNA Signature Might be a Potential Biomarker for Predicting the Prognosis of Papillary Thyroid Carcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 819-830.	0.6	5
14584	Plasma membrane phyloquinone biosynthesis in nonphotosynthetic parasitic plants. <i>Plant Physiology</i> , 2021, 185, 1443-1456.	2.3	8
14585	Whole exome sequencing and system biology analysis support the "two-hit" mechanism in the onset of Ameloblastoma. <i>Medicina Oral, Patologia Oral Y Cirugia Bucal</i> , 2021, 26, e510-e517.	0.7	4
14586	Dissection of the potential pharmacological mechanism of Rhizoma coptidis water extract against inflammation in diabetes mellitus via chemical profiling, network pharmacology and experimental validation. <i>New Journal of Chemistry</i> , 2021, 45, 16283-16297.	1.4	0
14587	Computational and network pharmacology analysis of bioflavonoids as possible natural antiviral compounds in COVID-19. <i>Informatics in Medicine Unlocked</i> , 2021, 22, 100504.	1.9	36
14588	Identification of hsa_circ_0002024 as a prognostic competing endogenous RNA (ceRNA) through the hsa_miR_129-5p/Anti-Silencing Function 1B Histone Chaperone (ASF1B) axis in renal cell carcinoma. <i>Bioengineered</i> , 2021, 12, 6579-6593.	1.4	8
14589	Unraveling the surface glycoprotein interaction network by integrating chemical crosslinking with MS-based proteomics. <i>Chemical Science</i> , 2021, 12, 2146-2155.	3.7	10
14590	Studying Autism Using Untargeted Metabolomics in Newborn Screening Samples. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 1378-1393.	1.1	17
14591	Molecular Pathways within Autism Spectrum Disorder Endophenotypes. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 1357-1367.	1.1	3
14592	Long noncoding RNAs are potentially involved in the degeneration of virulence in an aphid-obligate pathogen, <i>Conidiobolus obscurus</i> (Entomophthoromycotina). <i>Virulence</i> , 2021, 12, 1705-1716.	1.8	6
14593	A Holistic Systems Approach to Characterize the Impact of Pre- and Post-natal Oxycodone Exposure on Neurodevelopment and Behavior. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 619199.	1.8	12
14594	Databases for Proteinâ€™Protein Interactions. <i>Methods in Molecular Biology</i> , 2021, 2361, 229-248.	0.4	6
14595	Transcriptome analysis of porcine PBMCs reveals lipopolysaccharide-induced immunomodulatory responses and crosstalk of immune and glucocorticoid receptor signaling. <i>Virulence</i> , 2021, 12, 1808-1824.	1.8	8

#	ARTICLE	IF	CITATIONS
14596	Integrated analysis on mRNA microarray and microRNA microarray to screen immune-related biomarkers and pathways in myelodysplastic syndrome. <i>Hematology</i> , 2021, 26, 417-431.	0.7	4
14597	Two novel oxetane containing lignans and a new megastigmane from <i>Paronychia arabica</i> and <i>in silico</i> analysis of them as prospective SARS-CoV-2 inhibitors. <i>RSC Advances</i> , 2021, 11, 20151-20163.	1.7	9
14598	Construction of a prognostic model for lung squamous cell carcinoma based on seven N6-methyladenosine-related autophagy genes. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 6709-6723.	1.0	4
14599	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. <i>Cell Death and Disease</i> , 2021, 12, 122.	2.7	21
14600	Capivasertib restricts SARS-CoV-2 cellular entry: a potential clinical application for COVID-19. <i>International Journal of Biological Sciences</i> , 2021, 17, 2348-2355.	2.6	31
14601	The landscape of alternative splicing reveals novel events associated with tumorigenesis and the immune microenvironment in gastric cancer. <i>Aging</i> , 2021, 13, 4317-4334.	1.4	2
14602	Role of Bioinformatics in Biological Sciences. , 2021, , 37-57.		5
14603	System-Wide Pollution of Biomedical Data: Consequence of the Search for Hub Genes of Hepatocellular Carcinoma Without Spatiotemporal Consideration. <i>Molecular Diagnosis and Therapy</i> , 2021, 25, 9-27.	1.6	4
14604	Gene co-expression network analysis of <i>Trypanosoma brucei</i> in tsetse fly vector. <i>Parasites and Vectors</i> , 2021, 14, 74.	1.0	7
14605	An integrative microenvironment approach for laryngeal carcinoma: the role of immune/methylation/autophagy signatures on disease clinical prognosis and single-cell genotypes. <i>Journal of Cancer</i> , 2021, 12, 4148-4171.	1.2	19
14606	Visualizing the superfamily of metallo- $\beta$ -lactamases through sequence similarity network neighborhood connectivity analysis. <i>Heliyon</i> , 2021, 7, e05867.	1.4	18
14607	Identification of hsa-miR-106a-5p as an impact agent on promotion of multiple sclerosis using multi-step data analysis. <i>Neurological Sciences</i> , 2021, 42, 3791-3799.	0.9	9
14608	Potential targets and the action mechanism of food-derived dipeptides on colitis: network pharmacology and bioinformatics analysis. <i>Food and Function</i> , 2021, 12, 5989-6000.	2.1	18
14609	iCysMod: an integrative database for protein cysteine modifications in eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
14610	Withanolides from <i>Withania somnifera</i> as an immunity booster and their therapeutic options against COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 5295-5308.	2.0	43
14611	Bioactive Terpenes and Their Derivatives as Potential SARS-CoV-2 Proteases Inhibitors from Molecular Modeling Studies. <i>Biomolecules</i> , 2021, 11, 74.	1.8	40
14612	Mobile Health Applications and Cloud Computing in Cytopathology. , 2021, , 1011-1048.		2
14613	Emerging Technologies Serving Cytopathology. , 2021, , 1740-1769.		3

#	ARTICLE	IF	CITATIONS
14614	Experimental evidence of microbial inheritance in plants and transmission routes from seed to phyllosphere and root. <i>Environmental Microbiology</i> , 2021, 23, 2199-2214.	1.8	106
14615	A User Guide for the Identification of New RiPP Biosynthetic Gene Clusters Using a RiPPER-Based Workflow. <i>Methods in Molecular Biology</i> , 2021, 2296, 227-247.	0.4	8
14616	Dynamic Modeling of Transcriptional Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2021, 2328, 67-97.	0.4	2
14617	Single cell transcriptomic analysis of human pluripotent stem cell chondrogenesis. <i>Nature Communications</i> , 2021, 12, 362.	5.8	98
14618	Employing Cross-Species Approaches to Construct Humanized Genetic Interaction Networks. <i>Methods in Molecular Biology</i> , 2021, 2381, 115-133.	0.4	0
14619	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	0.8	2
14620	The human O-GlcNAcome database and meta-analysis. <i>Scientific Data</i> , 2021, 8, 25.	2.4	138
14621	Mapping the SARS-CoV-2â€Host Proteinâ€Protein Interactome by Affinity Purification Mass Spectrometry and Proximity-Dependent Biotin Labeling: A Rational and Straightforward Route to Discover Host-Directed Anti-SARS-CoV-2 Therapeutics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 532.	1.8	38
14623	Serum-Derived Exosomal Proteins as Potential Candidate Biomarkers for Hepatocellular Carcinoma. <i>ACS Omega</i> , 2021, 6, 827-835.	1.6	16
14624	Metabolomics: small molecules that matter more. <i>Molecular Omics</i> , 2021, 17, 210-229.	1.4	68
14625	Identification And validation of transcription factor genes involved in prostate cancer metastasis. <i>International Journal of Transgender Health</i> , 2021, 14, 287-299.	1.1	0
14626	Bioinformatics analysis of lncRNAâ€associated ceRNA network in melanoma. <i>Journal of Cancer</i> , 2021, 12, 2921-2932.	1.2	9
14627	Systematic analysis of the function and prognostic value of RNA binding proteins in Colon Adenocarcinoma. <i>Journal of Cancer</i> , 2021, 12, 2537-2549.	1.2	1
14628	Unbiased bioinformatics analysis of microRNA transcriptomics datasets and network theoretic target prediction. , 2021, , 441-457.		0
14629	Investigation of Candidate Genes and Pathways in Basal/TNBC Patients by Integrated Analysis. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110195.	0.8	7
14630	The cyanobacterium, <i>Nostoc punctiforme</i> can protect against programmed cell death and induce defence genes in <i>Arabidopsis thaliana</i> . <i>Journal of Plant Interactions</i> , 2021, 16, 64-74.	1.0	8
14631	Screening and identification of key genes in imatinib-resistant chronic myelogenous leukemia cells: a bioinformatics study. <i>Hematology</i> , 2021, 26, 408-414.	0.7	3
14632	UBE2T And CYP3A4: hub genes regulating the transformation of cirrhosis into hepatocellular carcinoma. <i>International Journal of Transgender Health</i> , 2021, 14, 509-521.	1.1	0

#	ARTICLE	IF	CITATIONS
14633	PRODUCTION OF NEW WAP-8294A CYCLODEPSIPEPTIDES BY THE BIOLOGICAL CONTROL AGENT LYSOBACTER ENZYMOGENES OH11. <i>Frontiers of Agricultural Science and Engineering</i> , 2022, 9, 120.	0.9	2
14634	A systems pharmacology approach to identify the autophagy-inducing effects of Traditional Persian medicinal plants. <i>Scientific Reports</i> , 2021, 11, 336.	1.6	7
14635	Micro-RNA Quantification, Target Gene Identification, and Pathway Analysis. <i>Methods in Molecular Biology</i> , 2021, 2284, 207-229.	0.4	1
14636	NMR-Based Metabolomics. , 2021, , 353-369.		1
14637	Quantifying Face-to-Face Communication among Multidisciplinary Medical Professions in a Convalescent Rehabilitation Ward by using a Name Tag-Type Information Communication Device. <i>The Journal of the International Society of Physical and Rehabilitation Medicine</i> , 2021, 4, 125-130.	0.1	0
14638	Identification of Key Histone Modifications and Their Regulatory Regions on Gene Expression Level Changes in Chronic Myelogenous Leukemia. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 621578.	1.8	6
14639	Injection site vaccinology of a recombinant vaccinia-based vector reveals diverse innate immune signatures. <i>PLoS Pathogens</i> , 2021, 17, e1009215.	2.1	13
14640	Detecting causal relations in time series with the new cross Markov Matrix technique. <i>Nonlinear Dynamics</i> , 2021, 103, 1937-1953.	2.7	0
14641	Immune Cluster and PPI Network Analyses Identified CXCR3 as a Key Node of Immunoregulation in Head and Neck Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 564306.	1.3	3
14642	Enrichment of Vomiting Gene Function and Drug Therapy of Glioblastoma Multiforme after Radiotherapy and Chemotherapy Based on Computer Text Mining. <i>Advances in Clinical Medicine</i> , 2021, 11, 78-86.	0.0	0
14643	A host-based whole genome sequencing study reveals novel risk loci associated with severity of influenza A(H1N1)pdm09 infection. <i>Emerging Microbes and Infections</i> , 2021, 10, 123-131.	3.0	3
14644	Large-scale regulatory and signaling network assembly through linked open data. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	1
14645	Host cell response and distinct gene expression profiles at different stages of <i>Chlamydia trachomatis</i> infection reveals stage-specific biomarkers of infection. <i>BMC Microbiology</i> , 2021, 21, 3.	1.3	10
14646	Accumulation of detached kelp biomass in a subtidal temperate coastal ecosystem induces succession of epiphytic and sediment bacterial communities. <i>Environmental Microbiology</i> , 2021, 23, 1638-1655.	1.8	20
14647	Novel and versatile artificial intelligence algorithms for investigating possible GHSR1 $\mu$ and DRD1 agonists for Alzheimer's disease. <i>RSC Advances</i> , 2021, 11, 6423-6446.	1.7	2
14648	Multi-omic dissection of the drought resistance traits of soybean landrace LX. <i>Plant, Cell and Environment</i> , 2021, 44, 1379-1398.	2.8	15
14649	Regulation of Pancreatic Fibrosis by Acinar Cell-Derived Exosomal miR-130a-3p via Targeting of Stellate Cell PPAR $\gamma$ . <i>Journal of Inflammation Research</i> , 2021, Volume 14, 461-477.	1.6	13
14651	Bioinformatic analysis of key biomarkers and immune filtration of skin biopsy in discoid lupus erythematosus. <i>Lupus</i> , 2021, 30, 807-817.	0.8	11



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14652	Mechanism of Modified Danggui Sini Decoction for Knee Osteoarthritis Based on Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-11.	0.5	18
14655	VRdb 2.0: Interactive analysis of comorbidity conditions associated with vitiligo pathogenesis using co-expression network-based approach. F1000Research, 2020, 9, 1055.	0.8	0
14656	Detailed Molecular Mechanism and Potential Drugs for COL1A1 in Carboplatin-Resistant Ovarian Cancer. Frontiers in Oncology, 2020, 10, 576565.	1.3	10
14659	CD3D has the Potential to be a Prognostic Factor for Endometrial Carcinoma and an Indicator of Tumor Immune Microenvironment Regulation: a Study based on TCGA Data Mining. Indian Journal of Gynecologic Oncology, 2021, 19, 1.	0.1	1
14660	Targeting critical kinases and anti-apoptotic molecules overcomes steroid resistance in MLL-rearranged leukaemia. EBioMedicine, 2021, 64, 103235.	2.7	2
14661	Network Pharmacology Strategy to Investigate the Pharmacological Mechanism of Siwu Decoction on Primary Dysmenorrhea and Molecular Docking Verification. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-13.	0.5	2
14662	Chromatin Accessibility Is Associated with Artemisinin Biosynthesis Regulation in Artemisia annua. Molecules, 2021, 26, 1194.	1.7	3
14663	A novel prognostic prediction model based on seven immune-related RNAs for predicting overall survival of patients in early cervical squamous cell carcinoma. BMC Medical Genomics, 2021, 14, 49.	0.7	7
14664	Genome-wide search and structural and functional analyses for late embryogenesis-abundant (LEA) gene family in poplar. BMC Plant Biology, 2021, 21, 110.	1.6	18
14665	Contribution of pathogenic fungi to N <sub>2</sub> O emissions increases temporally in intensively managed strawberry cropping soil. Applied Microbiology and Biotechnology, 2021, 105, 2043-2056.	1.7	8
14666	Gene Regulatory Network of ETS Domain Transcription Factors in Different Stages of Glioma. Journal of Personalized Medicine, 2021, 11, 138.	1.1	6
14667	Development of a prognostic signature for esophageal cancer based on nine immune related genes. BMC Cancer, 2021, 21, 113.	1.1	17
14668	Land-use change has a greater effect on soil diazotrophic community structure than the plant rhizosphere in acidic ferralsols in southern China. Plant and Soil, 2021, 462, 445-458.	1.8	11
14669	Conformational Changes of Glutamine 5-Phosphoribosylpyrophosphate Amidotransferase for Two Substrates Analogue Binding: Insight from Conventional Molecular Dynamics and Accelerated Molecular Dynamics Simulations. Frontiers in Chemistry, 2021, 9, 640994.	1.8	5
14670	Soybean Yellow Stripe-like 7 is a symbiosome membrane peptide transporter important for nitrogen fixation. Plant Physiology, 2021, 186, 581-598.	2.3	14
14671	Complex Response of the Chlorarachniophyte Bigeloviella natans to Iron Availability. MSystems, 2021, 6, .	1.7	5
14672	Die Wechselwirkung mit ribosomalen Proteinen begleitet die Stressinduktion des Wirkstoffkandidaten BOLD-100/KP1339 im endoplasmatischen Retikulum. Angewandte Chemie, 2021, 133, 5121-5126.	1.6	2
14674	A Comprehensive Evolutionary Scenario of Cell Division and Associated Processes in the Firmicutes. Molecular Biology and Evolution, 2021, 38, 2396-2412.	3.5	4

#	ARTICLE	IF	CITATIONS
14675	Quercetin-Conjugated Superparamagnetic Iron Oxide Nanoparticles Protect A $\beta$ 1-Induced Neurotoxicity in a Rat Model of Alzheimer's Disease via Antioxidant Genes, APP Gene, and miRNA-101. <i>Frontiers in Neuroscience</i> , 2020, 14, 598617.	1.4	23
14676	Development and validation of an immune gene-set based prognostic signature for soft tissue sarcoma. <i>BMC Cancer</i> , 2021, 21, 144.	1.1	9
14677	In silico identification of key regulators instigating the pre-meiotic phase during respiration in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	1
14678	Rapid changes in DNA methylation associated with the initiation of reproduction in a small songbird. <i>Molecular Ecology</i> , 2021, 30, 3645-3659.	2.0	24
14679	The aging-related risk signature in colorectal cancer. <i>Aging</i> , 2021, 13, 7330-7349.	1.4	49
14680	Comprehensive analysis of tumour mutational burden and its clinical significance in prostate cancer. <i>BMC Urology</i> , 2021, 21, 29.	0.6	15
14681	Whole-body cryostimulation application with age: A review. <i>Journal of Thermal Biology</i> , 2021, 96, 102861.	1.1	7
14682	Deciphering Biochemical and Molecular Signatures Associated with Obesity in Context of Metabolic Health. <i>Genes</i> , 2021, 12, 290.	1.0	5
14683	An OMICs-based meta-analysis to support infection state stratification. <i>Bioinformatics</i> , 2021, 37, 2347-2355.	1.8	2
14684	Genetic and functional interaction network analysis reveals global enrichment of regulatory T cell genes influencing basal cell carcinoma susceptibility. <i>Genome Medicine</i> , 2021, 13, 19.	3.6	20
14685	A four-genes based diagnostic signature for osteoarthritis. <i>Rheumatology International</i> , 2021, 41, 1815-1823.	1.5	3
14686	Transcriptome analysis evinces anti-neoplastic mechanisms of hypericin: A study on U87 glioblastoma cell line. <i>Life Sciences</i> , 2021, 266, 118874.	2.0	8
14687	Network-Based Target Prioritization and Drug Candidate Identification for Multiple Sclerosis: From Analyzing Omics Data to Druggability Simulations. <i>ACS Chemical Neuroscience</i> , 2021, 12, 917-929.	1.7	5
14688	Fully Integrated and Multiplexed Sample Preparation Technology for Sensitive Interactome Profiling. <i>Analytical Chemistry</i> , 2021, 93, 3026-3034.	3.2	9
14689	Alterations in the conjunctival surface bacterial microbiome in bacterial keratitis patients. <i>Experimental Eye Research</i> , 2021, 203, 108418.	1.2	27
14690	Case Report: Whole Exome Sequencing Revealed Disease-Causing Variants in Two Genes in a Patient With Autism Spectrum Disorder, Intellectual Disability, Hyperactivity, Sleep and Gastrointestinal Disturbances. <i>Frontiers in Genetics</i> , 2021, 12, 625564.	1.1	8
14691	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021, 12, 925.	5.8	18
14692	The molecular basis of gender disparities in smoking lung cancer patients. <i>Life Sciences</i> , 2021, 267, 118927.	2.0	8

#	ARTICLE	IF	CITATIONS
14693	Integration of transcriptomic and proteomic analyses for finger millet [ <i>Eleusine coracana</i> (L.) Gaertn.] in response to drought stress. <i>PLoS ONE</i> , 2021, 16, e0247181.	1.1	17
14694	Sequential Abiotic-Biotic Processes Drive Organic Carbon Transformation in Peat Bogs. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006079.	1.3	8
14695	The chromatin remodeler ISWI acts during <i>Drosophila</i> development to regulate adult sleep. <i>Science Advances</i> , 2021, 7, .	4.7	9
14696	Genome-wide analysis in response to nitrogen and carbon identifies regulators for root AtNRT2 transporters. <i>Plant Physiology</i> , 2021, 186, 696-714.	2.3	16
14697	An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 108-122.	3.0	7
14698	The histone demethylase KDM5 is required for synaptic structure and function at the <i>Drosophila</i> neuromuscular junction. <i>Cell Reports</i> , 2021, 34, 108753.	2.9	15
14699	BACH2 enforces the transcriptional and epigenetic programs of stem-like CD8+ T cells. <i>Nature Immunology</i> , 2021, 22, 370-380.	7.0	75
14700	Single Cell Omics for Musculoskeletal Research. <i>Current Osteoporosis Reports</i> , 2021, 19, 131-140.	1.5	10
14701	Identification of biomarkers and pathways for the SARS-CoV-2 infections that make complexities in pulmonary arterial hypertension patients. <i>Briefings in Bioinformatics</i> , 2021, 22, 1451-1465.	3.2	30
14702	Transcriptome Analysis Reveals Photoperiod-Associated Genes Expressed in Rice Anthers. <i>Frontiers in Plant Science</i> , 2021, 12, 621561.	1.7	14
14704	Characterization of metabolism feature and potential pharmacological changes of morusin-a promising anti-tumor drug-by ultra-high-performance liquid chromatography coupled time-of-flight mass spectrometry and network pharmacology. <i>Arabian Journal of Chemistry</i> , 2021, 14, 102964.	2.3	7
14705	Interaction with Ribosomal Proteins Accompanies Stress Induction of the Anticancer Metalloprotein BOLD-100/KP1339 in the Endoplasmic Reticulum. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 5063-5068.	7.2	39
14706	Uncovering Active Ingredients and Mechanisms of <i>Spica Prunellae</i> in the Treatment of Colon Adenocarcinoma: A Study Based on Network Pharmacology and Bioinformatics. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 306-318.	0.6	3
14707	A Five-microRNA Signature as Risk Stratification System in Uterine Corpus Endometrial Carcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 187-194.	0.6	3
14708	ENAM gene associated with T classification and inhibits proliferation in renal clear cell carcinoma. <i>Aging</i> , 2021, 13, 7035-7051.	1.4	8
14709	Metagenomics Reveals That Intravenous Injection of Beta-Hydroxybutyric Acid (BHBA) Disturbs the Nasopharynx Microflora and Increases the Risk of Respiratory Diseases. <i>Frontiers in Microbiology</i> , 2020, 11, 630280.	1.5	10
14710	In silico data mining of human body fluids to unravel the immunomes in breast cancer. <i>Journal of Proteins and Proteomics</i> , 2021, 12, 45-62.	1.0	1
14714	An Integrated Approach Based on Network Pharmacology Combined with Experimental Verification Reveals AMPK/PI3K/Akt Signaling is an Important Way for the Anti-Type 2 Diabetic Activity of Silkworm Excrement. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2021, Volume 14, 601-616.	1.1	4

#	ARTICLE	IF	CITATIONS
14715	Neutrophil degranulation interconnects over-represented biological processes in atrial fibrillation. <i>Scientific Reports</i> , 2021, 11, 2972.	1.6	7
14718	Protein and phytohormone profiles of <i>Mahanarva spectabilis</i> salivary glands infesting different forages. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 106, e21773.	0.6	1
14719	Identification of Potential Biomarkers Associated with Prognosis in Gastric Cancer via Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2021, 27, e929104.	0.5	3
14720	Identification of MEDAG as a Hub Candidate Gene in the Onset and Progression of Type 2 Diabetes Mellitus by Comprehensive Bioinformatics Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	3
14721	Graphene and Reproduction: A Love-Hate Relationship. <i>Nanomaterials</i> , 2021, 11, 547.	1.9	5
14722	Structure and functional properties of the cold-adapted catalase from <i>Acinetobacter</i> sp. Ver3 native to the Atacama plateau in northern Argentina. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 369-379.	1.1	4
14723	Dissecting the Gene Expression Networks Associated with Variations in the Major Components of the Fatty Acid Semimembranosus Muscle Profile in Large White Heavy Pigs. <i>Animals</i> , 2021, 11, 628.	1.0	8
14725	Molecular diversity of the Soft Coral <i>Lobophytum</i> in Sabang Island. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 674, 012071.	0.2	0
14726	Genetic characteristics of <i>Bursaphelenchus xylophilus</i> third-stage dispersal juveniles. <i>Scientific Reports</i> , 2021, 11, 3908.	1.6	4
14727	Alterations in the gut microbiome and metabolic profile in rats acclimated to high environmental temperature. <i>Microbial Biotechnology</i> , 2022, 15, 276-288.	2.0	15
14728	A single-cell atlas of mouse olfactory bulb chromatin accessibility. <i>Journal of Genetics and Genomics</i> , 2021, 48, 147-162.	1.7	3
14729	Characterization and Biomarker Analyses of Post-COVID-19 Complications and Neurological Manifestations. <i>Cells</i> , 2021, 10, 386.	1.8	125
14730	Proteomics of developing pea seeds reveals a complex antioxidant network underlying the response to sulfur deficiency and water stress. <i>Journal of Experimental Botany</i> , 2021, 72, 2611-2626.	2.4	12
14731	Integrative Transcriptomic Network Analysis of Butyrate Treated Colorectal Cancer Cells. <i>Cancers</i> , 2021, 13, 636.	1.7	11
14732	OsTPR boosts the superior grains through increase in upper secondary rachis branches without incurring a grain quality penalty. <i>Plant Biotechnology Journal</i> , 2021, 19, 1396-1411.	4.1	9
14733	Hypercapnia selectively modulates LPS-induced changes in innate immune and DNA replication-related gene transcription in the macrophage. <i>Interface Focus</i> , 2021, 11, 20200039.	1.5	9
14734	A Prognostic Model Based on RNA Binding Protein Predicts Clinical Outcomes in Hepatocellular Carcinoma Patients. <i>Frontiers in Oncology</i> , 2020, 10, 613102.	1.3	6
14735	Identification of FPR3 as a Unique Biomarker for Targeted Therapy in the Immune Microenvironment of Breast Cancer. <i>Frontiers in Pharmacology</i> , 2020, 11, 593247.	1.6	9

#	ARTICLE	IF	CITATIONS
14736	Development and validation of a novel circular RNA as an independent prognostic factor in acute myeloid leukemia. <i>BMC Medicine</i> , 2021, 19, 28.	2.3	11
14737	Prognostic Signatures Based on Thirteen Immune-Related Genes in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 591739.	1.3	15
14738	Arrayed CRISPR reveals genetic regulators of tau aggregation, autophagy and mitochondria in Alzheimer's disease model. <i>Scientific Reports</i> , 2021, 11, 2879.	1.6	14
14739	Transcriptome analysis of the procession from chronic pancreatitis to pancreatic cancer and metastatic pancreatic cancer. <i>Scientific Reports</i> , 2021, 11, 3409.	1.6	4
14740	A High-Throughput Method for Identifying Novel Genes That Influence Metabolic Pathways Reveals New Iron and Heme Regulation in <i>Pseudomonas aeruginosa</i> . <i>MSystems</i> , 2021, 6, .	1.7	11
14741	The DNA damage inducible lncRNA SCAT7 regulates genomic integrity and topoisomerase 1 turnover in lung adenocarcinoma. <i>NAR Cancer</i> , 2021, 3, zcab002.	1.6	6
14742	<i>Wolbachia</i> and Virus Alter the Host Transcriptome at the Interface of Nucleotide Metabolism Pathways. <i>MBio</i> , 2021, 12, .	1.8	23
14743	Metabolic Fingerprinting of Feces from Calves, Subjected to Gram-Negative Bacterial Endotoxin. <i>Metabolites</i> , 2021, 11, 108.	1.3	0
14744	Conserved IFN Signature between Adult and Pediatric Eosinophilic Esophagitis. <i>Journal of Immunology</i> , 2021, 206, 1361-1371.	0.4	17
14745	Identification of a Potentially Functional microRNA-mRNA Regulatory Network in Lung Adenocarcinoma Using a Bioinformatics Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 641840.	1.8	9
14746	An Early Stage Researcher's Primer on Systems Medicine Terminology. <i>Network and Systems Medicine</i> , 2021, 4, 2-50.	2.7	9
14747	m <sup>6</sup> A modification patterns and tumor immune landscape in clear cell renal carcinoma. , 2021, 9, e001646.		42
14748	Cerebrum, liver, and muscle regulatory networks uncover maternal nutrition effects in developmental programming of beef cattle during early pregnancy. <i>Scientific Reports</i> , 2021, 11, 2771.	1.6	26
14749	Characterization and functional analysis of the Hydroxycinnamoyl-CoA: shikimate hydroxycinnamoyl transferase (HCT) gene family in poplar. <i>PeerJ</i> , 2021, 9, e10741.	0.9	8
14750	Understanding glomerular diseases through proteomics. <i>Expert Review of Proteomics</i> , 2021, 18, 137-157.	1.3	7
14751	The long non-coding RNA GHSROS reprograms prostate cancer cell lines toward a more aggressive phenotype. <i>PeerJ</i> , 2021, 9, e10280.	0.9	5
14752	Silencing ZEB2 Induces Apoptosis and Reduces Viability in Glioblastoma Cell Lines. <i>Molecules</i> , 2021, 26, 901.	1.7	3
14753	Genome-wide characterization of the hyperaccumulator <i>Sedum alfredii</i> F-box family under cadmium stress. <i>Scientific Reports</i> , 2021, 11, 3023.	1.6	3

#	ARTICLE	IF	CITATIONS
14754	Integrative analysis of chloroplast DNA methylation in a marine alga "Saccharina japonica. <i>Plant Molecular Biology</i> , 2021, 105, 611-623.	2.0	5
14755	The Peripheral Blood Transcriptome Is Correlated With PET Measures of Lung Inflammation During Successful Tuberculosis Treatment. <i>Frontiers in Immunology</i> , 2020, 11, 596173.	2.2	6
14756	Antidepressants fluoxetine and amitriptyline induce alterations in intestinal microbiota and gut microbiome function in rats exposed to chronic unpredictable mild stress. <i>Translational Psychiatry</i> , 2021, 11, 131.	2.4	73
14757	Identification of key modules and hub genes in glioblastoma multiforme based on co-expression network analysis. <i>FEBS Open Bio</i> , 2021, 11, 833-850.	1.0	5
14758	NEK5 interacts with LonP1 and its kinase activity is essential for the regulation of mitochondrial functions and mtDNA maintenance. <i>FEBS Open Bio</i> , 2021, 11, 546-563.	1.0	10
14759	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734.	5.8	26
14760	CoExp: A Web Tool for the Exploitation of Co-expression Networks. <i>Frontiers in Genetics</i> , 2021, 12, 630187.	1.1	16
14761	Overexpression of miR-1306-5p, miR-3195, and miR-3914 Inhibits Ameloblast Differentiation through Suppression of Genes Associated with Human Amelogenesis Imperfecta. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2202.	1.8	9
14762	Comparison of the Fatty Acid Metabolism Pathway in Pan-Renal Cell Carcinoma: Evidence from Bioinformatics. <i>Analytical Cellular Pathology</i> , 2021, 2021, 1-25.	0.7	1
14763	Residue Interaction Network Analysis Predicts a Val24 " Ile31 Interaction May be Involved in Preventing Amyloid " Beta (1 " 42) Primary Nucleation. <i>Protein Journal</i> , 2021, 40, 175-183.	0.7	3
14764	Meta-omics characteristics of intestinal microbiota associated to HBeAg seroconversion induced by oral antiviral therapy. <i>Scientific Reports</i> , 2021, 11, 3253.	1.6	1
14765	Sinomenine Inhibits the Growth of Ovarian Cancer Cells Through the Suppression of Mitosis by Down-Regulating the Expression and the Activity of CDK1. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 823-834.	1.0	6
14766	Assembly of rhizosphere microbial communities in <i>Artemisia annua</i> : recruitment of plant growth-promoting microorganisms and inter-kingdom interactions between bacteria and fungi. <i>Plant and Soil</i> , 2022, 470, 127-139.	1.8	32
14767	Coronary artery disease: differential expression of ceRNAs and interaction analyses. <i>Annals of Translational Medicine</i> , 2021, 9, 229-229.	0.7	3
14768	Screening of JAK-STAT modulators from the antiviral plants of Indian traditional system of medicine with the potential to inhibit 2019 novel coronavirus using network pharmacology. <i>3 Biotech</i> , 2021, 11, 119.	1.1	8
14770	Gene-Microbiome Co-expression Networks in Colon Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 617505.	1.1	7
14771	Mutational Pattern in Multiple Pulmonary Nodules Are Associated With Early Stage Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 571521.	1.3	1
14773	Expression and Functional Relevance of ANXA1 in Hypopharyngeal Carcinoma with Lymph Node Metastasis. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 1387-1399.	1.0	6



#	ARTICLE	IF	CITATIONS
14774	Identification of potential biomarkers associated with immune infiltration in the esophageal carcinoma tumor microenvironment. <i>Bioscience Reports</i> , 2021, 41, .	1.1	10
14775	Analysis of MicroRNAs Associated With Carotid Atherosclerotic Plaque Rupture With Thrombosis. <i>Frontiers in Genetics</i> , 2021, 12, 599350.	1.1	4
14777	Uncovering the Pharmacological Mechanism of 2-Dodecyl-6-Methoxycyclohexa-2,5 -Diene-1,4-Dione Against Lung Cancer Based on Network Pharmacology and Experimental Evaluation. <i>Frontiers in Pharmacology</i> , 2021, 12, 617555.	1.6	5
14778	Proteomic Analysis of Cardioembolic and Large Artery Atherosclerotic Clots Using Reverse Phase Protein Array Technology Reveals Key Cellular Interactions Within Clot Microenvironments. <i>Cureus</i> , 2021, 13, e13499.	0.2	4
14779	Identification of Targets and Active Components of Yiqi Sanjie Formula Against Lung Neoplasms Based on Network Pharmacology Analysis and Molecular Docking. <i>Natural Product Communications</i> , 2021, 16, 1934578X2199767.	0.2	0
14780	Calcium-binding and coiled-coil domain 2 promotes the proliferation and suppresses apoptosis of prostate cancer cells. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 405.	0.8	3
14781	LncMachine: a machine learning algorithm for long noncoding RNA annotation in plants. <i>Functional and Integrative Genomics</i> , 2021, 21, 195-204.	1.4	17
14782	Network pharmacology-based study to explore the mechanism of the Yiqi Gubiao pill in lung cancer treatment. <i>Oncology Letters</i> , 2021, 21, 321.	0.8	4
14783	Single-cell RNA sequencing reveals developmental heterogeneity among <i>Plasmodium berghei</i> sporozoites. <i>Scientific Reports</i> , 2021, 11, 4127.	1.6	21
14784	Longitudinal transcriptomics define the stages of myeloid activation in the living human brain after intracerebral hemorrhage. <i>Science Immunology</i> , 2021, 6, .	5.6	31
14785	Transcriptomic analysis of granulosa cell populations proximal and distal to the germinal disc of chicken preovulatory follicles. <i>Scientific Reports</i> , 2021, 11, 4683.	1.6	10
14786	Investigation on Combined Inhalation Exposure Scenarios to Biocidal Mixtures: Biocidal and Household Chemical Products in South Korea. <i>Toxics</i> , 2021, 9, 32.	1.6	10
14787	High-throughput phenotypic screen and transcriptional analysis identify new compounds and targets for macrophage reprogramming. <i>Nature Communications</i> , 2021, 12, 773.	5.8	62
14788	Lifestyle of sponge symbiont phages by host prediction and correlative microscopy. <i>ISME Journal</i> , 2021, 15, 2001-2011.	4.4	19
14789	New insights into the response of maize to fluctuations in the light environment. <i>Molecular Genetics and Genomics</i> , 2021, 296, 615-629.	1.0	3
14790	Molecular characterization of atherosclerosis in HIV positive persons. <i>Scientific Reports</i> , 2021, 11, 3232.	1.6	5
14791	Profiling plasma-extracellular vesicle proteins and microRNAs in diabetes onset in middle-aged male participants in the ELSA-Brazil study. <i>Physiological Reports</i> , 2021, 9, e14731.	0.7	9
14792	Identification of LncRNA Prognostic Markers for Ovarian Cancer by Integration of Co-expression and CeRNA Network. <i>Frontiers in Genetics</i> , 2020, 11, 566497.	1.1	6

#	ARTICLE	IF	CITATIONS
14794	The analysis on the human protein domain targets and host-like interacting motifs for the MERS-CoV and SARS-CoV/CoV-2 infers the molecular mimicry of coronavirus. <i>PLoS ONE</i> , 2021, 16, e0246901.	1.1	6
14795	Phosphoproteomic Landscape of AML Cells Treated with the ATP-Competitive CK2 Inhibitor CX-4945. <i>Cells</i> , 2021, 10, 338.	1.8	7
14796	The Playbooks of Medicinal Chemistry Design Moves. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 729-742.	2.5	11
14797	High-pressure processing-induced transcriptome response during recovery of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2021, 22, 117.	1.2	18
14798	miR-193a-3p Promotes the Invasion, Migration, and Mesenchymal Transition in Glioma through Regulating BTRC. <i>BioMed Research International</i> , 2021, 2021, 1-22.	0.9	12
14799	Transcriptome Analysis Reveals the Genes Involved in <i>Bifidobacterium Longum</i> FGSZY16M3 Biofilm Formation. <i>Microorganisms</i> , 2021, 9, 385.	1.6	14
14800	Time-Course Changes of Extracellular Matrix Encoding Genes Expression Level in the Spinal Cord Following Contusion Injury—A Data-Driven Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1744.	1.8	5
14801	Local Geomorphological Gradients and Land Use Patterns Play Key Role on the Soil Bacterial Community Diversity and Dynamics in the Highly Endemic Indigenous Afrotropical Coastal Scarp Forest Biome. <i>Frontiers in Microbiology</i> , 2021, 12, 592725.	1.5	16
14802	Fluid shear stress generates a unique signaling response by activating multiple TGF $\beta$ family type I receptors in osteocytes. <i>FASEB Journal</i> , 2021, 35, e21263.	0.2	18
14803	The Coding and Small Non-coding Hippocampal Synaptic RNAome. <i>Molecular Neurobiology</i> , 2021, 58, 2940-2953.	1.9	10
14804	Immune response dynamics and <i>Lutzomyia longipalpis</i> exposure characterize a biosignature of visceral leishmaniasis susceptibility in a canine cohort. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009137.	1.3	6
14805	mTORC1 activity is supported by spatial association with focal adhesions. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	41
14806	The doxorubicin-induced cell motility network is under the control of the ceramide-activated protein phosphatase 1 alpha. <i>FASEB Journal</i> , 2021, 35, e21396.	0.2	6
14807	Tumor microenvironment characterization in triple-negative breast cancer identifies prognostic gene signature. <i>Aging</i> , 2021, 13, 5485-5505.	1.4	8
14808	Zinc Finger Protein CTCF Regulates Extracellular Matrix (ECM)-Related Gene Expression Associated With the Wnt Signaling Pathway in Gastric Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 625633.	1.3	13
14809	Haplotype-based genomic analysis reveals novel association of CNTNAP5 genic region with primary angle closure glaucoma. <i>Journal of Biosciences</i> , 2021, 46, 1.	0.5	6
14810	Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize ( <i>Zea mays</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	1.5	97
14811	A gene co-association network regulating gut microbial communities in a Duroc pig population. <i>Microbiome</i> , 2021, 9, 52.	4.9	19

#	ARTICLE	IF	CITATIONS
14812	Multi-organ proteomic landscape of COVID-19 autopsies. <i>Cell</i> , 2021, 184, 775-791.e14.	13.5	272
14813	Simultaneous Inhibition of SARS-CoV-2 Entry Pathways by Cyclosporine. <i>ACS Chemical Neuroscience</i> , 2021, 12, 930-944.	1.7	20
14814	Identification of Core Genes and Screening of Potential Targets in Glioblastoma Multiforme by Integrated Bioinformatic Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 615976.	1.3	14
14815	Comparative Genomics and Integrated Network Approach Unveiled Undirected Phylogeny Patterns, Co-mutational Hot Spots, Functional Cross Talk, and Regulatory Interactions in SARS-CoV-2. <i>MSystems</i> , 2021, 6, .	1.7	23
14816	Network Pharmacology Approach Uncovering Pathways Involved in Targeting Hsp90 Through Curcumin and Epigallocatechin to Control Inflammation. <i>Current Drug Discovery Technologies</i> , 2021, 18, 127-138.	0.6	2
14817	TWIST1 and chromatin regulatory proteins interact to guide neural crest cell differentiation. <i>ELife</i> , 2021, 10, .	2.8	26
14818	An Alternative Splicing Variant of PtRD26 Delays Leaf Senescence by Regulating Multiple NAC Transcription Factors in <i>Populus</i> . <i>Plant Cell</i> , 2021, 33, 1594-1614.	3.1	74
14819	Coupling of Co-expression Network Analysis and Machine Learning Validation Unearthed Potential Key Genes Involved in Rheumatoid Arthritis. <i>Frontiers in Genetics</i> , 2021, 12, 604714.	1.1	9
14822	Identification of Prognostic Stromal-Immune Score-Based Genes in Hepatocellular Carcinoma Microenvironment. <i>Frontiers in Genetics</i> , 2021, 12, 625236.	1.1	5
14824	Identification of UBE2C as hub gene in driving prostate cancer by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2021, 16, e0247827.	1.1	16
14825	Integrated analysis of competing endogenous RNA in esophageal carcinoma. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 11-27.	0.6	1
14826	Genome-wide identification and functional prediction of long non-coding RNAs in Sprague-Dawley rats during heat stress. <i>BMC Genomics</i> , 2021, 22, 122.	1.2	4
14828	The expression patterns and prognostic significance of pleckstrin homology-like domain family A (PHLDA) in lung cancer and malignant mesothelioma. <i>Journal of Thoracic Disease</i> , 2021, 13, 689-707.	0.6	3
14829	Exploration of Intrinsic Microbial Community Modulators in the Rice Endosphere Indicates a Key Role of Distinct Bacterial Taxa Across Different Cultivars. <i>Frontiers in Microbiology</i> , 2021, 12, 629852.	1.5	11
14831	DNA methylation and cancer incidence: lymphatic-hematopoietic versus solid cancers in the Strong Heart Study. <i>Clinical Epigenetics</i> , 2021, 13, 43.	1.8	8
14832	New from Old: Thorectandrin Alkaloids in a Southern Australian Marine Sponge, <i>Thorectandra choanoides</i> (CMB-01889). <i>Marine Drugs</i> , 2021, 19, 97.	2.2	6
14834	Construction and Analysis of Survival-Associated Competing Endogenous RNA Network in Lung Adenocarcinoma. <i>BioMed Research International</i> , 2021, 2021, 1-17.	0.9	5
14836	Transcriptomic Data Analyses Reveal That Sow Fertility-Related lincRNA NORFA Is Essential for the Normal States and Functions of Granulosa Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 610553.	1.8	10

#	ARTICLE	IF	CITATIONS
14838	A Molecular Interaction Map of <i>Klebsiella pneumoniae</i> and Its Human Host Reveals Potential Mechanisms of Host Cell Subversion. <i>Frontiers in Microbiology</i> , 2021, 12, 613067.	1.5	8
14840	Profiling the Philippine Blue: Liquid chromatography/mass spectrometry-based metabolomics study on Philippine <i>Indigofera</i> . <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e9037.	0.7	10
14841	T cell immune regulator 1 is a prognostic marker associated with immune infiltration in glioblastoma multiforme. <i>Oncology Letters</i> , 2021, 21, 252.	0.8	8
14842	The potential role of chemotaxis and the complement system in the formation and progression of thoracic aortic aneurysms inferred from the weighted gene coexpression network analysis. <i>Journal of Translational Medicine</i> , 2021, 19, 49.	1.8	6
14843	Enhanced Understanding of Molecular Interactions and Function Underlying Pain Processes Through Networks of Transcript Isoforms, Genes, and Gene Families. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2021, Volume 14, 49-69.	1.6	4
14844	Insulin-like 3 affects zebrafish spermatogenic cells directly and via Sertoli cells. <i>Communications Biology</i> , 2021, 4, 204.	2.0	11
14845	Uncovering the Anti-Lung-Cancer Mechanisms of the Herbal Drug FDY2004 by Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	0
14847	Network Analysis Identifies Drug Targets and Small Molecules to Modulate Apoptosis Resistant Cancers. <i>Cancers</i> , 2021, 13, 851.	1.7	6
14848	Genome-Wide Identification and Characterization of Potato Long Non-coding RNAs Associated With <i>Phytophthora infestans</i> Resistance. <i>Frontiers in Plant Science</i> , 2021, 12, 619062.	1.7	9
14849	Novel risk factors for craniofacial microsomia and assessment of their utility in clinic diagnosis. <i>Human Molecular Genetics</i> , 2021, 30, 1045-1056.	1.4	3
14850	Novel Ex Vivo Model to Examine the Mechanism and Relationship of Esophageal Microbiota and Disease. <i>Biomedicines</i> , 2021, 9, 142.	1.4	4
14851	Integrative analysis of circRNA/miRNA/mRNA regulatory network reveals the potential immune function of circRNAs in the <i>Bombyx mori</i> fat body. <i>Journal of Invertebrate Pathology</i> , 2021, 179, 107537.	1.5	10
14852	Scorpionicidal activity of secondary metabolites from <i>Paecilomyces</i> sp. CMAA1686 against <i>Tityus serrulatus</i> . <i>Journal of Invertebrate Pathology</i> , 2021, 179, 107541.	1.5	3
14853	Metabolic Analysis of Vitreous/Lens and Retina in Wild Type and Retinal Degeneration Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2345.	1.8	6
14854	Gene expression and epigenetics reveal species-specific mechanisms acting upon common molecular pathways in the evolution of task division in bees. <i>Scientific Reports</i> , 2021, 11, 3654.	1.6	12
14855	Functional Diversification, Redundancy, and Epistasis among Paralogs of the <i>Drosophila melanogaster</i> <i>Obp50a</i> Gene Cluster. <i>Molecular Biology and Evolution</i> , 2021, 38, 2030-2044.	3.5	11
14856	Identification of Predictor Genes for Feed Efficiency in Beef Cattle by Applying Machine Learning Methods to Multi-Tissue Transcriptome Data. <i>Frontiers in Genetics</i> , 2021, 12, 619857.	1.1	15
14857	Resveratrol Mediates the Apoptosis of Triple Negative Breast Cancer Cells by Reducing POLD1 Expression. <i>Frontiers in Oncology</i> , 2021, 11, 569295.	1.3	22

#	ARTICLE	IF	CITATIONS
14858	Hepatic Steatosis and Ectopic Fat Are Associated With Differences in Subcutaneous Adipose Tissue Gene Expression in People With HIV. <i>Hepatology Communications</i> , 2021, 5, 1224-1237.	2.0	9
14859	Molecular Features of Cancer-associated Fibroblast Subtypes and their Implication on Cancer Pathogenesis, Prognosis, and Immunotherapy Resistance. <i>Clinical Cancer Research</i> , 2021, 27, 2636-2647.	3.2	140
14860	Integrated Proteomics and Metabolomics Assessment Indicated Metabolic Alterations in Hypothalamus of Mice Exposed to Triclosan. <i>Chemical Research in Toxicology</i> , 2021, 34, 1319-1328.	1.7	4
14861	Activin A promotes the development of acquired heterotopic ossification and is an effective target for disease attenuation in mice. <i>Science Signaling</i> , 2021, 14, .	1.6	24
14862	Viralink: An integrated workflow to investigate the effect of SARS-CoV-2 on intracellular signalling and regulatory pathways. <i>PLoS Computational Biology</i> , 2021, 17, e1008685.	1.5	11
14863	Diverse cressdnaviruses and an anellovirus identified in the fecal samples of yellow-bellied marmots. <i>Virology</i> , 2021, 554, 89-96.	1.1	11
14864	North American Fireflies Host Low Bacterial Diversity. <i>Microbial Ecology</i> , 2021, 82, 793-804.	1.4	3
14865	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. <i>Nucleic Acids Research</i> , 2021, 49, 1951-1971.	6.5	23
14866	A novel prognostic mRNA/miRNA signature for esophageal cancer and its immune landscape in cancer progression. <i>Molecular Oncology</i> , 2021, 15, 1088-1109.	2.1	35
14867	Metabolite profile of <i>Nectandra oppositifolia</i> Nees & Mart. and assessment of antitrypanosomal activity of bioactive compounds through efficiency analyses. <i>PLoS ONE</i> , 2021, 16, e0247334.	1.1	2
14868	Transcriptome profiling of long noncoding RNAs and mRNAs in spinal cord of a rat model of paclitaxel-induced peripheral neuropathy identifies potential mechanisms mediating neuroinflammation and pain. <i>Journal of Neuroinflammation</i> , 2021, 18, 48.	3.1	36
14869	High-resolution transcriptomes provide insights into fruit development and ripening in <i>Citrus sinensis</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 1337-1353.	4.1	33
14870	Validated removal of nuclear pseudogenes and sequencing artefacts from mitochondrial metabarcoding data. <i>Molecular Ecology Resources</i> , 2021, 21, 1772-1787.	2.2	32
14871	Transcriptome Analysis of Subcutaneous Adipose Tissue from Severely Obese Patients Highlights Deregulation Profiles in Coding and Non-Coding Oncogenes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1989.	1.8	7
14872	Optimized expression of Hfq protein increases <i>Escherichia coli</i> growth. <i>Journal of Biological Engineering</i> , 2021, 15, 7.	2.0	5
14873	Comparison of SYK Signaling Networks Reveals the Potential Molecular Determinants of Its Tumor-Promoting and Suppressing Functions. <i>Biomolecules</i> , 2021, 11, 308.	1.8	5
14874	The kinetic landscape of an RNA-binding protein in cells. <i>Nature</i> , 2021, 591, 152-156.	13.7	50
14875	ADAP is a possible negative regulator of glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> based on clustering and gene expression analyses. <i>Journal of Plant Research</i> , 2021, 134, 327-339.	1.2	9

#	ARTICLE	IF	CITATIONS
14876	Transcriptome analysis of salt stress responsiveness in the seedlings of wild and cultivated <i>Ricinus communis</i> L. <i>Journal of Biotechnology</i> , 2021, 327, 106-116.	1.9	17
14877	Identification of flavonoid glycosides from leaves of <i>Casearia arborea</i> (Salicaceae) by UHPLC-ESI-MS/MS combined with molecular networking and NMR. <i>Phytochemical Analysis</i> , 2021, 32, 891-898.	1.2	14
14878	Global Transcriptomic Analyses Reveal Genes Involved in Conceptus Development During the Implantation Stages in Pigs. <i>Frontiers in Genetics</i> , 2021, 12, 584995.	1.1	10
14879	Integrated Protein-Protein Interaction and Weighted Gene Co-expression Network Analysis Uncover Three Key Genes in Hepatoblastoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 631982.	1.8	16
14880	Transcriptional Analysis of Lymphoid Tissues from Infected Nonhuman Primates Reveals the Basis for Attenuation and Immunogenicity of an Ebola Virus Encoding a Mutant VP35 Protein. <i>Journal of Virology</i> , 2021, 95, .	1.5	2
14881	Comparative genomic analysis reveals evolutionary and structural attributes of MCM gene family in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> . <i>Journal of Biotechnology</i> , 2021, 327, 117-132.	1.9	2
14882	The TRIM9/TRIM67 neuronal interactome reveals novel activators of morphogenesis. <i>Molecular Biology of the Cell</i> , 2021, 32, 314-330.	0.9	21
14883	circRNA-miRNA-mRNA network in age-related macular degeneration: From construction to identification. <i>Experimental Eye Research</i> , 2021, 203, 108427.	1.2	17
14884	Interactoma de predisposición y resistencia a SARS-CoV-2. Proteínas, genes y funciones.. <i>Revista Bionatura</i> , 2021, 6, 1555-1562.	0.1	0
14887	Development and Validation of a 5-Gene Autophagy-Based Prognostic Index in Endometrial Carcinoma. <i>Medical Science Monitor</i> , 2021, 27, e928949.	0.5	2
14888	Comprehensive analysis of the gene expression profile of wheat at the crossroads of heat, drought and combined stress. <i>Highlights in BioScience</i> , 0, , bs202104.	0.0	4
14889	Biogeographic and Evolutionary Patterns of Trace Element Utilization in Marine Microbial World. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 958-972.	3.0	1
14891	Novel Two-Component System-Like Elements Reveal Functional Domains Associated with Restriction-Modification Systems and paraMORC ATPases in Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
14892	Identification of RCC Subtype-Specific microRNAs: Meta-Analysis of High-Throughput RCC Tumor microRNA Expression Data. <i>Cancers</i> , 2021, 13, 548.	1.7	18
14893	In Silico Network Analysis of Ingredients of <i>Cornus officinalis</i> in Osteoporosis. <i>Medical Science Monitor</i> , 2021, 27, e929219.	0.5	4
14894	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 787-799.	3.0	7
14895	Elevation in viral entry genes and innate immunity compromise underlying increased infectivity and severity of COVID-19 in cancer patients. <i>Scientific Reports</i> , 2021, 11, 4533.	1.6	6
14896	Lipidomic and metabolomic profiles of <i>Coffea canephora</i> L. beans cultivated in Southwestern Nigeria. <i>PLoS ONE</i> , 2021, 16, e0234758.	1.1	7



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14897	Systematic and Multi-Omics Prognostic Analysis of Lysine Acetylation Regulators in Glioma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 587516.	1.6	3
14898	Identification of the Potential Biomarkers Involved in the Human Oral Mucosal Wound Healing: A Bioinformatic Study. <i>BioMed Research International</i> , 2021, 2021, 1-16.	0.9	3
14899	Expanding the Coverage of Metabolic Landscape in Cultivated Rice with Integrated Computational Approaches. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 702-714.	3.0	3
14900	Comprehensive Analysis of the Immune and Prognostic Implication of COL6A6 in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 633420.	1.3	6
14902	Characterization of lncRNAs and mRNAs Involved in Powdery Mildew Resistance in Cucumber. <i>Phytopathology</i> , 2021, 111, 1613-1624.	1.1	13
14903	Genomic Insights into the Origin and Evolution of Molluscan Red-Bloodedness in the Blood Clam <i>Tegillarca granosa</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2351-2365.	3.5	28
14906	Identifying the essential nodes in network pharmacology based on multilayer network combined with random walk algorithm. <i>Journal of Biomedical Informatics</i> , 2021, 114, 103666.	2.5	9
14907	The Autotrophic Core: An Ancient Network of 404 Reactions Converts H <sub>2</sub> , CO <sub>2</sub> , and NH <sub>3</sub> into Amino Acids, Bases, and Cofactors. <i>Microorganisms</i> , 2021, 9, 458.	1.6	19
14908	A Multi-OMICS Approach Sheds Light on the Higher Yield Phenotype and Enhanced Abiotic Stress Tolerance in Tobacco Lines Expressing the Carrot lycopene β-cyclase1 Gene. <i>Frontiers in Plant Science</i> , 2021, 12, 624365.	1.7	12
14909	A Network Pharmacology Study on the Molecular Mechanisms of FDY003 for Breast Cancer Treatment. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-18.	0.5	6
14910	Screening of Significant Biomarkers Related to Prognosis of Cervical Cancer and Functional Study Based on lncRNA-associated ceRNA Regulatory Network. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 472-482.	0.6	8
14911	Ileum Gene Expression in Response to Acute Systemic Inflammation in Mice Chronically Fed Ethanol: Beneficial Effects of Elevated Tissue n-3 PUFAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1582.	1.8	5
14913	DeORFanizing <i>Candida albicans</i> Genes using Coexpression. <i>MSphere</i> , 2021, 6, .	1.3	11
14914	A tale of two fish: Comparative transcriptomics of resistant and susceptible steelhead following exposure to <i>Ceratonova shasta</i> highlights differences in parasite recognition. <i>PLoS ONE</i> , 2021, 16, e0234837.	1.1	16
14916	Effects of long-acting, broad spectra anthelmintic treatments on the rumen microbial community compositions of grazing sheep. <i>Scientific Reports</i> , 2021, 11, 3836.	1.6	13
14917	Differential Interactome Proposes Subtype-Specific Biomarkers and Potential Therapeutics in Renal Cell Carcinomas. <i>Journal of Personalized Medicine</i> , 2021, 11, 158.	1.1	8
14918	The role of ARHGAP9: clinical implication and potential function in acute myeloid leukemia. <i>Journal of Translational Medicine</i> , 2021, 19, 65.	1.8	10
14919	Identification of Primary and Metastatic Lung Cancer-Related lncRNAs and Potential Targeted Drugs Based on ceRNA Network. <i>Frontiers in Oncology</i> , 2020, 10, 628930.	1.3	6

#	ARTICLE	IF	CITATIONS
14920	Exploring the conservation of Alzheimer-related pathways between <i>H. sapiens</i> and <i>C. elegans</i> : a network alignment approach. <i>Scientific Reports</i> , 2021, 11, 4572.	1.6	10
14921	Gas chromatography-mass spectrometry based metabolomic approach to investigate the changes in goat milk yoghurt during storage. <i>Food Research International</i> , 2021, 140, 110072.	2.9	30
14922	In silico Analyses of Immune System Protein Interactome Network, Single-Cell RNA Sequencing of Human Tissues, and Artificial Neural Networks Reveal Potential Therapeutic Targets for Drug Repurposing Against COVID-19. <i>Frontiers in Pharmacology</i> , 2021, 12, 598925.	1.6	16
14923	Post-Translational Modifications That Drive Prostate Cancer Progression. <i>Biomolecules</i> , 2021, 11, 247.	1.8	21
14924	Comparative Genomic Analysis of <i>Mycobacteriaceae</i> Reveals Horizontal Gene Transfer-Mediated Evolution of the CRISPR-Cas System in the <i>Mycobacterium tuberculosis</i> Complex. <i>MSystems</i> , 2021, 6, .	1.7	11
14925	Research Trends and Regulation of CCL5 in Prostate Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 1417-1427.	1.0	19
14926	Cryo-EM structures of human RNA polymerase III in its unbound and transcribing states. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 210-219.	3.6	59
14927	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. <i>Nature</i> , 2021, 590, 649-654.	13.7	104
14928	Fecal microbiota transplant overcomes resistance to anti-PD-1 therapy in melanoma patients. <i>Science</i> , 2021, 371, 595-602.	6.0	746
14929	Shotgun Proteomics of Isolated Urinary Extracellular Vesicles for Investigating Respiratory Impedance in Healthy Preschoolers. <i>Molecules</i> , 2021, 26, 1258.	1.7	2
14930	A Five Immune-Related lncRNA Signature as a Prognostic Target for Glioblastoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 632837.	1.6	15
14931	Identification of microRNA-16-5p and microRNA-21-5p in feces as potential noninvasive biomarkers for inflammatory bowel disease. <i>Aging</i> , 2021, 13, 4634-4646.	1.4	18
14932	Development and validation of an individual alternative splicing prognostic signature in gastric cancer. <i>Aging</i> , 2021, 13, 5824-5844.	1.4	3
14933	Long non-coding RNA LINC00491 promotes proliferation and inhibits apoptosis in esophageal squamous cell carcinoma. <i>International Journal of Molecular Medicine</i> , 2021, 47, .	1.8	6
14934	Network Pharmacology-Based Approach to Investigate the Molecular Targets of Sinomenine for Treating Breast Cancer. <i>Cancer Management and Research</i> , 2021, Volume 13, 1189-1204.	0.9	14
14935	Transcriptomic Signatures and Functional Network Analysis of Chronic Rhinosinusitis With Nasal Polyps. <i>Frontiers in Genetics</i> , 2021, 12, 609754.	1.1	6
14936	Exploring the mechanism of aidi injection for lung cancer by network pharmacology approach and molecular docking validation. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
14938	Regulation of Gut Microbiota Disrupts the Glucocorticoid Receptor Pathway and Inflammation-related Pathways in the Mouse Hippocampus. <i>Experimental Neurobiology</i> , 2021, 30, 59-72.	0.7	1

#	ARTICLE	IF	CITATIONS
14939	GFI1/HDAC1 axis differentially regulates immunosuppressive CD73 in human tumor-associated FOXP3 <sup>+</sup> Th17 and inflammation-linked Th17 cells. <i>European Journal of Immunology</i> , 2021, 51, 1206-1217.	1.6	6
14940	Genome-scale meta-analysis of breast cancer datasets identifies promising targets for drug development. <i>Journal of Biological Research</i> , 2021, 28, 5.	2.2	5
14941	Integrated analysis of differentially expressed genes and construction of a competing endogenous RNA network in human Huntington neural progenitor cells. <i>BMC Medical Genomics</i> , 2021, 14, 48.	0.7	2
14942	Knowledge-Guided "Community Network" Analysis Reveals the Functional Modules and Candidate Targets in Non-Small-Cell Lung Cancer. <i>Cells</i> , 2021, 10, 402.	1.8	10
14943	Compound-Target Prediction and Network-Target Analysis on Jamu Formula. <i>Journal of Physics: Conference Series</i> , 2021, 1752, 012028.	0.3	2
14944	Decoding the Mechanism of Huanglian Jiedu Decoction in Treating Pneumonia Based on Network Pharmacology and Molecular Docking. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 638366.	1.8	32
14945	Histone deacetylase inhibitor givinostat alleviates liver fibrosis by regulating hepatic stellate cell activation. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	8
14946	Effect of Ocean Acidification on Bacterial Metabolic Activity and Community Composition in Oligotrophic Oceans, Inferred From Short-Term Bioassays. <i>Frontiers in Microbiology</i> , 2021, 12, 583982.	1.5	8
14947	Identifying critical protein-coding genes and long non-coding RNAs in non-functioning pituitary adenoma recurrence. <i>Oncology Letters</i> , 2021, 21, 264.	0.8	8
14948	Potential Molecular Mechanism of TNF Superfamily-Related Genes in Glioblastoma Multiforme Based on Transcriptome and Epigenome. <i>Frontiers in Neurology</i> , 2021, 12, 576382.	1.1	6
14949	Targeted Isolation of Xenicane Diterpenoids From Taiwanese Soft Coral <i>Asterospicularia laurae</i> . <i>Marine Drugs</i> , 2021, 19, 123.	2.2	4
14950	Decreased HLF Expression Predicts Poor Survival in Lung Adenocarcinoma. <i>Medical Science Monitor</i> , 2021, 27, e929333.	0.5	9
14951	Correlation of Metabolic Profiles of Plasma and Cerebrospinal Fluid of High-Grade Glioma Patients. <i>Metabolites</i> , 2021, 11, 133.	1.3	13
14952	Alternatively Splicing Interactomes Identify Novel Isoform-Specific Partners for NSD2. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 612019.	1.8	0
14953	Identification of key pathways and genes in polycystic ovary syndrome via integrated bioinformatics analysis and prediction of small therapeutic molecules. <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 31.	1.4	16
14954	Biochar decreased rhizodeposits stabilization via opposite effects on bacteria and fungi: diminished fungi-promoted aggregation and enhanced bacterial mineralization. <i>Biology and Fertility of Soils</i> , 2021, 57, 533-546.	2.3	15
14955	Putative Circulating MicroRNAs Are Able to Identify Patients with Mitral Valve Prolapse and Severe Regurgitation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2102.	1.8	6
14956	Biocontrol of potato common scab by <i>Brevibacillus laterosporus</i> BL12 is related to the reduction of pathogen and changes in soil bacterial community. <i>Biological Control</i> , 2021, 153, 104496.	1.4	18

#	ARTICLE	IF	CITATIONS
14957	Non-target metabolomics revealed the differences between <i>Rh. tanguticum</i> plants growing under canopy and open habitats. <i>BMC Plant Biology</i> , 2021, 21, 119.	1.6	11
14959	Identification of hub genes and key pathways in the emphysema phenotype of COPD. <i>Aging</i> , 2021, 13, 5120-5135.	1.4	10
14960	Revealing <i>Candida glabrata</i> biofilm matrix proteome: global characterization and pH response. <i>Biochemical Journal</i> , 2021, 478, 961-974.	1.7	2
14961	MSN, MWCNT and ZnO nanoparticle-induced CHO-K1 cell polarisation is linked to cytoskeleton ablation. <i>Journal of Nanobiotechnology</i> , 2021, 19, 45.	4.2	12
14963	Proteomic Analysis of Low-Grade, Early-Stage Endometrial Carcinoma Reveals New Dysregulated Pathways Associated with Cell Death and Cell Signaling. <i>Cancers</i> , 2021, 13, 794.	1.7	31
14964	MicroRNA-mRNA Networks in Pregnancy Complications: A Comprehensive Downstream Analysis of Potential Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2313.	1.8	43
14965	Hsa_circ_0038383-mediated competitive endogenous RNA network in recurrent implantation failure. <i>Aging</i> , 2021, 13, 6076-6090.	1.4	12
14966	Acute oral treatment with resveratrol and <i>Lactococcus Lactis</i> Subsp. <i>Lactis</i> decrease body weight and improve liver proinflammatory markers in C57BL/6 mice. <i>Molecular Biology Reports</i> , 2021, 48, 1725-1734.	1.0	8
14967	Functional interrogation of a SARS-CoV-2 host protein interactome identifies unique and shared coronavirus host factors. <i>Cell Host and Microbe</i> , 2021, 29, 267-280.e5.	5.1	127
14968	Exosome-Derived Mediators as Potential Biomarkers for Cardiovascular Diseases: A Network Approach. <i>Proteomes</i> , 2021, 9, 8.	1.7	21
14969	Integrated miRNA and mRNA expression profiling reveals dysregulated miRNA-mRNA regulatory networks in eosinophilic and non-eosinophilic chronic rhinosinusitis with nasal polyps. <i>International Forum of Allergy and Rhinology</i> , 2021, 11, 1207-1219.	1.5	9
14971	Gut Microbiomes of Freshwater Mussels (Unionidae) Are Taxonomically and Phylogenetically Variable across Years but Remain Functionally Stable. <i>Microorganisms</i> , 2021, 9, 411.	1.6	14
14972	Identification of the relationship between the gut microbiome and feed efficiency in a commercial pig cohort. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	22
14973	Metabolomics and <i>In Silico</i> Docking-Directed Discovery of Small-Molecule Enzyme Targets. <i>Analytical Chemistry</i> , 2021, 93, 3072-3081.	3.2	15
14974	Dynamic characteristics and co-occurrence patterns of microbial community in tobacco leaves during the 24-month aging process. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	17
14975	Genome-wide comparative transcriptome analysis of the A4-CMS line ICPA 2043 and its maintainer ICPB 2043 during the floral bud development of pigeonpea. <i>Functional and Integrative Genomics</i> , 2021, 21, 251-263.	1.4	11
14976	Discovery of an ene-reductase for initiating flavone and flavonol catabolism in gut bacteria. <i>Nature Communications</i> , 2021, 12, 790.	5.8	46
14977	Inhibitory effect of sodium butyrate on colorectal cancer cells and construction of the related molecular network. <i>BMC Cancer</i> , 2021, 21, 127.	1.1	18

#	ARTICLE	IF	CITATIONS
14978	LncRNA NKX2-1 AS1 promotes tumor progression and angiogenesis via upregulation of SERPINE1 expression and activation of the VEGFR2 signaling pathway in gastric cancer. <i>Molecular Oncology</i> , 2021, 15, 1234-1255.	2.1	48
14979	In silico identification of natural products from Traditional Chinese Medicine for cancer immunotherapy. <i>Scientific Reports</i> , 2021, 11, 3332.	1.6	14
14980	Glucocorticoid counteracts cellular mechanoresponses by LINC01569-dependent glucocorticoid receptor-mediated mRNA decay. <i>Science Advances</i> , 2021, 7, .	4.7	11
14981	Prognostic Signatures of Metabolic Genes and Metabolism-Related Long Non-coding RNAs Accurately Predict Overall Survival for Osteosarcoma Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 644220.	1.8	8
14982	Functional and Structural Characterization of the UDP-Glucose Dehydrogenase Involved in Capsular Polysaccharide Biosynthesis from <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2021, 60, 725-734.	1.2	5
14983	Pineal gland transcriptomic profiling reveals the differential regulation of lncRNA and mRNA related to prolificacy in STH sheep with two FecB genotypes. <i>BMC Genomic Data</i> , 2021, 22, 9.	0.7	6
14984	Temporal modulation of the NF- $\kappa$ B RelA network in response to different types of DNA damage. <i>Biochemical Journal</i> , 2021, 478, 533-551.	1.7	10
14985	Exhausted-like CD8+ T cell phenotypes linked to C-peptide preservation in alefacept-treated T1D subjects. <i>JCI Insight</i> , 2021, 6, .	2.3	37
14986	Adipocytokine Profile Reveals Resistin Forming a Prognostic-Related Cytokine Network in the Acute Phase of Sepsis. <i>Shock</i> , 2021, 56, 718-726.	1.0	17
14988	Genome-wide analysis and expression profile of the bZIP gene family in poplar. <i>BMC Plant Biology</i> , 2021, 21, 122.	1.6	59
14989	Two predicted models based on ceRNAs and immune cells in lung adenocarcinoma. <i>PeerJ</i> , 2021, 9, e11029.	0.9	1
14990	The identification of neutrophils-mediated mechanisms and potential therapeutic targets for the management of sepsis-induced acute immunosuppression using bioinformatics. <i>Medicine (United Tj ETQq1 1 0.784314 rgB2/Overlo</i>		
14991	An Integrative <i>in silico</i> Drug Repurposing Approach for Identification of Potential Inhibitors of SARS-CoV-2 Main Protease. <i>Molecular Informatics</i> , 2021, 40, e2000187.	1.4	7
14993	Primary cilia and the reciprocal activation of AKT and SMAD2/3 regulate stretch-induced autophagy in trabecular meshwork cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
14994	Small-molecule mimicry hunting strategy in the imperial cone snail, <i>Conus imperialis</i> . <i>Science Advances</i> , 2021, 7, .	4.7	18
14995	Genome-Wide Identification and Characterization of the IGT Gene Family in Allotetraploid Rapeseed ( <i>Brassica napus</i> L.). <i>DNA and Cell Biology</i> , 2021, 40, 441-456.	0.9	4
14996	Phylostratigraphic analysis of gene networks of human diseases. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2021, 25, 46-56.	0.4	1
14997	Targeting of FK506 binding protein5 by miR-203 affects the progression of breast cancer via regulating the fatty acid degradation pathway and potential drug repurposing. <i>Oncology Letters</i> , 2021, 21, 346.	0.8	1

#	ARTICLE	IF	CITATIONS
14999	Machine learning analysis of gene expression profile reveals a novel diagnostic signature for osteoporosis. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 189.	0.9	8
15000	Bioprospecting of Soil-Derived Actinobacteria Along the Alar-Hotan Desert Highway in the Taklamakan Desert. <i>Frontiers in Microbiology</i> , 2021, 12, 604999.	1.5	9
15001	Identification of Transcriptomic Differences between Lower Extremities Arterial Disease, Abdominal Aortic Aneurysm and Chronic Venous Disease in Peripheral Blood Mononuclear Cells Specimens. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3200.	1.8	4
15002	EDLMFC: an ensemble deep learning framework with multi-scale features combination for ncRNA-protein interaction prediction. <i>BMC Bioinformatics</i> , 2021, 22, 133.	1.2	18
15003	Transcriptomic Analysis of Mouse Brain After Traumatic Brain Injury Reveals That the Angiotensin Receptor Blocker Candesartan Acts Through Novel Pathways. <i>Frontiers in Neuroscience</i> , 2021, 15, 636259.	1.4	13
15004	Construction of a Signature Composed of 14 Immune Genes to Judge the Prognosis and Immune Infiltration of Colon Cancer. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 163-178.	0.3	0
15005	Spatial familial networks to infer demographic structure of wild populations. <i>Ecology and Evolution</i> , 2021, 11, 4507-4519.	0.8	2
15007	Onecut Regulates Core Components of the Molecular Machinery for Neurotransmission in Photoreceptor Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 602450.	1.8	5
15008	Comprehensive circRNA-microRNA-mRNA network analysis revealed the novel regulatory mechanism of <i>Trichosporon asahii</i> infection. <i>Military Medical Research</i> , 2021, 8, 19.	1.9	7
15009	Computational Analysis of Rice Transcriptomic and Genomic Datasets in Search for SNPs Involved in Flavonoid Biosynthesis. , 0, , .		0
15010	The diversity of microbial communities in Chinese milk fan and their effects on volatile organic compound profiles. <i>Journal of Dairy Science</i> , 2021, 104, 2581-2593.	1.4	14
15011	Comparative analyses of hypothalamus transcriptomes reveal fertility-, growth-, and immune-related genes and signal pathways in different ploidy cyprinid fish. <i>Genomics</i> , 2021, 113, 595-605.	1.3	13
15013	Epigenetic Mechanisms Are Involved in the Oncogenic Properties of ZNF518B in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 1433.	1.7	4
15014	Identification and validation of a glycolysis-associated multiomics prognostic model for hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 7481-7498.	1.4	5
15015	The Protozoan Inhibitor Atovaquone Affects Mitochondrial Respiration and Shows In Vitro Efficacy Against Glucocorticoid-Resistant Cells in Childhood B-Cell Acute Lymphoblastic Leukaemia. <i>Frontiers in Oncology</i> , 2021, 11, 632181.	1.3	3
15017	Deciphering the multi-scale mechanisms of <i>Tephrosia purpurea</i> against polycystic ovarian syndrome (PCOS) and its major psychiatric comorbidities: Studies from network pharmacological perspective. <i>Gene</i> , 2021, 773, 145385.	1.0	12
15018	Identifying CNS-colonizing T cells as potential therapeutic targets to prevent progression of multiple sclerosis. <i>Med</i> , 2021, 2, 296-312.e8.	2.2	43
15019	Screening of osteoarthritis diagnostic markers based on immune-related genes and immune infiltration. <i>Scientific Reports</i> , 2021, 11, 7032.	1.6	16



#	ARTICLE	IF	CITATIONS
15020	A Molecular Networking Strategy: High-Throughput Screening and Chemical Analysis of Brazilian Cerrado Plant Extracts against Cancer Cells. <i>Cells</i> , 2021, 10, 691.	1.8	12
15021	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. <i>ISME Journal</i> , 2021, 15, 2366-2378.	4.4	93
15022	RRM2B Is Frequently Amplified Across Multiple Tumor Types: Implications for DNA Repair, Cellular Survival, and Cancer Therapy. <i>Frontiers in Genetics</i> , 2021, 12, 628758.	1.1	9
15023	In silico guided design of non-covalent inhibitors of DprE1: synthesis and biological evaluation. <i>SAR and QSAR in Environmental Research</i> , 2021, 32, 333-352.	1.0	6
15024	Decision support systems based on scientific evidence: bibliometric networks of invasive <i>Lantana camara</i> . <i>Proceedings of the Indian National Science Academy</i> , 2021, 87, 133-138.	0.5	1
15025	The Repertoire of Glycan Alterations and Glycoproteins in Human Cancers. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 139-168.	1.0	4
15026	Aging and pathological aging signatures of the brain: through the focusing lens of SIRT6. <i>Aging</i> , 2021, 13, 6420-6441.	1.4	11
15027	Investigation of the putative role of antisense transcripts as regulators of sense transcripts by correlation analysis of sense-antisense pairs in colorectal cancers. <i>FASEB Journal</i> , 2021, 35, e21482.	0.2	3
15028	The "Matrisome" reveals the characterization of skin keloid microenvironment. <i>FASEB Journal</i> , 2021, 35, e21237.	0.2	3
15029	Experimental competition induces immediate and lasting effects on the neurogenome in free-living female birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
15030	TSPAN1, TMPRSS4, SDR16C5, and CTSE as Novel Panel for Pancreatic Cancer: A Bioinformatics Analysis and Experiments Validation. <i>Frontiers in Immunology</i> , 2021, 12, 649551.	2.2	15
15031	De novo histidine biosynthesis protects <i>Mycobacterium tuberculosis</i> from host IFN- $\gamma$ mediated histidine starvation. <i>Communications Biology</i> , 2021, 4, 410.	2.0	15
15032	Global proteomic analysis of extracellular matrix in mouse and human brain highlights relevance to cerebrovascular disease. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2021, 41, 2423-2438.	2.4	14
15033	Integrated analysis of miRNA-mRNA networks reveals a strong anti-skin cancer signature in vitiligo epidermis. <i>Experimental Dermatology</i> , 2021, 30, 1309-1319.	1.4	6
15034	IGF2BP1, a Conserved Regulator of RNA Turnover in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 632219.	1.6	24
15036	Bacteria could help ectomycorrhizae establishment under climate variations. <i>Mycorrhiza</i> , 2021, 31, 395-401.	1.3	7
15037	A Network Pharmacology-Based Approach to Investigating the Mechanisms of Fushen Granule Effects on Intestinal Barrier Injury in Chronic Renal Failure. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	1
15038	Analysis of the Neuroproteome Associated With Cell Therapy After Intranigral Grafting in a Mouse Model of Parkinson Disease. <i>Frontiers in Neuroscience</i> , 2021, 15, 621121.	1.4	1

#	ARTICLE	IF	CITATIONS
15039	A developmental lineage-based gene co-expression network for mouse pancreatic $\beta^2$ -cells reveals a role for <i>Zfp800</i> in pancreas development. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	12
15040	An integrated model of N6-methyladenosine regulators to predict tumor aggressiveness and immune evasion in pancreatic cancer. <i>EBioMedicine</i> , 2021, 65, 103271.	2.7	33
15041	The anti-vaccination infodemic on social media: A behavioral analysis. <i>PLoS ONE</i> , 2021, 16, e0247642.	1.1	205
15042	MKRN3-mediated ubiquitination of Poly(A)-binding proteins modulates the stability and translation of <i>GNRH1</i> mRNA in mammalian puberty. <i>Nucleic Acids Research</i> , 2021, 49, 3796-3813.	6.5	44
15044	Genetic-variant hotspots and hotspot clusters in the human genome facilitating adaptation while increasing instability. <i>Human Genomics</i> , 2021, 15, 19.	1.4	9
15045	Network Pharmacology and Pharmacological Evaluation Reveals the Mechanism of the <i>Sanguisorba officinalis</i> in Suppressing Hepatocellular Carcinoma. <i>Frontiers in Pharmacology</i> , 2021, 12, 618522.	1.6	19
15047	DNA repair pathway activation features in follicular and papillary thyroid tumors, interrogated using 95 experimental RNA sequencing profiles. <i>Heliyon</i> , 2021, 7, e06408.	1.4	10
15048	Nasopharyngeal Microbial Communities of Patients Infected With SARS-CoV-2 That Developed COVID-19. <i>Frontiers in Microbiology</i> , 2021, 12, 637430.	1.5	53
15049	Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.	2.9	44
15050	Network pharmacology study on the mechanism of the herb pair of prepared <i>Rehmannia root-Chinese arborvitae</i> kernel for anxiety disorders. <i>Annals of Palliative Medicine</i> , 2021, 10, 3313-3327.	0.5	10
15051	Molecular Characteristics, Prognostic Value, and Immune Characteristics of m6A Regulators Identified in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 629718.	1.3	9
15052	Sex-Related Differences in Protein Expression in Sarcomere Mutation-Positive Hypertrophic Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 612215.	1.1	11
15053	The Genetic and Epigenetic Mechanisms Involved in Irreversible Pulp Neural Inflammation. <i>Disease Markers</i> , 2021, 2021, 1-26.	0.6	7
15054	Flexible Semantic Network Structure Supports the Production of Creative Metaphor. <i>Creativity Research Journal</i> , 2021, 33, 209-223.	1.7	22
15055	Comparative transcriptomics and WGCNA reveal candidate genes involved in petaloid stamens in <i>Paeonia lactiflora</i> . <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 588-603.	0.9	10
15056	Microbial Characteristics of Locally Advanced Rectal Cancer Patients After Neoadjuvant Chemoradiation Therapy According to Pathologic Response. <i>Cancer Management and Research</i> , 2021, Volume 13, 2655-2667.	0.9	4
15057	Identifying Molecular Signatures of Distinct Modes of Collective Migration in Response to the Microenvironment Using Three-Dimensional Breast Cancer Models. <i>Cancers</i> , 2021, 13, 1429.	1.7	7
15058	On Defining and Finding Islands of Trees and Mitigating Large Island Bias. <i>Systematic Biology</i> , 2021, 70, 1282-1294.	2.7	8

#	ARTICLE	IF	CITATIONS
15060	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , 2021, 15, 2779-2791.	4.4	30
15061	Identification of four key prognostic genes and three potential drugs in human papillomavirus negative head and neck squamous cell carcinoma. <i>Cancer Cell International</i> , 2021, 21, 167.	1.8	7
15062	Identification of circular RNA expression profiles and potential biomarkers for intracerebral hemorrhage. <i>Epigenomics</i> , 2021, 13, 379-395.	1.0	4
15063	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. <i>Microbiome</i> , 2021, 9, 78.	4.9	101
15064	Comparison of path-based centrality measures in protein-protein interaction networks revealed proteins with phenotypic relevance during adaptation to changing nitrogen environments. <i>Journal of Proteomics</i> , 2021, 235, 104114.	1.2	32
15065	The factors for the early and late development of midbrain dopaminergic neurons segregate into two distinct evolutionary clusters. <i>Brain Disorders</i> , 2021, 1, 100002.	1.1	3
15066	Comparative proteomic analysis reveals insights into the dynamic responses of maize ( <i>Zea mays</i> L.) to <i>Setosphaeria turcica</i> infection. <i>Plant Science</i> , 2021, 304, 110811.	1.7	4
15067	A proteomic analysis of skeletal tissue anomaly in the brain coral <i>Platygyra carnosa</i> . <i>Marine Pollution Bulletin</i> , 2021, 164, 111982.	2.3	6
15068	Exploring the druggable proteome of <i>Candida</i> species through comprehensive computational analysis. <i>Genomics</i> , 2021, 113, 728-739.	1.3	8
15069	Behavioral and Gene Expression Analysis of <i>Stxbp6</i> -Knockout Mice. <i>Brain Sciences</i> , 2021, 11, 436.	1.1	3
15070	RNAseq Reveals Differential Gene Expression Contributing to <i>Phytophthora nicotianae</i> Adaptation to Partial Resistance in Tobacco. <i>Agronomy</i> , 2021, 11, 656.	1.3	1
15071	A New Epigenetic Model to Stratify Glioma Patients According to Their Immunosuppressive State. <i>Cells</i> , 2021, 10, 576.	1.8	7
15072	Interactome Mapping of eIF3A in a Colon Cancer and an Immortalized Embryonic Cell Line Using Proximity-Dependent Biotin Identification. <i>Cancers</i> , 2021, 13, 1293.	1.7	1
15073	Lipidomic Perturbations in <i>Cynomolgus</i> Monkeys are Regulated by Thyroid Stimulating Hormone. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 640387.	1.6	3
15074	Characterization of Photosynthetic Pathway Genes Using Transcriptome Sequences in Drought-treated Leaves of <i>Paulownia catalpifolia</i> Gong Tong. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 889-905.	2.8	0
15075	Major ceRNA regulation and key metabolic signature analysis of intervertebral disc degeneration. <i>BMC Musculoskeletal Disorders</i> , 2021, 22, 249.	0.8	8
15076	Comparative Metagenomics Reveals Microbial Signatures of Sugarcane Phyllosphere in Organic Management. <i>Frontiers in Microbiology</i> , 2021, 12, 623799.	1.5	17
15077	Identification of MEC8/miR-378d/SOBP axis as a novel regulatory network and associated with immune infiltrates in ovarian carcinoma by integrated bioinformatics analysis. <i>Cancer Medicine</i> , 2021, 10, 2924-2939.	1.3	9

#	ARTICLE	IF	CITATIONS
15078	Identification of vital prognostic genes related to tumor microenvironment in pheochromocytoma and paraganglioma based on weighted gene co-expression network analysis. <i>Aging</i> , 2021, 13, 9976-9990.	1.4	6
15079	Causal effects in microbiomes using interventional calculus. <i>Scientific Reports</i> , 2021, 11, 5724.	1.6	10
15080	Longitudinal multi-omics transition associated with fatality in critically ill COVID-19 patients. <i>Intensive Care Medicine Experimental</i> , 2021, 9, 13.	0.9	9
15081	Comprehensive Analysis of the Functions and Prognostic Value of RNA-Binding Proteins in Thyroid Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 625007.	1.3	6
15082	m5U54 tRNA Hypomodification by Lack of TRMT2A Drives the Generation of tRNA-Derived Small RNAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2941.	1.8	31
15083	The characteristics of circRNA as competing endogenous RNA in pathogenesis of acute myeloid leukemia. <i>BMC Cancer</i> , 2021, 21, 277.	1.1	8
15085	FOX D1 regulates cell division in clear cell renal cell carcinoma. <i>BMC Cancer</i> , 2021, 21, 312.	1.1	11
15087	Identification, characterization, and expression profiles of the GASA genes in cotton. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	13
15089	Comparative analysis of long noncoding RNAs in angiosperms and characterization of long noncoding RNAs in response to heat stress in Chinese cabbage. <i>Horticulture Research</i> , 2021, 8, 48.	2.9	38
15092	Regional association analysis coupled with transcriptome analyses reveal candidate genes affecting seed oil accumulation in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 1545-1555.	1.8	7
15093	Comprehensive metabolomic study of the response of HK-2 cells to hyperglycemic hypoxic diabetic-like milieu. <i>Scientific Reports</i> , 2021, 11, 5058.	1.6	24
15094	Identification of key genes in type 2 diabetes-induced erectile dysfunction rats with stem cell therapy through high-throughput sequencing and bioinformatic analysis. <i>Andrologia</i> , 2021, 53, e14031.	1.0	2
15095	The risk of oral transmission in an area of a Chagas disease outbreak in the Brazilian northeast evaluated through entomological, socioeconomic and schooling indicators. <i>Acta Tropica</i> , 2021, 215, 105803.	0.9	15
15096	The Banana Root Endophytome: Differences between Mother Plants and Suckers and Evaluation of Selected Bacteria to Control <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 194.	1.5	26
15097	Poplar acetylome profiling reveals lysine acetylation dynamics in seasonal bud dormancy release. <i>Plant, Cell and Environment</i> , 2021, 44, 1830-1845.	2.8	12
15099	Dissociable Roles of Pallidal Neuron Subtypes in Regulating Motor Patterns. <i>Journal of Neuroscience</i> , 2021, 41, 4036-4059.	1.7	36
15100	Analysis of m6A-Related Signatures in the Tumor Immune Microenvironment and Identification of Clinical Prognostic Regulators in Adrenocortical Carcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 637933.	2.2	54
15101	The <i>Arabidopsis</i> mediator complex subunit 8 regulates oxidative stress responses. <i>Plant Cell</i> , 2021, 33, 2032-2057.	3.1	23

#	ARTICLE	IF	CITATIONS
15102	Single-cell transcriptomic analysis of somatosensory neurons uncovers temporal development of neuropathic pain. <i>Cell Research</i> , 2021, 31, 904-918.	5.7	79
15104	Single-cell analysis reveals metastatic cell heterogeneity in clear cell renal cell carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 4260-4274.	1.6	16
15105	Melanoma subpopulations that rapidly escape MAPK pathway inhibition incur DNA damage and rely on stress signalling. <i>Nature Communications</i> , 2021, 12, 1747.	5.8	39
15106	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	42
15107	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	5.8	69
15108	Repurposing novel therapeutic candidate drugs for coronavirus disease-19 based on protein-protein interaction network analysis. <i>BMC Biotechnology</i> , 2021, 21, 22.	1.7	29
15109	Combination of biochar and immobilized bacteria accelerates polyacrylamide biodegradation in soil by both bio-augmentation and bio-stimulation strategies. <i>Journal of Hazardous Materials</i> , 2021, 405, 124086.	6.5	51
15110	Abnormal upregulation of cardiovascular disease biomarker PLA2G7 induced by proinflammatory macrophages in COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 6811.	1.6	19
15111	A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. <i>Cell Reports</i> , 2021, 34, 108856.	2.9	101
15112	Epigenetic Lens to Visualize the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) Infection in COVID-19 Pandemic. <i>Frontiers in Genetics</i> , 2021, 12, 581726.	1.1	28
15113	Computational approach to decipher cellular interactors and drug targets during co-infection of SARS-CoV-2, Dengue, and Chikungunya virus. <i>VirusDisease</i> , 2021, 32, 55-64.	1.0	4
15114	The Effects of <i>Helicobacter pylori</i> Infection on Microbiota Associated With Gastric Mucosa and Immune Factors in Children. <i>Frontiers in Immunology</i> , 2021, 12, 625586.	2.2	13
15115	Exogenous Probiotics Improve Fermentation Quality, Microflora Phenotypes, and Trophic Modes of Fermented Vegetable Waste for Animal Feed. <i>Microorganisms</i> , 2021, 9, 644.	1.6	10
15117	FunHoP: Enhanced Visualization and Analysis of Functionally Homologous Proteins in Complex Metabolic Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 848-859.	3.0	2
15119	Methylation of rRNA as a host defense against rampant group II intron retrotransposition. <i>Mobile DNA</i> , 2021, 12, 9.	1.3	2
15120	Inhibition of HSP90 as a Strategy to Radiosensitize Glioblastoma: Targeting the DNA Damage Response and Beyond. <i>Frontiers in Oncology</i> , 2021, 11, 612354.	1.3	12
15124	Identification of potential oncogenes in triple-negative breast cancer based on bioinformatics analyses. <i>Oncology Letters</i> , 2021, 21, 363.	0.8	6
15125	Metagenomic Insight Into Patterns and Mechanism of Nitrogen Cycle During Biocrust Succession. <i>Frontiers in Microbiology</i> , 2021, 12, 633428.	1.5	14

#	ARTICLE	IF	CITATIONS
15126	A Network Pharmacology to Explore the Mechanism of Calculus Bovis in the Treatment of Ischemic Stroke. <i>BioMed Research International</i> , 2021, 2021, 1-20.	0.9	9
15127	Identification of molecular biomarkers and pathways of NSCLC: insights from a systems biomedicine perspective. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 43.	1.5	8
15128	Evidence for a synergistic effect of post-translational modifications and genomic composition of eEF1 $\alpha$ on the adaptation of <i>Phytophthora infestans</i> . <i>Ecology and Evolution</i> , 2021, 11, 5484-5496.	0.8	2
15129	Identification ACTA2 and KDR as key proteins for prognosis of PD-1/PD-L1 blockade therapy in melanoma. <i>Animal Models and Experimental Medicine</i> , 2021, 4, 138-150.	1.3	4
15130	Identification of genes and pathways related to breast cancer metastasis in an integrated cohort. <i>European Journal of Clinical Investigation</i> , 2021, 51, e13525.	1.7	3
15131	Genome-wide regulation of CpG methylation by ecCEBP1 in acute myeloid leukemia. <i>F1000Research</i> , 2021, 10, 204.	0.8	1
15133	Protein aggregates contain RNA and DNA, entrapped by misfolded proteins but largely rescued by slowing translational elongation. <i>Aging Cell</i> , 2021, 20, e13326.	3.0	16
15134	Down-regulation of HLA-DRs and HLA-DPs reflects the deficiency of antigen-presenting cells in endometrium from infertile women with and without ovarian endometriosis. <i>Human Fertility</i> , 2022, 25, 716-727.	0.7	1
15135	Weighted Correlation Gene Network Analysis Reveals New Potential Mechanisms and Biomarkers in Non-obstructive Azoospermia. <i>Frontiers in Genetics</i> , 2021, 12, 617133.	1.1	10
15136	Non-coding RNA Identification in Osteonecrosis of the Femoral Head Using Competitive Endogenous RNA Network Analysis. <i>Orthopaedic Surgery</i> , 2021, 13, 1067-1076.	0.7	8
15137	Associations Between Obesity and Alzheimer's Disease: Multiple Bioinformatic Analyses. <i>Journal of Alzheimer's Disease</i> , 2021, 80, 271-281.	1.2	14
15138	Panacea: Visual exploration system for analyzing trends in annual recruitment using time-varying graphs. <i>PLoS ONE</i> , 2021, 16, e0247587.	1.1	2
15139	Label-free proteomics uncovers SMC1A expression is Down-regulated in AUB-E. <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 35.	1.4	1
15140	Semantic Data Set Construction from Human Clustering and Spatial Arrangement. <i>Computational Linguistics</i> , 2021, 47, 69-116.	2.5	6
15141	Structural and Functional Analyses of Hub MicroRNAs in An Integrated Gene Regulatory Network of Arabidopsis. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 747-764.	3.0	10
15142	Quantitative acetylome analysis reveals histone modifications that may predict prognosis in hepatitis B-related hepatocellular carcinoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e313.	1.7	19
15143	Identification of Potential Therapeutic Genes and Pathways in Phytoestrogen Emodin Treated Breast Cancer Cell Lines via Network Biology Approaches. <i>Nutrition and Cancer</i> , 2022, 74, 592-604.	0.9	2
15144	Transcriptome analysis of sinensetin-treated liver cancer cells guided by biological network analysis. <i>Oncology Letters</i> , 2021, 21, 355.	0.8	3



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15145	Identification of key non-coding RNAs and transcription factors regulators and their potential drugs for steroid-induced femoral head necrosis. <i>Genomics</i> , 2021, 113, 490-496.	1.3	2
15147	Biological mechanisms of growth performance and meat quality in porcine muscle tissue. <i>Animal Biotechnology</i> , 2022, 33, 1246-1254.	0.7	3
15148	Urinary Exosomes Identify Inflammatory Pathways in Vancomycin Associated Acute Kidney Injury. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2784.	1.8	17
15149	New insights for precision treatment of glioblastoma from analysis of single-cell lncRNA expression. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 1881-1895.	1.2	3
15151	Blocks in the pseudouridimycin pathway unlock hidden metabolites in the <i>Streptomyces</i> producer strain. <i>Scientific Reports</i> , 2021, 11, 5827.	1.6	8
15152	A prognostic model for hepatocellular carcinoma based on apoptosis-related genes. <i>World Journal of Surgical Oncology</i> , 2021, 19, 70.	0.8	17
15153	The transcriptome characteristics of vestibular organs from delayed endolymphatic hydrops patients (Meniere's disease). <i>Clinical Otolaryngology</i> , 2021, 46, 823-833.	0.6	3
15154	XlinkCyNET: A Cytoscape Application for Visualization of Protein Interaction Networks Based on Cross-Linking Mass Spectrometry Identifications. <i>Journal of Proteome Research</i> , 2021, 20, 1943-1950.	1.8	8
15155	An Information Theoretical Multilayer Network Approach to Breast Cancer Transcriptional Regulation. <i>Frontiers in Genetics</i> , 2021, 12, 617512.	1.1	6
15157	The metabolic network of the last bacterial common ancestor. <i>Communications Biology</i> , 2021, 4, 413.	2.0	33
15158	N-Glycan Degradation Pathways in Gut- and Soil-Dwelling Actinobacteria Share Common Core Genes. <i>ACS Chemical Biology</i> , 2021, 16, 701-711.	1.6	6
15159	Targeted Isolation of Saalfelduracin B from <i>Amycolatopsis saalfeldensis</i> Using LC-MS/MS-Based Molecular Networking. <i>Journal of Natural Products</i> , 2021, 84, 1002-1011.	1.5	6
15160	Environmental and Anthropogenic Factors Shape Major Bacterial Community Types Across the Complex Mountain Landscape of Switzerland. <i>Frontiers in Microbiology</i> , 2021, 12, 581430.	1.5	13
15161	Tumor Microenvironment Analysis Identified Subtypes Associated With the Prognosis and the Tumor Response to Immunotherapy in Bladder Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 551605.	1.1	10
15162	A gene module identification algorithm and its applications to identify gene modules and key genes of hepatocellular carcinoma. <i>Scientific Reports</i> , 2021, 11, 5517.	1.6	11
15163	Identification of a Six Gene Prognosis Signature for Papillary Thyroid Cancer Using Multi-Omics Methods and Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 624421.	1.3	12
15164	Systematic analysis of gut microbiome reveals the role of bacterial folate and homocysteine metabolism in Parkinson's disease. <i>Cell Reports</i> , 2021, 34, 108807.	2.9	77
15165	OverCOVID: an integrative web portal for SARS-CoV-2 bioinformatics resources. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 9-17.	1.0	11

#	ARTICLE	IF	CITATIONS
15166	Proteomic profiling of human uterine extracellular vesicles reveal dynamic regulation of key players of embryo implantation and fertility during menstrual cycle. <i>Proteomics</i> , 2021, 21, e2000211.	1.3	37
15167	Identification of IFN-Induced Transmembrane Protein 1 With Prognostic Value in Pancreatic Cancer Using Network Module-Based Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 626883.	1.3	5
15168	Exploring the Role of Epicardial Adipose Tissue in Coronary Artery Disease From the Difference of Gene Expression. <i>Frontiers in Physiology</i> , 2021, 12, 605811.	1.3	3
15169	Growth, physiological, biochemical, and molecular responses of Pacific white shrimp <i>Litopenaeus vannamei</i> fed different levels of dietary selenium. <i>Aquaculture</i> , 2021, 535, 736393.	1.7	26
15170	Does global food trade close the dietary nutrient gap for the world's poorest nations?. <i>Global Food Security</i> , 2021, 28, 100490.	4.0	24
15171	Design and evaluation of synthetic bacterial consortia for optimized phenanthrene degradation through the integration of genomics and shotgun proteomics. <i>Biotechnology Reports (Amsterdam, Nj)</i> 10.1016/j.btre.2021.100714	0.7	2
15172	Circadian rhythms in bipolar disorder patient-derived neurons predict lithium response: preliminary studies. <i>Molecular Psychiatry</i> , 2021, 26, 3383-3394.	4.1	29
15173	Chemoinformatic Screening for the Selection of Potential Senolytic Compounds from Natural Products. <i>Biomolecules</i> , 2021, 11, 467.	1.8	14
15174	Assessing Cultural Heritage Adaptive Reuse Practices: Multi-Scale Challenges and Solutions in Rijeka. <i>Sustainability</i> , 2021, 13, 3603.	1.6	25
15175	Network-based analysis using chromosomal microdeletion syndromes as a model. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2021, 187, 337-348.	0.7	2
15176	Repurposing of thalidomide and its derivatives for the treatment of SARS-CoV-2 infections: Hints on molecular action. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 3835-3850.	1.1	10
15177	Noise regularization removes correlation artifacts in single-cell RNA-seq data preprocessing. <i>Patterns</i> , 2021, 2, 100211.	3.1	9
15178	The Role of Autophagy and lncRNAs in the Maintenance of Cancer Stem Cells. <i>Cancers</i> , 2021, 13, 1239.	1.7	14
15179	Auto-aggressive CXCR6+ CD8 T cells cause liver immune pathology in NASH. <i>Nature</i> , 2021, 592, 444-449.	13.7	233
15180	Weighted gene co-expression network analysis revealed host transcriptional response to H1N1 influenza A virus infection. <i>Journal of Infection</i> , 2021, 82, e4-e7.	1.7	2
15181	Functional elucidation of TfuA in peptide backbone thioamidation. <i>Nature Chemical Biology</i> , 2021, 17, 585-592.	3.9	21
15182	Metabolome and Transcriptome Analyses Reveal the Regulatory Mechanisms of Photosynthesis in Developing <i>Ginkgo biloba</i> Leaves. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2601.	1.8	7
15183	The Genomic Architecture of Adaptation to Larval Malnutrition Points to a Trade-off with Adult Starvation Resistance in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2732-2749.	3.5	14

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15184	A chromosome level genome assembly of <i>Propillocerus akamusi</i> to understand its response to heavy metal exposure. <i>Molecular Ecology Resources</i> , 2021, 21, 1996-2012.	2.2	11
15185	Exploration of binary protein-protein interactions between tick-borne flaviviruses and <i>Ixodes ricinus</i> . <i>Parasites and Vectors</i> , 2021, 14, 144.	1.0	11
15186	Multi-factor mediated functional modules identify novel classification of ulcerative colitis and functional gene panel. <i>Scientific Reports</i> , 2021, 11, 5669.	1.6	7
15187	Comprehensive in silico survey of the <i>Mycobacterium</i> mobilome reveals an as yet underexplored diversity. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
15188	Full-Length Transcriptome Sequencing and Comparative Transcriptome Analysis to Evaluate Drought and Salt Stress in <i>Iris lactea</i> var. <i>chinensis</i> . <i>Genes</i> , 2021, 12, 434.	1.0	14
15190	Novel Molecular Hallmarks of Group 3 Medulloblastoma by Single-Cell Transcriptomics. <i>Frontiers in Oncology</i> , 2021, 11, 622430.	1.3	4
15192	Integrative Analysis of the Expression of SIGLEC Family Members in Lung Adenocarcinoma via Data Mining. <i>Frontiers in Oncology</i> , 2021, 11, 608113.	1.3	7
15194	Prenatal testosterone triggers long-term behavioral changes in male zebra finches: unravelling the neurogenomic mechanisms. <i>BMC Genomics</i> , 2021, 22, 158.	1.2	7
15195	Insights on the Structural Variations of the Furin-Like Cleavage Site Found Among the December 2019-July 2020 SARS-CoV-2 Spike Glycoprotein: A Computational Study Linking Viral Evolution and Infection. <i>Frontiers in Medicine</i> , 2021, 8, 613412.	1.2	5
15196	Screening potential FDA-approved inhibitors of the SARS-CoV-2 major protease 3CLpro through high-throughput virtual screening and molecular dynamics simulation. <i>Aging</i> , 2021, 13, 6258-6272.	1.4	11
15197	Transcriptome Analysis Reveals Genes Involved in Thermogenesis in Two Cold-Exposed Sheep Breeds. <i>Genes</i> , 2021, 12, 375.	1.0	4
15199	Identification of novel interactions between host and non-structural protein 2C of foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2021, 102, .	1.3	1
15200	Integrative analysis of the microbiome and metabolome in understanding the causes of sugarcane bitterness. <i>Scientific Reports</i> , 2021, 11, 6024.	1.6	21
15202	Bioinformatic analysis reveals possible molecular mechanism of PXR on regulating ulcerative colitis. <i>Scientific Reports</i> , 2021, 11, 5428.	1.6	3
15204	Rapid selection response to ethanol in <i>Saccharomyces eubayanus</i> emulates the domestication process under brewing conditions. <i>Microbial Biotechnology</i> , 2022, 15, 967-984.	2.0	9
15205	In Search of Newer Targets for Inflammatory Bowel Disease: A Systems and a Network Medicine Approach. <i>Network and Systems Medicine</i> , 2021, 4, 74-87.	2.7	0
15206	Identification of Potential Diagnostic Gene Targets for Pediatric Sepsis Based on Bioinformatics and Machine Learning. <i>Frontiers in Pediatrics</i> , 2021, 9, 576585.	0.9	2
15207	Deep Learning Reveals Key Immunosuppression Genes and Distinct Immunotypes in Periodontitis. <i>Frontiers in Genetics</i> , 2021, 12, 648329.	1.1	12

#	ARTICLE	IF	CITATIONS
15208	REG4 is a Potential Biomarker for Radiochemotherapy Sensitivity in Colorectal Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 1605-1611.	1.0	6
15210	Development of a Comprehensive Toxicity Pathway Model for 17 $\beta$ -Ethinylestradiol in Early Life Stage Fathead Minnows ( <i>Pimephales promelas</i> ). <i>Environmental Science &amp; Technology</i> , 2021, 55, 5024-5036.	4.6	13
15211	Chlorinated bianthrone from the cyanolichen <i>Nephroma laevigatum</i> . <i>F<math>\ddot{A}</math>-totrap<math>\ddot{A}</math></i> , 2021, 149, 104811.	1.1	6
15212	Network pharmacology-based research uncovers cold resistance and thermogenesis mechanism of <i>Cinnamomum cassia</i> . <i>F<math>\ddot{A}</math>-totrap<math>\ddot{A}</math></i> , 2021, 149, 104824.	1.1	12
15213	Transglutaminase $\alpha$ 2, RNA-binding proteins and mitochondrial proteins selectively traffic to MDCK cell-derived microvesicles following H $\alpha$ Ras-induced epithelial $\rightarrow$ mesenchymal transition. <i>Proteomics</i> , 2021, 21, 2000221.	1.3	5
15214	Gene Set Index Based on Different Modules May Help Differentiate the Mechanisms of Alzheimer's Disease and Vascular Dementia. <i>Clinical Interventions in Aging</i> , 2021, Volume 16, 451-463.	1.3	8
15215	Inactivation of cytosolic FUMARASE2 enhances growth and photosynthesis under simultaneous copper and iron deprivation in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2021, 106, 766-784.	2.8	4
15216	Genomic scanning enabling discovery of a new antibacterial bicyclic carbamate-containing alkaloid. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 12-19.	1.8	5
15218	Identification and validation of three core genes in p53 signaling pathway in hepatitis B virus-related hepatocellular carcinoma. <i>World Journal of Surgical Oncology</i> , 2021, 19, 66.	0.8	11
15219	Large-scale transcriptomics to dissect 2 $\frac{1}{2}$ years of the life of a fungal phytopathogen interacting with its host plant. <i>BMC Biology</i> , 2021, 19, 55.	1.7	21
15220	Elucidating evolutionarily conserved mechanisms of diapause regulation using an in silico approach. <i>FEBS Letters</i> , 2021, 595, 1350-1374.	1.3	0
15221	Genome analyses of 174 strains of <i>Mycobacterium tuberculosis</i> provide insight into the evolution of drug resistance and reveal potential drug targets. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
15222	Bioinformatics Analysis of Candidate Genes and Pathways Related to Hepatocellular Carcinoma in China: A Study Based on Public Databases. <i>Pathology and Oncology Research</i> , 2021, 27, 588532.	0.9	17
15223	Genome-wide RNAi screen for regulators of UPR $^{mt}$ in <i>Caenorhabditis elegans</i> mutants with defects in mitochondrial fusion. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
15224	A 2 miRNAs-based signature for the diagnosis of atherosclerosis. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 150.	0.7	8
15225	Processed foods drive intestinal barrier permeability and microvascular diseases. <i>Science Advances</i> , 2021, 7, .	4.7	80
15226	Removal of antibiotic resistance genes from swine wastewater by membrane filtration treatment. <i>Ecotoxicology and Environmental Safety</i> , 2021, 210, 111885.	2.9	77
15227	Endometrium On-a-Chip Reveals Insulin- and Glucose-induced Alterations in the Transcriptome and Proteomic Secretome. <i>Endocrinology</i> , 2021, 162, .	1.4	18

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15228	Genome Analysis of <i>Endotrypanum</i> and <i>Porcisia</i> spp., Closest Phylogenetic Relatives of <i>Leishmania</i> , Highlights the Role of Amastins in Shaping Pathogenicity. <i>Genes</i> , 2021, 12, 444.	1.0	12
15229	Detection of H3K4me3 Identifies NeuroHIV Signatures, Genomic Effects of Methamphetamine and Addiction Pathways in Postmortem HIV+ Brain Specimens that Are Not Amenable to Transcriptome Analysis. <i>Viruses</i> , 2021, 13, 544.	1.5	5
15230	Data processing strategies for non-targeted analysis of foods using liquid chromatography/high-resolution mass spectrometry. <i>TrAC - Trends in Analytical Chemistry</i> , 2021, 136, 116188.	5.8	36
15231	LncRNA-mRNA co-expression analysis discovered the diagnostic and prognostic biomarkers and potential therapeutic agents for myocardial infarction. <i>Aging</i> , 2021, 13, 8944-8959.	1.4	8
15232	Dynamic bacterial community response to <i>Akashiwo sanguinea</i> (Dinophyceae) bloom in indoor marine microcosms. <i>Scientific Reports</i> , 2021, 11, 6983.	1.6	14
15233	Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. <i>Molecular Systems Biology</i> , 2021, 17, e9923.	3.2	152
15234	Persistent microbiome members in the common bean rhizosphere: an integrated analysis of space, time, and plant genotype. <i>ISME Journal</i> , 2021, 15, 2708-2722.	4.4	76
15235	Construction of Competitive Endogenous RNA Network and Verification of 3-Key LncRNA Signature Associated With Distant Metastasis and Poor Prognosis in Patients With Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 640150.	1.3	21
15236	C11orf95-RELA fusion drives aberrant gene expression through the unique epigenetic regulation for ependymoma formation. <i>Acta Neuropathologica Communications</i> , 2021, 9, 36.	2.4	14
15239	Dihydrouridine synthesis in tRNAs is under reductive evolution in Mollicutes. <i>RNA Biology</i> , 2021, 18, 2278-2289.	1.5	7
15240	The overexpression of DNA repair genes in invasive ductal and lobular breast carcinomas: Insights on individual variations and precision medicine. <i>PLoS ONE</i> , 2021, 16, e0247837.	1.1	6
15243	Bioinformatics identification of the candidate microRNAs and construction of a competing endogenous RNA regulatory network in lacrimal gland adenoid cystic carcinoma high-grade transformation. <i>Oncology Letters</i> , 2021, 21, 360.	0.8	4
15245	A Streamlined Approach to Pathway Analysis from RNA-Sequencing Data. <i>Methods and Protocols</i> , 2021, 4, 21.	0.9	0
15247	Weighted Gene Coexpression Network Analysis Reveals Essential Genes and Pathways in Bipolar Disorder. <i>Frontiers in Psychiatry</i> , 2021, 12, 553305.	1.3	10
15248	Prognostic significance and immune infiltration of microenvironment-related signatures in pancreatic cancer. <i>Medicine (United States)</i> , 2021, 100, e24957.	0.4	3
15249	High oil accumulation in tuber of yellow nutsedge compared to purple nutsedge is associated with more abundant expression of genes involved in fatty acid synthesis and triacylglycerol storage. <i>Biotechnology for Biofuels</i> , 2021, 14, 54.	6.2	6
15250	Antibiotic tolerance is associated with a broad and complex transcriptional response in <i>E. coli</i> . <i>Scientific Reports</i> , 2021, 11, 6112.	1.6	22
15251	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	4.4	24

#	ARTICLE	IF	CITATIONS
15252	mRNA-lncRNA Co-Expression Network Analysis Reveals the Role of lncRNAs in Immune Dysfunction during Severe SARS-CoV-2 Infection. <i>Viruses</i> , 2021, 13, 402.	1.5	30
15253	Upregulation of GNPAT1 Predicts Poor Prognosis and Correlates With Immune Infiltration in Lung Adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 605754.	1.6	21
15254	M2 macrophage-derived exosomal microRNAs inhibit cell migration and invasion in gliomas through PI3K/AKT/mTOR signaling pathway. <i>Journal of Translational Medicine</i> , 2021, 19, 99.	1.8	31
15255	Overexpression of CCNE1 confers a poorer prognosis in triple-negative breast cancer identified by bioinformatic analysis. <i>World Journal of Surgical Oncology</i> , 2021, 19, 86.	0.8	13
15256	Current status and future perspectives of computational studies on human-virus protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
15257	Mechanisms behind polyphagia in a pest insect: Responses of <i>Spodoptera frugiperda</i> (J.E. Smith) strains to preferential and alternative larval host plants assessed with gene regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194687.	0.9	2
15258	Interception Targets of <i>Angelica Gigas</i> Nakai Root Extract versus Pyranocoumarins in Prostate Early Lesions and Neuroendocrine Carcinomas in TRAMP Mice. <i>Cancer Prevention Research</i> , 2021, 14, 635-648.	0.7	1
15259	CNVs inform the biological network of Autism spectrum disorder. <i>Psychiatry Research</i> , 2021, 297, 113729.	1.7	0
15260	Cloning, expression and immunological characterisation of Coc n 1, the first major allergen from Coconut pollen. <i>Molecular Immunology</i> , 2021, 131, 33-43.	1.0	2
15262	MicroRNA-665 Regulates Cell Proliferation and Apoptosis of Vascular Smooth Muscle Cells by Targeting TGFBR1. <i>International Heart Journal</i> , 2021, 62, 371-380.	0.5	3
15264	Herb-target virtual screening and network pharmacology for prediction of molecular mechanism of Danggui Beimu Kushen Wan for prostate cancer. <i>Scientific Reports</i> , 2021, 11, 6656.	1.6	18
15265	Prediction of lncRNA-encoded small peptides in glioma and oligomer channel functional analysis using in silico approaches. <i>PLoS ONE</i> , 2021, 16, e0248634.	1.1	6
15266	Electronic health record and patterns of care for children with cerebral palsy. <i>Developmental Medicine and Child Neurology</i> , 2021, 63, 1337-1343.	1.1	6
15267	Integrative Analysis of Gene Expression and miRNAs Reveal Biological Pathways Associated with Bud Paradormancy and Endodormancy in Grapevine. <i>Plants</i> , 2021, 10, 669.	1.6	5
15268	Characterization of Biological Pathways Regulating Acute Cold Resistance of Zebrafish. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3028.	1.8	28
15269	Revisiting the Relationship Between Alzheimer's Disease and Cancer With a circRNA Perspective. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647197.	1.8	6
15270	MET transcriptional regulator/serine peptidase inhibitor kunitz type 1 panel operating through HGF/c-MET axis as a prognostic signature in pan-cancer. <i>Cancer Medicine</i> , 2021, 10, 2442-2460.	1.3	4
15271	EphA2 super-enhancer promotes tumor progression by recruiting FOSL2 and TCF7L2 to activate the target gene EphA2. <i>Cell Death and Disease</i> , 2021, 12, 264.	2.7	18



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15272	Network pharmacology based high throughput screening for identification of multi targeted anti-diabetic compound from traditionally used plants. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 8004-8017.	2.0	6
15273	Bioinformatic Analysis of Key Genes and Pathways Related to Keloids. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	6
15275	Integrated MicroRNA-mRNA Analyses of Distinct Expression Profiles in Hyperoxia-Induced Bronchopulmonary Dysplasia in Neonatal Mice. <i>American Journal of Perinatology</i> , 2022, 39, 1702-1710.	0.6	1
15277	Single Cell Label-Free Probing of Chromatin Dynamics During B Lymphocyte Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 646616.	1.8	9
15278	Comprehensive analysis of immune-related prognostic genes in the tumour microenvironment of hepatocellular carcinoma. <i>BMC Cancer</i> , 2021, 21, 331.	1.1	1
15279	A Comprehensive Understanding of the Anticancer Mechanisms of FDY2004 Against Cervical Cancer Based on Network Pharmacology. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110043.	0.2	2
15280	Comprehensive analysis of ceRNA networks reveals prognostic lncRNAs related to immune infiltration in colorectal cancer. <i>BMC Cancer</i> , 2021, 21, 255.	1.1	28
15281	Nanostructured lipid carrier co-delivering paclitaxel and doxorubicin restrains the proliferation and promotes apoptosis of glioma stem cells via regulating PI3K/Akt/mTOR signaling. <i>Nanotechnology</i> , 2021, 32, 225101.	1.3	8
15282	Improvement of Atopic Dermatitis by Synbiotic Baths. <i>Microorganisms</i> , 2021, 9, 527.	1.6	8
15283	Differential Response of Grapevine to Infection with <i>Candidatus Phytoplasma solani</i> ™ in Early and Late Growing Season through Complex Regulation of mRNA and Small RNA Transcriptomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3531.	1.8	10
15284	Blood Coagulation Factor Fibrinogen in Tumor Pathogenesis of Central Nervous System B-Cell Lymphoma. <i>American Journal of Pathology</i> , 2021, 191, 575-583.	1.9	5
15285	Extracellular Vesicles for the Treatment of Radiation-Induced Normal Tissue Toxicity in the Lung. <i>Frontiers in Oncology</i> , 2020, 10, 602763.	1.3	7
15286	Characteristics of soil bacterial and fungal communities on interval seawater covering Linchang Island, China. <i>Archives of Microbiology</i> , 2021, 203, 2453-2461.	1.0	1
15287	Identification and Analysis of Potential Key Genes Associated With Hepatocellular Carcinoma Based on Integrated Bioinformatics Methods. <i>Frontiers in Genetics</i> , 2021, 12, 571231.	1.1	25
15288	Integration of summary data from GWAS and eQTL studies identified novel risk genes for coronary artery disease. <i>Medicine (United States)</i> , 2021, 100, e24769.	0.4	9
15289	Mapping specificity, cleavage entropy, allosteric changes and substrates of blood proteases in a high-throughput screen. <i>Nature Communications</i> , 2021, 12, 1693.	5.8	17
15290	Exploring short k-mer profiles in cells and mobile elements from Archaea highlights the major influence of both the ecological niche and evolutionary history. <i>BMC Genomics</i> , 2021, 22, 186.	1.2	8
15291	High BLM Expression Predicts Poor Clinical Outcome and Contributes to Malignant Progression in Human Cholangiocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 633899.	1.3	8

#	ARTICLE	IF	CITATIONS
15292	Remodeling of the cell wall as a drought-tolerance mechanism of a soybean genotype revealed by global gene expression analysis. <i>ABIOTECH</i> , 2021, 2, 14-31.	1.8	10
15293	Rhizosphere microbiome modulated effects of biochar on ryegrass 15N uptake and rhizodeposited 13C allocation in soil. <i>Plant and Soil</i> , 2021, 463, 359-377.	1.8	17
15294	Identification of hub genes associated with neutrophils infiltration in colorectal cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 3371-3380.	1.6	15
15295	Screening of Hub Genes Associated with Pulmonary Arterial Hypertension by Integrated Bioinformatic Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-16.	0.9	9
15297	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. <i>Frontiers in Genetics</i> , 2021, 12, 599261.	1.1	64
15298	A bird eye view on cystic fibrosis: An underestimated multifaceted chronic disorder. <i>Life Sciences</i> , 2021, 268, 118959.	2.0	10
15299	Transcriptome Analysis Identifies Candidate Genes and Signaling Pathways Associated With Feed Efficiency in Xiayan Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 607719.	1.1	12
15300	Coagulation factor IX analysis in bioreactor cell culture supernatant predicts quality of the purified product. <i>Communications Biology</i> , 2021, 4, 390.	2.0	8
15301	Identification of a Novel Cis-Acting Regulator of HIV-1 Genome Packaging. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3435.	1.8	6
15302	Functional analysis of SARS-CoV-2 proteins in <i>Drosophila</i> identifies Orf6-induced pathogenic effects with Selinexor as an effective treatment. <i>Cell and Bioscience</i> , 2021, 11, 59.	2.1	18
15303	Phytochrome B links the environment to transcription. <i>Journal of Experimental Botany</i> , 2021, 72, 4068-4084.	2.4	11
15304	Multi-country investigation of the diversity and associated microorganisms isolated from tick species from domestic animals, wildlife and vegetation in selected african countries. <i>Experimental and Applied Acarology</i> , 2021, 83, 427-448.	0.7	6
15305	Glycosylation of N-hydroxy-pipecolic acid equilibrates between systemic acquired resistance response and plant growth. <i>Molecular Plant</i> , 2021, 14, 440-455.	3.9	44
15306	A KDM5 transcriptional axis functions during early neurodevelopment to regulate mushroom body formation. <i>ELife</i> , 2021, 10, .	2.8	17
15307	Discovery of RSV-Induced BRD4 Protein Interactions Using Native Immunoprecipitation and Parallel Accumulation Serial Fragmentation (PASEF) Mass Spectrometry. <i>Viruses</i> , 2021, 13, 454.	1.5	20
15308	Integrated Proteomics and Bioinformatics to Identify Potential Prognostic Biomarkers in Hepatocellular Carcinoma. <i>Cancer Management and Research</i> , 2021, Volume 13, 2307-2317.	0.9	12
15309	Preclinical modeling of chronic inhibition of the Parkinson's disease associated kinase LRRK2 reveals altered function of the endolysosomal system in vivo. <i>Molecular Neurodegeneration</i> , 2021, 16, 17.	4.4	29
15310	Identification of Meat Quality Determining Marker Genes in Fibroblasts of Bovine Muscle Using Transcriptomic Profiling. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 3776-3786.	2.4	10

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15311	Multiomics Analysis of Genetics and Epigenetics Reveals Pathogenesis and Therapeutic Targets for Atrial Fibrillation. <i>BioMed Research International</i> , 2021, 2021, 1-36.	0.9	4
15312	Identification of Hub Genes and Key Pathways Associated with Anti-VEGF Resistant Glioblastoma Using Gene Expression Data Analysis. <i>Biomolecules</i> , 2021, 11, 403.	1.8	12
15314	Inhibition of Intestinal Lipid Absorption by Cyanobacterial Strains in Zebrafish Larvae. <i>Marine Drugs</i> , 2021, 19, 161.	2.2	7
15315	Evolutionary Contribution of Duplicated Genes to Genome Evolution in the Ginseng Species Complex. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
15316	Identification of Genetic Modifiers of TDP-43: Inflammatory Activation of Astrocytes for Neuroinflammation. <i>Cells</i> , 2021, 10, 676.	1.8	9
15317	Transcriptomic analysis of the trade-off between endurance and burst-performance in the frog <i>Xenopus allofraseri</i> . <i>BMC Genomics</i> , 2021, 22, 204.	1.2	1
15318	Potential Association Between Asthma, Helicobacter pylori Infection, and Gastric Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 630235.	1.3	8
15319	TSC1 Affects the Process of Renal Ischemia-Reperfusion Injury by Controlling Macrophage Polarization. <i>Frontiers in Immunology</i> , 2021, 12, 637335.	2.2	14
15320	A long non-coding RNAs expression signature to improve prognostic prediction of Wilms tumor in children. <i>Translational Pediatrics</i> , 2021, 10, 525-540.	0.5	3
15321	IL-8, MSPa, MIF, FGF-9, ANG-2 and AgRP collection were identified for the diagnosis of colorectal cancer based on the support vector machine model. <i>Cell Cycle</i> , 2021, 20, 781-791.	1.3	8
15322	Comprehensive analysis of autophagy-related genes and patterns of immune cell infiltration in valvular atrial fibrillation. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 132.	0.7	10
15323	Study on the Mechanism of Jiawei Shengjiang Powder in Improving Male Asthma-Induced Asthenospermia Based on Network Pharmacology and Bioinformatics. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 1245-1259.	2.0	5
15324	Transcriptome analysis and candidate gene identification reveals insights into the molecular mechanisms of hypermelanosis in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Aquaculture and Fisheries</i> , 2021, , .	1.2	4
15326	The Main Alkaloids in <i>Uncaria rhynchophylla</i> and Their Anti-Alzheimer's Disease Mechanism Determined by a Network Pharmacology Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3612.	1.8	39
15327	Composition and diversity of bacterial communities in the rhizosphere of the Chinese medicinal herb <i>Dendrobium</i> . <i>BMC Plant Biology</i> , 2021, 21, 127.	1.6	36
15328	Transcriptional markers of excitation-inhibition balance in germ-free mice show region-specific dysregulation and rescue after bacterial colonization. <i>Journal of Psychiatric Research</i> , 2021, 135, 248-255.	1.5	9
15329	Network-Based Analysis of Cognitive Impairment and Memory Deficits from Transcriptome Data. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 2415-2428.	1.1	4
15330	Arginase 1 (Arg1) as an Up-Regulated Gene in COVID-19 Patients: A Promising Marker in COVID-19 Immunopathy. <i>Journal of Clinical Medicine</i> , 2021, 10, 1051.	1.0	34

#	ARTICLE	IF	CITATIONS
15331	Metagenomic insights into the taxonomy, function, and dysbiosis of prokaryotic communities in octocorals. <i>Microbiome</i> , 2021, 9, 72.	4.9	34
15332	Human Wharton's Jelly Mesenchymal Stromal Cell-Derived Small Extracellular Vesicles Drive Oligodendroglial Maturation by Restraining MAPK/ERK and Notch Signaling Pathways. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 622539.	1.8	13
15333	Exploring the significance of novel immune-related gene signatures in the prognosis and immune features of pancreatic adenocarcinoma. <i>International Immunopharmacology</i> , 2021, 92, 107359.	1.7	8
15334	Novel gene signatures for stage classification of the squamous cell carcinoma of the lung. <i>Scientific Reports</i> , 2021, 11, 4835.	1.6	4
15335	Deciphering the Pharmacological Mechanisms of Guizhi-Fuling Capsule on Primary Dysmenorrhea Through Network Pharmacology. <i>Frontiers in Pharmacology</i> , 2021, 12, 613104.	1.6	17
15336	Microbiome variation during culture growth of the European house dust mite, <i>Dermatophagoides pteronyssinus</i> . <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	10
15337	GRAS-domain transcription factor PAT1 regulates jasmonic acid biosynthesis in grape cold stress response. <i>Plant Physiology</i> , 2021, 186, 1660-1678.	2.3	53
15338	Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. <i>Plant Cell</i> , 2021, 33, 1430-1446.	3.1	55
15339	Gene co-expression analysis of tomato seed maturation reveals tissue-specific regulatory networks and hubs associated with the acquisition of desiccation tolerance and seed vigour. <i>BMC Plant Biology</i> , 2021, 21, 124.	1.6	15
15340	Metagenomic Analysis of the Respiratory Microbiome of a Broiler Flock from Hatching to Processing. <i>Microorganisms</i> , 2021, 9, 721.	1.6	9
15341	The Constitutive Extracellular Protein Release by Acute Myeloid Leukemia Cells—A Proteomic Study of Patient Heterogeneity and Its Modulation by Mesenchymal Stromal Cells. <i>Cancers</i> , 2021, 13, 1509.	1.7	11
15342	COVID-19 engages clinical markers for the management of cancer and cancer-relevant regulators of cell proliferation, death, migration, and immune response. <i>Scientific Reports</i> , 2021, 11, 5228.	1.6	6
15343	Transcriptome analyses and weighted gene coexpression network analysis reveal key pathways and genes involved in the rapid cold resistance of the Chinese white wax scale insect. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21781.	0.6	11
15344	Endothelial Jak3 expression enhances pro-hematopoietic angiocrine function in mice. <i>Communications Biology</i> , 2021, 4, 406.	2.0	9
15346	Identification of Chlorophyll Metabolism- and Photosynthesis-Related Genes Regulating Green Flower Color in Chrysanthemum by Integrative Transcriptome and Weighted Correlation Network Analyses. <i>Genes</i> , 2021, 12, 449.	1.0	9
15347	Identification of differentially expressed circular <i>scn</i> RNAs associated with thymoma. <i>Thoracic Cancer</i> , 2021, 12, 1312-1319.	0.8	10
15348	Identification of disease treatment mechanisms through the multiscale interactome. <i>Nature Communications</i> , 2021, 12, 1796.	5.8	72
15349	Molecular differential analysis of uterine leiomyomas and leiomyosarcomas through weighted gene network and pathway tracing approaches. <i>Systems Biology in Reproductive Medicine</i> , 2021, 67, 209-220.	1.0	7

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15350	Protection against Glucolipototoxicity by High Density Lipoprotein in Human PANC-1 Hybrid 1.1B4 Pancreatic Beta Cells: The Role of microRNA. <i>Biology</i> , 2021, 10, 218.	1.3	5
15352	The comprehensive changes in soil properties are continuous cropping obstacles associated with American ginseng ( <i>Panax quinquefolius</i> ) cultivation. <i>Scientific Reports</i> , 2021, 11, 5068.	1.6	37
15353	Molecular characterization of long-term survivors of hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 7517-7537.	1.4	5
15354	Proteome dynamics at broken replication forks reveal a distinct ATM-directed repair response suppressing DNA double-strand break ubiquitination. <i>Molecular Cell</i> , 2021, 81, 1084-1099.e6.	4.5	57
15355	Inducible mechanisms of disease tolerance provide an alternative strategy of acquired immunity to malaria. <i>ELife</i> , 2021, 10, .	2.8	43
15356	Identification of a tumor microenvironment-related gene signature to improve the prediction of cervical cancer prognosis. <i>Cancer Cell International</i> , 2021, 21, 182.	1.8	10
15357	Biodiversity and antimicrobial potential of bacterial endophytes from halophyte <i>Salicornia brachiata</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 591-608.	0.7	10
15359	Elucidating the influence of environmentally relevant toxic metal mixture on molecular mechanisms involved in the development of neurodegenerative diseases: In silico toxicogenomic data-mining. <i>Environmental Research</i> , 2021, 194, 110727.	3.7	17
15360	Association analysis framework of genetic and exposure risks for COVID-19 in middle-aged and elderly adults. <i>Mechanisms of Ageing and Development</i> , 2021, 194, 111433.	2.2	18
15361	Mesenchymal stem cell-derived extracellular vesicles reduce senescence and extend health span in mouse models of aging. <i>Aging Cell</i> , 2021, 20, e13337.	3.0	63
15362	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. <i>Plant Cell</i> , 2021, 33, 1863-1887.	3.1	27
15364	High-content phenotypic and pathway profiling to advance drug discovery in diseases of unmet need. <i>Cell Chemical Biology</i> , 2021, 28, 338-355.	2.5	27
15365	Innate immune signatures to a partially-efficacious HIV vaccine predict correlates of HIV-1 infection risk. <i>PLoS Pathogens</i> , 2021, 17, e1009363.	2.1	19
15366	Higher Abundance of Sediment Methanogens and Methanotrophs Do Not Predict the Atmospheric Methane and Carbon Dioxide Flows in Eutrophic Tropical Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2021, 12, 647921.	1.5	13
15367	Revealing taxon-specific heavy metal-resistance mechanisms in denitrifying phosphorus removal sludge using genome-centric metaproteomics. <i>Microbiome</i> , 2021, 9, 67.	4.9	34
15368	Genome-wide association studies reveal the coordinated regulatory networks underlying photosynthesis and wood formation in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 5372-5389.	2.4	12
15369	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
15370	Metallothioneins alter macrophage phenotype and represent novel therapeutic targets for acetaminophen-induced liver injury. <i>Journal of Leukocyte Biology</i> , 2021, 111, 123-133.	1.5	8

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15371	Differential MicroRNA Expression Involved in Endometrial Receptivity of Goats. <i>Biomolecules</i> , 2021, 11, 472.	1.8	11
15372	Isolation and Characterization of <i>Klebsiella</i> Phages for Phage Therapy. <i>Phage</i> , 2021, 2, 26-42.	0.8	36
15373	Identification of immune-related lncRNA signature for predicting immune checkpoint blockade and prognosis in hepatocellular carcinoma. <i>International Immunopharmacology</i> , 2021, 92, 107333.	1.7	62
15374	Hybrid assembly of an agricultural slurry virome reveals a diverse and stable community with the potential to alter the metabolism and virulence of veterinary pathogens. <i>Microbiome</i> , 2021, 9, 65.	4.9	182
15376	Pharmacological Mechanisms Underlying the Anti-asthmatic Effects of Modified Guomin Decoction Determined by Network Pharmacology and Molecular Docking. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 644561.	1.6	6
15377	Identification and Validation of SNP-Containing Genes With Prognostic Value in Gastric Cancer via Integrated Bioinformatics Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 564296.	1.3	10
15378	Transcriptomic analysis and competing endogenous RNA network in the human endometrium between proliferative and mid-secretory phases. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 660.	0.8	11
15379	Protective and Risk Factors for Medical and Nursing Staff Suffering From Psychological Symptoms During COVID-19. <i>Frontiers in Psychology</i> , 2021, 12, 603553.	1.1	5
15380	Analysis of temporal gene regulation of <i>Listeria monocytogenes</i> revealed distinct regulatory response modes after exposure to high pressure processing. <i>BMC Genomics</i> , 2021, 22, 266.	1.2	5
15381	MicroRNA Biomarkers of High-Grade Cervical Intraepithelial Neoplasia in Liquid Biopsy. <i>BioMed Research International</i> , 2021, 2021, 1-9.	0.9	9
15382	A Combination of RNA-Seq Analysis and Use of TCGA Database for Determining the Molecular Mechanism and Identifying Potential Drugs for GJB1 in Ovarian Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 2623-2633.	1.0	1
15384	Identification of the Key Regulators of Spina Bifida Through Graph-Theoretical Approach. <i>Frontiers in Genetics</i> , 2021, 12, 597983.	1.1	3
15386	Probing Conformational Dynamics by Protein Contact Networks: Comparison with NMR Relaxation Studies and Molecular Dynamics Simulations. <i>Biophysica</i> , 2021, 1, 157-167.	0.6	1
15387	Integrative microRNAome analysis of skeletal muscle of <i>Colossoma macropomum</i> (tambaqui), <i>Piaractus mesopotamicus</i> (pacu), and the hybrid tambacu, based on next-generation sequencing data. <i>BMC Genomics</i> , 2021, 22, 237.	1.2	3
15388	Quantitative Phosphoproteomic Analysis Reveals Dendritic Cell- Specific STAT Signaling After $\alpha$ 2-3-Linked Sialic Acid Ligand Binding. <i>Frontiers in Immunology</i> , 2021, 12, 673454.	2.2	3
15389	Network Analyses Predict Small RNAs That Might Modulate Gene Expression in the Testis and Epididymis of <i>Bos indicus</i> Bulls. <i>Frontiers in Genetics</i> , 2021, 12, 610116.	1.1	7
15390	Computational Identification of the Plausible Molecular Vaccine Candidates of Multidrug-Resistant <i>Salmonella enterica</i> . , 0, , .		1
15391	Dynamic and Temporal Transcriptomic Analysis Reveals Ferroptosis-Mediated Antileukemia Activity of S-Dimethylarsino-Glutathione: Insights into Novel Therapeutic Strategy. <i>CCS Chemistry</i> , 2022, 4, 963-974.	4.6	1



#	ARTICLE	IF	CITATIONS
15392	Comprehensive RNA-Seq Analysis of Potential Therapeutic Targets of Ganâ€“Douâ€“Fuâ€“Mu Decoction for Treatment of Wilson Disease Using a Toxic Milk Mouse Model. <i>Frontiers in Pharmacology</i> , 2021, 12, 622268.	1.6	5
15393	The European Bioinformatics Community for Mass Spectrometry (EuBICâ€“MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9087.	0.7	3
15394	Network Pharmacology-Based Prediction of Mechanism of Shenzhuo Formula for Application to DKD. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	2
15397	Multi-schema computational prediction of the comprehensive SARS-CoV-2 vs. human interactome. <i>PeerJ</i> , 2021, 9, e11117.	0.9	8
15398	Organic Electron Donors and Terminal Electron Acceptors Structure Anaerobic Microbial Communities and Interactions in a Permanently Stratified Sulfidic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 620424.	1.5	9
15400	Network pharmacology and RNA-sequencing reveal the molecular mechanism of Xuebijing injection on COVID-19-induced cardiac dysfunction. <i>Computers in Biology and Medicine</i> , 2021, 131, 104293.	3.9	14
15401	Computational and experimental characterization of the novel ECM glycoprotein SNED1 and prediction of its interactome. <i>Biochemical Journal</i> , 2021, 478, 1413-1434.	1.7	10
15402	Finding What Is Inaccessible: Antimicrobial Resistance Language Use among the One Health Domains. <i>Antibiotics</i> , 2021, 10, 385.	1.5	4
15403	Screening and identification of haptoglobin showing its important role in pathophysiological process of gallbladder carcinoma. <i>Gene</i> , 2021, 776, 145429.	1.0	2
15404	Integrated analysis of miRNAome and transcriptome reveals miRNA-mRNA network regulation in <i>Vibrio alginolyticus</i> infected thick shell mussel <i>Mytilus coruscus</i> . <i>Molecular Immunology</i> , 2021, 132, 217-226.	1.0	6
15405	The Na/Kâ€“ATPase Î±1/Src interaction regulates metabolic reserve and Western diet intolerance. <i>Acta Physiologica</i> , 2021, 232, e13652.	1.8	12
15406	Single-cell RNA-seq reveals dynamic change in tumor microenvironment during pancreatic ductal adenocarcinoma malignant progression. <i>EBioMedicine</i> , 2021, 66, 103315.	2.7	105
15407	Similarity and difference of pathogenesis among lung cancer subtypes suggested by expression profile data. <i>Pathology Research and Practice</i> , 2021, 220, 153365.	1.0	4
15408	Arena3Dweb: interactive 3D visualization of multilayered networks. <i>Nucleic Acids Research</i> , 2021, 49, W36-W45.	6.5	22
15409	MicroRNAs in the aqueous humor of patients with different types of glaucoma. <i>Graefe's Archive for Clinical and Experimental Ophthalmology</i> , 2021, 259, 2337-2349.	1.0	14
15410	Isoform-specific and signaling-dependent propagation of acute myeloid leukemia by Wilms tumor 1. <i>Cell Reports</i> , 2021, 35, 109010.	2.9	12
15411	Proteogenomic landscape of uterine leiomyomas from hereditary leiomyomatosis and renal cell cancer patients. <i>Scientific Reports</i> , 2021, 11, 9371.	1.6	9
15412	Varied clinical significance of ATP-binding cassette C sub-family members for lung adenocarcinoma. <i>Medicine (United States)</i> , 2021, 100, e25246.	0.4	3

#	ARTICLE	IF	CITATIONS
15413	Uncultivated Viral Populations Dominate Estuarine Viromes on the Spatiotemporal Scale. <i>MSystems</i> , 2021, 6, .	1.7	13
15414	Elucidation of the Pathogenicity-Associated Regulatory Network in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>MSystems</i> , 2021, 6, .	1.7	5
15415	PolyQ length co-evolution in neural proteins. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab032.	1.5	4
15416	Transcriptional changes through menstrual cycle reveal a global transcriptional derepression underlying the molecular mechanism involved in the window of implantation. <i>Molecular Human Reproduction</i> , 2021, 27, .	1.3	5
15417	Exogenous GLP-1 stimulates TCA cycle and suppresses gluconeogenesis and ketogenesis in late-fasted northern elephant seals pups. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2021, 320, R393-R403.	0.9	2
15418	Nucleolin Rescues TDP-43 Toxicity in Yeast and Human Cell Models. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 625665.	1.8	12
15419	Identification of Key Genes Involved in Pancreatic Ductal Adenocarcinoma with Diabetes Mellitus Based on Gene Expression Profiling Analysis. <i>Pathology and Oncology Research</i> , 2021, 27, 604730.	0.9	4
15420	The Underlying Molecular Mechanisms Involved in Traditional Chinese Medicine <i>Smilax china</i> L. for the Treatment of Pelvic Inflammatory Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-18.	0.5	5
15421	Bioinformatic analysis identifies potential biomarkers and therapeutic targets of septic-shock-associated acute kidney injury. <i>Hereditas</i> , 2021, 158, 13.	0.5	30
15422	Systems Biology behind Immunoprotection of Both Sheep and Goats after Sungri/96 PPRV Vaccination. <i>MSystems</i> , 2021, 6, .	1.7	6
15423	Comparative proteome analyses highlight several exercise-like responses of mouse sciatic nerve after IP injection of irisin. <i>European Journal of Neuroscience</i> , 2021, 53, 3262-3277.	1.2	6
15424	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. <i>Nature Plants</i> , 2021, 7, 481-499.	4.7	247
15425	Consolidation of network and experimental pharmacology to divulge the antidiabetic action of <i>Ficus benghalensis</i> L. bark. <i>3 Biotech</i> , 2021, 11, 238.	1.1	10
15426	A widespread pathway for substitution of adenine by diaminopurine in phage genomes. <i>Science</i> , 2021, 372, 512-516.	6.0	55
15428	Integrative microbiomics in bronchiectasis exacerbations. <i>Nature Medicine</i> , 2021, 27, 688-699.	15.2	105
15429	Multi-Omics Approaches to Define Calcific Aortic Valve Disease Pathogenesis. <i>Circulation Research</i> , 2021, 128, 1371-1397.	2.0	39
15431	Intelligent analysis of methylation data in Head and Neck Squamous Cell Carcinoma (HNSCC) interactomes. , 2021, , .		0
15433	Transcriptomic and microRNA Expression Profiles Identify Biomarkers for Predicting Neo-Chemoradiotherapy Response in Esophageal Squamous Cell Carcinomas (ESCC). <i>Frontiers in Pharmacology</i> , 2021, 12, 626972.	1.6	9

#	ARTICLE	IF	CITATIONS
15434	Use of Network Pharmacology to Explore the Mechanism of Gegen ( <i>Puerariae lobatae Radix</i> ) in the Treatment of Type 2 Diabetes Mellitus Associated with Hyperlipidemia. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-14.	0.5	18
15435	Different Responses of Bacterial and Archaeal Communities in River Sediments to Water Diversion and Seasonal Changes. Microorganisms, 2021, 9, 782.	1.6	12
15436	Ecosystem services provided by aculeate wasps. Biological Reviews, 2021, 96, 1645-1675.	4.7	75
15437	Metatranscriptomic Comparison of Endophytic and Pathogenic <i>Fusarium</i> – <i>Arabidopsis</i> Interactions Reveals Plant Transcriptional Plasticity. Molecular Plant-Microbe Interactions, 2021, 34, 1071-1083.	1.4	25
15438	Fibroblast GATA-4 and GATA-6 promote myocardial adaptation to pressure overload by enhancing cardiac angiogenesis. Basic Research in Cardiology, 2021, 116, 26.	2.5	34
15439	Genomic and Metabolomic Analysis of the Potato Common Scab Pathogen <i>Streptomyces scabiei</i> . ACS Omega, 2021, 6, 11474-11487.	1.6	21
15440	Ciprofloxacin-Resistant <i>Staphylococcus aureus</i> Displays Enhanced Resistance and Virulence in Iron-Restricted Conditions. Journal of Proteome Research, 2021, 20, 2839-2850.	1.8	10
15441	Comparative Phosphoproteomics Reveals a Role for AMPK in Hypoxia Signaling in Testes of Oriental River Prawn ( <i>Macrobrachium nipponense</i> ). Journal of Proteome Research, 2021, 20, 2923-2934.	1.8	9
15442	Biomarker Identification for Liver Hepatocellular Carcinoma and Cholangiocarcinoma Based on Gene Regulatory Network Analysis. Current Bioinformatics, 2021, 16, 31-43.	0.7	4
15443	Long-term inorganic nitrogen application changes the ammonia-oxidizing archaeal community composition in paddy soils. European Journal of Soil Science, 2021, 72, 2246-2260.	1.8	4
15445	HIV-associated nephropathy: Protocol and rationale for an exploratory genotype-phenotype study in a sub-Saharan African population. PLoS ONE, 2021, 16, e0249567.	1.1	0
15446	Identification of blood-derived candidate gene markers and a new 7-gene diagnostic model for multiple sclerosis. Biological Research, 2021, 54, 12.	1.5	15
15447	Identification of a MicroRNA Signature Associated With Lymph Node Metastasis in Endometrial Endometrioid Cancer. Frontiers in Genetics, 2021, 12, 650102.	1.1	3
15448	Actin and Microtubules Differently Contribute to Vacuolar Targeting Specificity during the Export from the ER. Membranes, 2021, 11, 299.	1.4	5
15449	A novel comprehensive immune-related gene signature as a promising survival predictor for the patients with head and neck squamous cell carcinoma. Aging, 2021, 13, 11507-11527.	1.4	4
15450	Expression and Co-expression Analyses of WRKY, MYB, bHLH and bZIP Transcription Factor Genes in Potato ( <i>Solanum tuberosum</i> ) Under Abiotic Stress Conditions: RNA-seq Data Analysis. Potato Research, 2021, 64, 721-741.	1.2	6
15451	Influence of Non-canonical DNA Bases on the Genomic Diversity of Tevenvirinae. Frontiers in Microbiology, 2021, 12, 632686.	1.5	3
15452	Weighted gene co expression network analysis (WGCNA) with key pathways and hub-genes related to micro RNAs in ischemic stroke. IET Systems Biology, 2021, 15, 93-100.	0.8	4

#	ARTICLE	IF	CITATIONS
15453	Molecular Basis of GABA Hypofunction in Adolescent Schizophrenia-Like Animals. <i>Neural Plasticity</i> , 2021, 2021, 1-15.	1.0	6
15454	Network analysis in aged <i>C. elegans</i> reveals candidate regulatory genes of ageing. <i>Biogerontology</i> , 2021, 22, 345-367.	2.0	0
15456	Feature-Based Molecular Network-Guided Dereplication of Natural Bioactive Products from Leaves of <i>Stryphnodendron pulcherrimum</i> (Willd.) Hochr. <i>Metabolites</i> , 2021, 11, 281.	1.3	15
15458	The GUL-1 Protein Binds Multiple RNAs Involved in Cell Wall Remodeling and Affects the MAK-1 Pathway in <i>Neurospora crassa</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	4
15459	The Regulation of Adaptation to Cold and Drought Stresses in <i>Poa crymophila</i> Keng Revealed by Integrative Transcriptomics and Metabolomics Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 631117.	1.7	8
15461	CXCL1 Clone Evolution Induced by the HDAC Inhibitor Belinostat Might Be a Favorable Prognostic Indicator in Triple-Negative Breast Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	4
15462	Advantages of using graph databases to explore chromatin conformation capture experiments. <i>BMC Bioinformatics</i> , 2021, 22, 43.	1.2	1
15463	The Mechanism of Lavender Essential Oil in the Treatment of Acute Colitis Based on "Quantity" Effect Weight Coefficient Network Pharmacology. <i>Frontiers in Pharmacology</i> , 2021, 12, 644140.	1.6	13
15464	Investigation of candidate genes and mechanisms underlying obesity associated type 2 diabetes mellitus using bioinformatics analysis and screening of small drug molecules. <i>BMC Endocrine Disorders</i> , 2021, 21, 80.	0.9	12
15465	Systematic in silico Evaluation of <i>Leishmania</i> spp. Proteomes for Drug Discovery. <i>Frontiers in Chemistry</i> , 2021, 9, 607139.	1.8	4
15466	Identification of Hub Genes and MicroRNAs Associated With Idiopathic Pulmonary Arterial Hypertension by Integrated Bioinformatics Analyses. <i>Frontiers in Genetics</i> , 2021, 12, 667406.	1.1	9
15467	Pinpointing cysteine oxidation sites by high-resolution proteomics reveals a mechanism of redox-dependent inhibition of human STING. <i>Science Signaling</i> , 2021, 14, .	1.6	15
15468	Cross-species transcriptomics uncovers genes underlying genetic accommodation of developmental plasticity in spadefoot toads. <i>Molecular Ecology</i> , 2021, 30, 2220-2234.	2.0	5
15469	Gene expression patterns associated with tumor-infiltrating CD4+ and CD8+ T cells in invasive breast carcinomas. <i>Human Immunology</i> , 2021, 82, 279-287.	1.2	5
15470	Clinical and In Silico Outcomes of the Expression of miR-130a-5p and miR-615-3p in Tumor Compared with Non-Tumor Adjacent Tissues of Patients with BC. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2021, 21, 927-935.	0.9	4
15471	The influence of delay in mononuclear cell isolation on acute myeloid leukemia phosphorylation profiles. <i>Journal of Proteomics</i> , 2021, 238, 104134.	1.2	3
15472	Epigenetic analysis of Paget's disease of bone identifies differentially methylated loci that predict disease status. <i>ELife</i> , 2021, 10, .	2.8	9
15473	eIF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. <i>Cell Reports</i> , 2021, 35, 108941.	2.9	56

#	ARTICLE	IF	CITATIONS
15474	Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. <i>Nature Communications</i> , 2021, 12, 2340.	5.8	43
15475	Genome-wide identification and analysis of long non-coding RNAs involved in fatty acid biosynthesis in young soybean pods. <i>Scientific Reports</i> , 2021, 11, 7603.	1.6	11
15476	Probiogenomics of <i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> CIDCA 133: In Silico, In Vitro, and In Vivo Approaches. <i>Microorganisms</i> , 2021, 9, 829.	1.6	12
15477	M6ADD: a comprehensive database of m <sup>6</sup> A modifications in diseases. <i>RNA Biology</i> , 2021, 18, 2354-2362.	1.5	8
15478	Antimicrobial Bombinin-like Peptide 3 Selectively Recognizes and Inserts into Bacterial Biomimetic Bilayers in Multiple Steps. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 5185-5197.	2.9	5
15480	Tumor microenvironment characterization in cervical cancer identifies prognostic relevant gene signatures. <i>PLoS ONE</i> , 2021, 16, e0249374.	1.1	6
15481	Accumulation of organic compounds in paddy soils after biochar application is controlled by iron hydroxides. <i>Science of the Total Environment</i> , 2021, 764, 144300.	3.9	18
15482	Integrated Biophysical Modeling of the SARS-CoV-2 Spike Protein Binding and Allosteric Interactions with Antibodies. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4596-4619.	1.2	60
15483	Increased SGK1 activity potentiates mineralocorticoid/NaCl-induced kidney injury. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, F628-F643.	1.3	15
15484	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021, 594, 246-252.	13.7	475
15485	Nanopore long-read RNAseq reveals regulatory mechanisms of thermally variable reef environments promoting heat tolerance of scleractinian coral <i>Pocillopora damicornis</i> . <i>Environmental Research</i> , 2021, 195, 110782.	3.7	14
15486	Deciphering the Methylation Landscape in Breast Cancer: Diagnostic and Prognostic Biosignatures through Automated Machine Learning. <i>Cancers</i> , 2021, 13, 1677.	1.7	24
15487	Correlation Analysis of Compounds in Essential Oil of <i>Amomum tsaoko</i> Seed and Fruit Morphological Characteristics, Geographical Conditions, Locality of Growth. <i>Agronomy</i> , 2021, 11, 744.	1.3	11
15488	Methamphetamine-induced changes in myocardial gene transcription are sex-dependent. <i>BMC Genomics</i> , 2021, 22, 259.	1.2	7
15489	Differential Expression Analysis of Phytohormone-Related Genes of Korean Wheat ( <i>Triticum aestivum</i> ) in Response to Preharvest Sprouting and Abscisic Acid (ABA). <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3562.	1.3	2
15490	Comparative transcriptome profiling reveals the basis of differential sheath blight disease response in tolerant and susceptible rice genotypes. <i>Protoplasma</i> , 2022, 259, 61-73.	1.0	9
15491	TLR4/IL-6/IRF1 signaling regulates androgen receptor expression: A potential therapeutic target to overcome taxol resistance in ovarian cancer. <i>Biochemical Pharmacology</i> , 2021, 186, 114456.	2.0	8
15492	Bioinformatics analysis of mRNA and miRNA microarray to identify the key miRNA-mRNA pairs in cisplatin-resistant ovarian cancer. <i>BMC Cancer</i> , 2021, 21, 452.	1.1	3

#	ARTICLE	IF	CITATIONS
15494	Analysis and Classification of Word Co-Occurrence Networks From Alzheimer's Patients and Controls. <i>Frontiers in Computer Science</i> , 2021, 3, .	1.7	7
15495	Carbon Dioxide Concentration Mechanisms in Natural Populations of Marine Diatoms: Insights From Tara Oceans. <i>Frontiers in Plant Science</i> , 2021, 12, 657821.	1.7	26
15496	Identification of gene signatures and potential therapeutic targets for acquired chemotherapy resistance in gastric cancer patients. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 407-422.	0.6	13
15497	Global Genome Mining Reveals the Distribution of Diverse Thioamidated RiPP Biosynthesis Gene Clusters. <i>Frontiers in Microbiology</i> , 2021, 12, 635389.	1.5	8
15500	Computational and In Vitro Analysis of Plumbagin's Molecular Mechanism for the Treatment of Hepatocellular Carcinoma. <i>Frontiers in Pharmacology</i> , 2021, 12, 594833.	1.6	6
15501	Gene network analyses unveil possible molecular basis underlying drug-induced glaucoma. <i>BMC Medical Genomics</i> , 2021, 14, 109.	0.7	3
15502	Identification of novel autophagy-related lncRNAs associated with a poor prognosis of colon adenocarcinoma through bioinformatics analysis. <i>Scientific Reports</i> , 2021, 11, 8069.	1.6	44
15504	Identification of Metastasis-Associated MicroRNAs in Metastatic Melanoma by miRNA Expression Profile and Experimental Validation. <i>Frontiers in Genetics</i> , 2021, 12, 663110.	1.1	9
15505	Investigation of the Mechanism of Traditional Chinese Medicines in Angiogenesis through Network Pharmacology and Data Mining. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	7
15506	Identification and Functional Analysis of Long Non-coding RNAs in Human Pulmonary Microvascular Endothelial Cells Subjected to Cyclic Stretch. <i>Frontiers in Physiology</i> , 2021, 12, 655971.	1.3	4
15507	Comprehensive analyses of competing endogenous RNA networks reveal potential biomarkers for predicting hepatocellular carcinoma recurrence. <i>BMC Cancer</i> , 2021, 21, 436.	1.1	3
15508	AGAP2-AS1 May Promote the Occurrence and Development of Glioblastoma by Sponging miR-9-5p: Evidence From a ceRNA Network. <i>Frontiers in Oncology</i> , 2021, 11, 607989.	1.3	4
15509	CDC20 and PTTG1 are Important Biomarkers and Potential Therapeutic Targets for Metastatic Prostate Cancer. <i>Advances in Therapy</i> , 2021, 38, 2973-2989.	1.3	18
15510	Regulatory role of non-coding RNA in ginseng rusty root symptom tissue. <i>Scientific Reports</i> , 2021, 11, 9211.	1.6	7
15511	A deep convolutional neural network for segmentation of whole-slide pathology images identifies novel tumour cell-perivascular niche interactions that are associated with poor survival in glioblastoma. <i>British Journal of Cancer</i> , 2021, 125, 337-350.	2.9	18
15512	Complementary transcriptomic and proteomic analysis of <i>Bombyx mori</i> middle silk glands reveals a predominant ribosome-biogenesis regulating network during silkworm yellow-cocoon color formation. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 260-270.	0.4	2
15513	Changes in salivary proteins can reflect beneficial physiological effects of ejaculation in the dog. <i>Theriogenology</i> , 2021, 164, 51-57.	0.9	0
15514	Gut microbiota affects the efficacy of Danggui Buxue Tang by affecting plasma concentration of active ingredients. <i>Journal of Ethnopharmacology</i> , 2021, 270, 113835.	2.0	5



#	ARTICLE	IF	CITATIONS
15515	Urban ecology of hosts and vectors of Rickettsia in a rickettsiosis-endemic city of the Yucatan peninsula, Mexico. Acta Tropica, 2021, 216, 105832.	0.9	4
15516	Identification of compounds responsible for the anthelmintic effects of chicory (Cichorium intybus) by molecular networking and bio-guided fractionation. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 15, 105-114.	1.4	17
15517	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
15518	Comprehensive analyses of correlation and survival reveal informative lncRNA prognostic signatures in colon cancer. World Journal of Surgical Oncology, 2021, 19, 104.	0.8	14
15519	Identification of the specific long-noncoding RNAs involved in night-break mediated flowering retardation in Chenopodium quinoa. BMC Genomics, 2021, 22, 284.	1.2	8
15520	A family of pathogen-induced cysteine-rich transmembrane proteins is involved in plant disease resistance. Planta, 2021, 253, 102.	1.6	8
15522	Analysis of differences in the transcriptomic profiles of eutopic and ectopic endometriums in women with ovarian endometriosis. PeerJ, 2021, 9, e11045.	0.9	6
15523	<i>Brassica juncea</i> (L.) Czern. leaves alleviate adjuvant-induced rheumatoid arthritis in rats via modulating the finest disease targets - IL2RA, IL18 and VEGFA. Journal of Biomolecular Structure and Dynamics, 2022, 40, 8155-8168.	2.0	12
15524	Proteomic Studies of Primary Acute Myeloid Leukemia Cells Derived from Patients Before and during Disease-Stabilizing Treatment Based on All-Trans Retinoic Acid and Valproic Acid. Cancers, 2021, 13, 2143.	1.7	6
15525	New World Cactaceae Plants Harbor Diverse Geminiviruses. Viruses, 2021, 13, 694.	1.5	8
15526	Identification of key regulators responsible for dysregulated networks in osteoarthritis by large-scale expression analysis. Journal of Orthopaedic Surgery and Research, 2021, 16, 259.	0.9	8
15527	Identification of key genes and pathways in discoid lupus skin via bioinformatics analysis. Medicine (United States), 2021, 100, e25433.	0.4	10
15528	Identification of Hub Genes Associated With Melanoma Development by Comprehensive Bioinformatics Analysis. Frontiers in Oncology, 2021, 11, 621430.	1.3	8
15529	Identification of differentially expressed miRNAs in human cells infected with different Zika virus strains. Archives of Virology, 2021, 166, 1681-1689.	0.9	4
15530	Fungal biodiversity and metabolic potential of selected fluvisols from the Vistula River valley in Lubelskie, Poland. Applied Soil Ecology, 2021, 160, 103866.	2.1	5
15531	Molecular Dockings and Molecular Dynamics Simulations Reveal the Potency of Different Inhibitors against Xanthine Oxidase. ACS Omega, 2021, 6, 11639-11649.	1.6	20
15532	Quantitative proteomic analysis of extracellular vesicle subgroups isolated by an optimized method combining polymer-based precipitation and size exclusion chromatography. Journal of Extracellular Vesicles, 2021, 10, e12087.	5.5	55
15533	Distinct diagnostic and prognostic values of Glypicans gene expression in patients with hepatocellular carcinoma. BMC Cancer, 2021, 21, 462.	1.1	6

#	ARTICLE	IF	CITATIONS
15534	Chronic HIV infection induces transcriptional and functional reprogramming of innate immune cells. <i>JCI Insight</i> , 2021, 6, .	2.3	33
15535	Identification of Potential Biomarkers From Hepatocellular Carcinoma With MT1 Deletion. <i>Pathology and Oncology Research</i> , 2021, 27, 597527.	0.9	5
15536	Integrated analysis of lncRNA, miRNA and mRNA profiles reveals potential lncRNA functions during early HIV infection. <i>Journal of Translational Medicine</i> , 2021, 19, 135.	1.8	7
15537	Malignant Pleural Mesothelioma Interactome with 364 Novel Protein-Protein Interactions. <i>Cancers</i> , 2021, 13, 1660.	1.7	8
15538	Combined Analysis of Volatile Terpenoid Metabolism and Transcriptome Reveals Transcription Factors Related to Terpene Synthase in Two Cultivars of <i>Dendrobium officinale</i> Flowers. <i>Frontiers in Genetics</i> , 2021, 12, 661296.	1.1	23
15540	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	6.5	25
15541	Identification of VWF as a Novel Biomarker in Lung Adenocarcinoma by Comprehensive Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 639600.	1.3	10
15542	Three-Dimensional Molecular Cartography of the Caribbean Reef-Building Coral <i>Orbicella faveolata</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
15543	Mapping Metabolic Networks in the Brain by Ambient Mass Spectrometry Imaging and Metabolomics. <i>Analytical Chemistry</i> , 2021, 93, 6746-6754.	3.2	35
15544	In Silico Mining of Terpenes from Red-Sea Invertebrates for SARS-CoV-2 Main Protease (Mpro) Inhibitors. <i>Molecules</i> , 2021, 26, 2082.	1.7	39
15545	Whole transcriptome sequencing and integrated network analysis elucidates the effects of 3,8-Di-O-methylellagic acid 2-O-glucoside derived from <i>Sanguisorba officinalis</i> L., a novel differentiation inducer on erythroleukemia cells. <i>Pharmacological Research</i> , 2021, 166, 105491.	3.1	7
15546	Systemic analysis of the expression levels and prognosis of breast cancer-related cadherins. <i>Experimental Biology and Medicine</i> , 2021, 246, 1706-1720.	1.1	8
15547	Next-generation yeast-two-hybrid analysis with Y2H-SCORES identifies novel interactors of the MLA immune receptor. <i>PLoS Computational Biology</i> , 2021, 17, e1008890.	1.5	14
15548	Transcriptome analysis of placentae reveals HELLP syndrome exhibits a greater extent of placental metabolic dysfunction than preeclampsia. <i>Hypertension in Pregnancy</i> , 2021, 40, 134-143.	0.5	3
15549	Quantitative Assessment of Nucleocytoplasmic Large DNA Virus and Host Interactions Predicted by Co-occurrence Analyses. <i>MSphere</i> , 2021, 6, .	1.3	22
15550	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. <i>Molecular Cell</i> , 2021, 81, 1453-1468.e12.	4.5	31
15551	A Novel Transcription Factor-Based Prognostic Signature in Endometrial Cancer: Establishment and Validation. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 2579-2598.	1.0	7
15552	Plasma Proteins As Biodosimetric Markers of Low-Dose Radiation in Mice. <i>Dose-Response</i> , 2021, 19, 155932582110162.	0.7	2

#	ARTICLE	IF	CITATIONS
15553	Quantitative proteomic analysis of cortex in the depressive-like behavior of rats induced by the simulated complex space environment. <i>Journal of Proteomics</i> , 2021, 237, 104144.	1.2	4
15554	Utilizing network pharmacology and molecular docking to explore the underlying mechanism of Guizhi Fuling Wan in treating endometriosis. <i>PeerJ</i> , 2021, 9, e11087.	0.9	7
15555	Identification of shell-color-related microRNAs in the Manila clam <i>Ruditapes philippinarum</i> using high-throughput sequencing of small RNA transcriptomes. <i>Scientific Reports</i> , 2021, 11, 8044.	1.6	10
15556	CYP1A2, 2A13, and 3A4 network and interaction with aflatoxin B <sub>1</sub> . <i>World Mycotoxin Journal</i> , 2021, 14, 179-189.	0.8	1
15557	Construction of Unified Human Antimicrobial and Immunomodulatory Peptide Database and Examination of Antimicrobial and Immunomodulatory Peptides in Alzheimer's Disease Using Network Analysis of Proteomics Datasets. <i>Frontiers in Genetics</i> , 2021, 12, 633050.	1.1	8
15558	Distribution and diversity of eukaryotic microalgae in Kuwait waters assessed using 18S rRNA gene sequencing. <i>PLoS ONE</i> , 2021, 16, e0250645.	1.1	7
15560	Transcriptomic Profiling of Fe-Responsive lncRNAs and Their Regulatory Mechanism in Rice. <i>Genes</i> , 2021, 12, 567.	1.0	6
15561	Specialized Metabolites from Ribosome Engineered Strains of <i>Streptomyces clavuligerus</i> . <i>Metabolites</i> , 2021, 11, 239.	1.3	13
15562	multiSLIDE is a web server for exploring connected elements of biological pathways in multi-omics data. <i>Nature Communications</i> , 2021, 12, 2279.	5.8	12
15563	Putative plasmid prophages of <i>Bacillus cereus sensu lato</i> may hold the key to undiscovered phage diversity. <i>Scientific Reports</i> , 2021, 11, 7611.	1.6	15
15564	Integrated Omics Strategy Reveals Cyclic Lipopeptides Empedopeptins from <i>Massilia</i> sp. YMA4 and Their Biosynthetic Pathway. <i>Marine Drugs</i> , 2021, 19, 209.	2.2	5
15565	Identification of Key Genes and Underlying Mechanisms in Acute Kawasaki Disease Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2021, 27, e930547.	0.5	6
15568	Induced Torpor as a Countermeasure for Low Dose Radiation Exposure in a Zebrafish Model. <i>Cells</i> , 2021, 10, 906.	1.8	8
15569	Gaussian graphical modeling of the serum exposome and metabolome reveals interactions between environmental chemicals and endogenous metabolites. <i>Scientific Reports</i> , 2021, 11, 7607.	1.6	12
15570	Sex-Biased lncRNA Signature in Fetal Growth Restriction (FGR). <i>Cells</i> , 2021, 10, 921.	1.8	5
15571	Integrated bioinformatics analysis to identify key genes related to the prognosis of esophageal squamous cell carcinoma. <i>Translational Cancer Research</i> , 2021, 10, 1679-1691.	0.4	1
15572	Transcriptomic analysis to infer key molecular players involved during host response to NDV challenge in <i>Gallus gallus</i> (Leghorn & Fayoumi). <i>Scientific Reports</i> , 2021, 11, 8486.	1.6	4
15573	Activation of Blood Vessel Development in Endometrial Stromal Cells In Vitro Cocultured with Human Peri-Implantation Embryos Revealed by Single-Cell RNA-Seq. <i>Life</i> , 2021, 11, 367.	1.1	4

#	ARTICLE	IF	CITATIONS
15574	Fibrotic expression profile analysis reveals repurposed drugs with potential anti-fibrotic mode of action. PLoS ONE, 2021, 16, e0249687.	1.1	6
15575	Similarity Calculation, Enrichment Analysis, and Ontology Visualization of Biomedical Ontologies using UFO. Current Protocols, 2021, 1, e115.	1.3	1
15576	Targeted transcriptome analysis using synthetic long read sequencing uncovers isoform reprogramming in the progression of colon cancer. Communications Biology, 2021, 4, 506.	2.0	10
15578	In Silico Exploration of the Potential Role of Acetaminophen and Pesticides in the Etiology of Autism Spectrum Disorder. Toxics, 2021, 9, 97.	1.6	0
15579	Algae Biofilm Reduces Microbe-Derived Dissolved Organic Nitrogen Discharges: Performance and Mechanisms. Environmental Science & Technology, 2021, 55, 6227-6238.	4.6	42
15580	Seasonal marine microorganisms change neighbours under contrasting environmental conditions. Environmental Microbiology, 2021, 23, 2592-2604.	1.8	18
15581	Transcriptomic, proteomic, and physiological studies reveal key players in wheat nitrogen use efficiency under both high and low nitrogen supply. Journal of Experimental Botany, 2021, 72, 4435-4456.	2.4	19
15582	Species-Specific Deamidation of RIG-I Reveals Collaborative Action between Viral and Cellular Deamidases in HSV-1 Lytic Replication. MBio, 2021, 12, .	1.8	9
15583	Small extracellular vesicle-encapsulated miR-181b-5p, miR-222-3p and let-7a-5p: Next generation plasma biopsy-based diagnostic biomarkers for inflammatory breast cancer. PLoS ONE, 2021, 16, e0250642.	1.1	26
15584	Interacting impact of maternal inflammatory response and stress on the amygdala transcriptome of pigs. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	13
15585	Single-Cell RNA Sequencing in Parkinson's Disease. Biomedicines, 2021, 9, 368.	1.4	20
15586	An <i>in vivo</i> Interaction Network of DNA-Repair Proteins: A Snapshot at Double Strand Break Repair in <i>Deinococcus radiodurans</i> . Journal of Proteome Research, 2021, 20, 3242-3255.	1.8	7
15587	Nuclear Leukocyte Immunoglobulin-like Receptor A3 Is Monomeric and Is Involved in Multiple Layers of Regulated Gene Expression and Translation. Journal of Proteome Research, 2021, 20, 3078-3089.	1.8	1
15588	The transcriptomic landscapes of rice cultivars with diverse root system architectures grown in upland field conditions. Plant Journal, 2021, 106, 1177-1190.	2.8	17
15589	Mild reductions in guard cell sucrose synthase 2 expression leads to slower stomatal opening and decreased whole plant transpiration in <i>Nicotiana tabacum</i> L. Environmental and Experimental Botany, 2021, 184, 104370.	2.0	8
15590	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. Biomolecules, 2021, 11, 622.	1.8	18
15591	Single human oocyte transcriptome analysis reveals distinct maturation stage-dependent pathways impacted by age. Aging Cell, 2021, 20, e13360.	3.0	43
15592	Effect of milk replacer allowance on calf faecal bacterial community profiles and fermentation. Animal Microbiome, 2021, 3, 27.	1.5	14

#	ARTICLE	IF	CITATIONS
15593	Molecular Mechanism of Small-Molecule Inhibitors in Blocking the PD-1/PD-L1 Pathway through PD-L1 Dimerization. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4766.	1.8	21
15594	Alterations to the Cardiac Metabolome Induced by Chronic <i>T. cruzi</i> Infection Relate to the Degree of Cardiac Pathology. <i>ACS Infectious Diseases</i> , 2021, 7, 1638-1649.	1.8	17
15595	Reboot: a straightforward approach to identify genes and splicing isoforms associated with cancer patient prognosis. <i>NAR Cancer</i> , 2021, 3, zcab024.	1.6	8
15596	Simultaneous removal of nitrite and organics in a biofilm-enhanced high-salt wastewater treatment system via mixotrophic denitrification coupled with sulfate reduction. <i>Journal of Water Process Engineering</i> , 2021, 40, 101976.	2.6	24
15597	Discovery and functional interrogation of SARS-CoV-2 RNA-host protein interactions. <i>Cell</i> , 2021, 184, 2394-2411.e16.	13.5	141
15598	Transcriptome architecture reveals genetic networks of bolting regulation in spinach. <i>BMC Plant Biology</i> , 2021, 21, 179.	1.6	13
15599	Comparative Transcriptomic Analysis of the Hematopoietic System between Human and Mouse by Single Cell RNA Sequencing. <i>Cells</i> , 2021, 10, 973.	1.8	6
15600	Identification of a prognostic long noncoding RNA signature in lung squamous cell carcinoma: a population-based study with a mean follow-up of 3.5 years. <i>Archives of Public Health</i> , 2021, 79, 61.	1.0	9
15601	Deciphering Pharmacological Mechanism of Buyang Huanwu Decoction for Spinal Cord Injury by Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-20.	0.5	3
15604	Genetic diversity in global chicken breeds in relation to their genetic distances to wild populations. <i>Genetics Selection Evolution</i> , 2021, 53, 36.	1.2	9
15605	Discovering key transcriptomic regulators in pancreatic ductal adenocarcinoma using Dirichlet process Gaussian mixture model. <i>Scientific Reports</i> , 2021, 11, 7853.	1.6	11
15606	Genomic Correlates of DNA Damage in Breast Cancer Subtypes. <i>Cancers</i> , 2021, 13, 2117.	1.7	3
15607	CTNNB1 S37C mutation causing cells proliferation and migration coupled with molecular mechanisms in lung adenocarcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 681-681.	0.7	2
15608	Development of a prognostic index and screening of prognosis related genes based on an immunogenomic landscape analysis of bladder cancer. <i>Aging</i> , 2021, 13, 12099-12112.	1.4	19
15609	Transcriptional signatures in prefrontal cortex confer vulnerability versus resilience to food and cocaine addiction-like behavior. <i>Scientific Reports</i> , 2021, 11, 9076.	1.6	17
15610	Network Pharmacology-Based Investigation of the Therapeutic Mechanisms of Action of Danning Tablets in Nonalcoholic Fatty Liver Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	6
15611	Weighted Gene Co-expression Network Analysis Identifies CALD1 as a Biomarker Related to M2 Macrophages Infiltration in Stage III and IV Mismatch Repair-Proficient Colorectal Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 649363.	1.6	10
15612	NREM delta power and AD-relevant tauopathy are associated with shared cortical gene networks. <i>Scientific Reports</i> , 2021, 11, 7797.	1.6	2

#	ARTICLE	IF	CITATIONS
15613	Stability Assessment of the Rumen Bacterial and Archaeal Communities in Dairy Cows Within a Single Lactation and Its Association With Host Phenotype. <i>Frontiers in Microbiology</i> , 2021, 12, 636223.	1.5	4
15614	Identification of hub genes related to the progression of type 1 diabetes by computational analysis. <i>BMC Endocrine Disorders</i> , 2021, 21, 61.	0.9	11
15615	Investigation of the Initial Host Response of Na <sup>+</sup> -ve Atlantic Salmon ( <i>Salmo salar</i> ) Inoculated with <i>Paramoeba perurans</i> . <i>Microorganisms</i> , 2021, 9, 746.	1.6	2
15616	The VRNetzer platform enables interactive network analysis in Virtual Reality. <i>Nature Communications</i> , 2021, 12, 2432.	5.8	33
15617	Genome-wide identification, evolutionary relationship and expression analysis of AGO, DCL and RDR family genes in tea. <i>Scientific Reports</i> , 2021, 11, 8679.	1.6	11
15618	Altered Food Habits? Understanding the Feeding Preference of Free-Ranging Gray Langurs Within an Urban Settlement. <i>Frontiers in Psychology</i> , 2021, 12, 649027.	1.1	6
15619	Integrating Network Pharmacology and Experimental Validation to Decipher the Mechanism of Action of Huanglian Jiedu Decoction in Treating Atherosclerosis. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 1779-1795.	2.0	11
15620	Expression and regulatory roles of lncRNAs in G-CIMP-low vs G-CIMP-high Glioma: an in-silico analysis. <i>Journal of Translational Medicine</i> , 2021, 19, 182.	1.8	5
15623	Genome-wide association study and transcriptome comparison reveal novel QTL and candidate genes that control petal size in rapeseed. <i>Journal of Experimental Botany</i> , 2021, 72, 3597-3610.	2.4	7
15624	Building Protein-Protein and Protein-Glycosaminoglycan Interaction Networks Using MatrixDB, the Extracellular Matrix Interaction Database. <i>Current Protocols</i> , 2021, 1, e47.	1.3	9
15625	Integrative Systems Biology Approaches to Identify Potential Biomarkers and Pathways of Cervical Cancer. <i>Journal of Personalized Medicine</i> , 2021, 11, 363.	1.1	9
15626	Genomic diversity and CRISPR-Cas systems in the cyanobacterium <i>Nostoc</i> in the High Arctic. <i>Environmental Microbiology</i> , 2021, 23, 2955-2968.	1.8	7
15627	LncRNA Inc_13814 promotes the cells apoptosis in granulosa cells of duck by acting as a miR-145-4 sponge. <i>Cell Cycle</i> , 2021, 20, 927-942.	1.3	4
15628	SETS: A Seed-Dense-Expanding Model-Based Topological Structure for the Prediction of Overlapping Protein Complexes. <i>Pertanika Journal of Science and Technology</i> , 2021, 29, .	0.3	1
15629	Terpenoid Biosynthesis Dominates among Secondary Metabolite Clusters in Mucoromycotina Genomes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 285.	1.5	14
15630	Integrated Bioinformatics Analysis for the Screening of Associated Pathways and Therapeutic Drugs in Coronavirus Disease 2019. <i>Archives of Medical Research</i> , 2021, 52, 304-310.	1.5	4
15631	CD2 Is a Novel Immune-Related Prognostic Biomarker of Invasive Breast Carcinoma That Modulates the Tumor Microenvironment. <i>Frontiers in Immunology</i> , 2021, 12, 664845.	2.2	22
15632	Discovering novel cancer bio-markers in acquired lapatinib resistance using Bayesian methods. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	1



#	ARTICLE	IF	CITATIONS
15633	Same but different â€” Molecular comparison of human KTI12 and PSTK. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021, 1868, 118945.	1.9	1
15634	Proteomic pipeline for biomarker hunting of defective bovine meat assisted by liquid chromatography-mass spectrometry analysis and chemometrics. <i>Journal of Proteomics</i> , 2021, 238, 104153.	1.2	14
15635	A novel immune-related prognostic signature in epithelial ovarian carcinoma. <i>Aging</i> , 2021, 13, 10289-10311.	1.4	8
15637	The Use of Traditional Chinese Medicine in Relieving EGFR-TKI-Associated Diarrhea Based on Network Pharmacology and Data Mining. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-16.	0.5	3
15638	Transcriptional circuitry atlas of genetic diverse unstimulated murine and human macrophages define disparity in population-wide innate immunity. <i>Scientific Reports</i> , 2021, 11, 7373.	1.6	7
15639	A Comparative Cross-Platform Meta-Analysis to Identify Potential Biomarker Genes Common to Endometriosis and Recurrent Pregnancy Loss. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3349.	1.3	1
15640	Identification of a Gene Prognostic Signature for Oral Squamous Cell Carcinoma by RNA Sequencing and Bioinformatics. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	8
15641	Identification of hub genes associated with obesity-induced hepatocellular carcinoma risk based on integrated bioinformatics analysis. <i>Medical Oncology</i> , 2021, 38, 63.	1.2	19
15642	Enhanced Targeting and Immune Activation of Tumor Microenvironment by Nanomodified Antiâ€”PD1 in Liver Cancer. <i>Advanced Therapeutics</i> , 2021, 4, 2100048.	1.6	7
15643	Soil microbial interconnections along ecological restoration gradients of lowland forests after slash-and-burn agriculture. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
15644	Zebrafish modeling mimics developmental phenotype of patients with <sc><i>RAPGEF1</i></sc> mutation. <i>Clinical Genetics</i> , 2021, 100, 144-155.	1.0	1
15645	The fourth scientific discovery paradigm for precision medicine and healthcare: Challenges ahead. <i>Precision Clinical Medicine</i> , 2021, 4, 80-84.	1.3	21
15646	Integrative analysis of the gastric cancer long nonâ€”coding RNAâ€”associated competing endogenous RNA network. <i>Oncology Letters</i> , 2021, 21, 456.	0.8	6
15647	Global Effects of Heroin Self-Administration on microRNA Expression Profiles in Rat Brain. <i>Neurochemical Journal</i> , 2021, 15, 187-195.	0.2	0
15648	Dual RNA Sequencing Meta-analysis in Plasmodium Infection Identifies Host-Parasite Interactions. <i>MSystems</i> , 2021, 6, .	1.7	5
15650	The Protein Interactome of Glycolysis in Escherichia coli. <i>Proteomes</i> , 2021, 9, 16.	1.7	3
15651	Not just shrivelling: time-series profiling of the biochemical changes in Corvina (&lt;i>Vitis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	0.7	6
15652	Identification of Plasmodium falciparum-specific protein PIESP2 as a novel virulence factor related to cerebral malaria. <i>International Journal of Biological Macromolecules</i> , 2021, 177, 535-547.	3.6	4

#	ARTICLE	IF	CITATIONS
15653	Comprehensive analysis of IgA nephropathy expression profiles: identification of potential biomarkers and therapeutic agents. <i>BMC Nephrology</i> , 2021, 22, 137.	0.8	9
15654	Prenatal Skeletal Muscle Transcriptome Analysis Reveals Novel MicroRNA-mRNA Networks Associated with Intrauterine Growth Restriction in Pigs. <i>Cells</i> , 2021, 10, 1007.	1.8	15
15656	Weighted gene co-expression network analysis and drug-gene interaction bioinformatics uncover key genes associated with various presentations of malaria infection in African children and major drug candidates. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104723.	1.0	4
15657	Inositol treatment inhibits medulloblastoma through suppression of epigenetic-driven metabolic adaptation. <i>Nature Communications</i> , 2021, 12, 2148.	5.8	20
15658	Exploring the Pharmacological Mechanism of Duhuo Jisheng Decoction in Treating Osteoporosis Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-21.	0.5	16
15659	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. <i>Immunity</i> , 2021, 54, 737-752.e10.	6.6	58
15660	Comprehensive Analysis of Prognostic and Genetic Signatures for General Transcription Factor III (GTF3) in Clinical Colorectal Cancer Patients Using Bioinformatics Approaches. <i>Current Issues in Molecular Biology</i> , 2021, 43, 2-20.	1.0	20
15661	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .	6.0	91
15662	A single-cell analysis of the Arabidopsis vegetative shoot apex. <i>Developmental Cell</i> , 2021, 56, 1056-1074.e8.	3.1	145
15663	Rubisco activase A (RcaA) is a central node in overlapping gene network of drought and salinity in Barley ( <i>Hordeum vulgare</i> L.) and may contribute to combined stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2021, 161, 248-258.	2.8	17
15664	RNA-seq Characterization of Sex-Differences in Adipose Tissue of Obesity Affected Patients: Computational Analysis of Differentially Expressed Coding and Non-Coding RNAs. <i>Journal of Personalized Medicine</i> , 2021, 11, 352.	1.1	8
15665	Analysis of crucial genes, pathways and construction of the molecular regulatory networks in vascular smooth muscle cell calcification. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 589.	0.8	3
15667	Screening of gene markers related to the prognosis of metastatic skin cutaneous melanoma based on Logit regression and survival analysis. <i>BMC Medical Genomics</i> , 2021, 14, 96.	0.7	4
15669	An order independent algorithm for inferring gene regulatory network using quantile value for conditional independence tests. <i>Scientific Reports</i> , 2021, 11, 7605.	1.6	7
15671	Transcriptome-Wide Gene Expression in a Murine Model of Ventilator-Induced Lung Injury. <i>Disease Markers</i> , 2021, 2021, 1-23.	0.6	1
15672	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
15673	Screening and Identification of Key Microenvironment-Related Genes in Non-functioning Pituitary Adenoma. <i>Frontiers in Genetics</i> , 2021, 12, 627117.	1.1	6
15674	Investigating the effects of chronic perinatal alcohol and combined nicotine and alcohol exposure on dopaminergic and non-dopaminergic neurons in the VTA. <i>Scientific Reports</i> , 2021, 11, 8706.	1.6	2

#	ARTICLE	IF	CITATIONS
15675	Diagnostic, Therapeutic, and Prognostic Value of the Thrombospondin Family in Gastric Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647095.	1.6	10
15676	Expression analysis of progesterone-regulated miRNAs in cells derived from human glioblastoma. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	0
15677	Extracting knowledge networks from plant scientific literature: potato tuber flesh color as an exemplary trait. <i>BMC Plant Biology</i> , 2021, 21, 198.	1.6	3
15679	A Complex Gene Network Mediated by Ethylene Signal Transduction TFs Defines the Flower Induction and Differentiation in <i>Olea europaea</i> L.. <i>Genes</i> , 2021, 12, 545.	1.0	2
15680	Exploration of targets and molecular mechanisms of cinnamaldehyde in overcoming fulvestrant-resistant breast cancer: a bioinformatics study. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2021, 10, 1.	1.2	2
15681	Prediction of <i>Streptococcus uberis</i> clinical mastitis treatment success in dairy herds by means of mass spectrometry and machine-learning. <i>Scientific Reports</i> , 2021, 11, 7736.	1.6	3
15682	Shared Neurodevelopmental Perturbations Can Lead to Intellectual Disability in Individuals with Distinct Rare Chromosome Duplications. <i>Genes</i> , 2021, 12, 632.	1.0	0
15684	Establishing a consensus for the hallmarks of cancer based on gene ontology and pathway annotations. <i>BMC Bioinformatics</i> , 2021, 22, 178.	1.2	15
15685	Potential Genes and Mechanisms Linking Intracerebral Hemorrhage and Depression: A Bioinformatics-Based Study. <i>International Journal of General Medicine</i> , 2021, Volume 14, 1213-1226.	0.8	2
15686	Identification of Key Genes Related to the Prognosis of Esophageal Squamous Cell Carcinoma Based on Chip Re-Annotation. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3229.	1.3	3
15689	Novel Insight Into the Role of Immune Dysregulation in Amyotrophic Lateral Sclerosis Based on Bioinformatic Analysis. <i>Frontiers in Neuroscience</i> , 2021, 15, 657465.	1.4	9
15690	Biomarkers mining for spinal cord injury based on integrated multi-transcriptome expression profile data. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 267.	0.9	9
15692	Integrating transcriptome, co-expression and QTL-seq analysis reveals that primary root growth in maize is regulated via flavonoid biosynthesis and auxin signal transduction. <i>Journal of Experimental Botany</i> , 2021, 72, 4773-4795.	2.4	26
15693	Integrative biochemical, proteomics and metabolomics cerebrospinal fluid biomarkers predict clinical conversion to multiple sclerosis. <i>Brain Communications</i> , 2021, 3, fcab084.	1.5	14
15694	Sifting environmental DNA metabarcoding data sets for rapid reconstruction of marine food webs. <i>Fish and Fisheries</i> , 2021, 22, 822-833.	2.7	16
15695	An Alternative and Conserved Cell Wall Enzyme That Can Substitute for the Lipid II Synthase MurG. <i>MBio</i> , 2021, 12, .	1.8	6
15696	Identification of Hub Genes and Construction of a Transcriptional Regulatory Network Associated With Tumor Recurrence in Colorectal Cancer by Weighted Gene Co-expression Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 649752.	1.1	9
15697	Five long non-coding RNAs establish a prognostic nomogram and construct a competing endogenous RNA network in the progression of non-small cell lung cancer. <i>BMC Cancer</i> , 2021, 21, 457.	1.1	9

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15698	The First Contact of Human Dendritic Cells With <i>Trypanosoma cruzi</i> Reveals Response to Virus as an Unexplored Central Pathway. <i>Frontiers in Immunology</i> , 2021, 12, 638020.	2.2	5
15699	The evaluation of the antidiabetic effects of red wine polyphenols with the view of in silico prediction methods. <i>Food Bioscience</i> , 2021, 40, 100920.	2.0	6
15700	Long-term chronic caloric restriction alters miRNA profiles in the brain of ageing mice. <i>British Journal of Nutrition</i> , 2022, 127, 641-652.	1.2	4
15701	Sex-Specific Control of Human Heart Maturation by the Progesterone Receptor. <i>Circulation</i> , 2021, 143, 1614-1628.	1.6	42
15702	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021, 19, e3001144.	2.6	23
15703	Identification of Expression Patterns and Potential Prognostic Significance of m5C-Related Regulators in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 592107.	1.3	12
15704	Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development. <i>Alzheimer's and Dementia</i> , 2021, 17, 1509-1527.	0.4	50
15705	A Network Pharmacology Study to Uncover the Multiple Molecular Mechanism of the Chinese Patent Medicine Toujiequwen Granules in the Treatment of Corona Virus Disease 2019 (COVID-19). <i>Current Medical Science</i> , 2021, 41, 297-305.	0.7	2
15706	Exploring effects of DNA methylation and gene expression on pan-cancer drug response by mathematical models. <i>Experimental Biology and Medicine</i> , 2021, 246, 1626-1642.	1.1	1
15707	Combining 1H-NMR-based metabolomics and network pharmacology to dissect the mechanism of antidepressant effect of <i>Milletia speciosa</i> Champ on mouse with chronic unpredictable mild stress-induced depression. <i>Journal of Pharmacy and Pharmacology</i> , 2021, 73, 881-892.	1.2	5
15708	Bioinformatics and system biology approach to identify the influences of SARS-CoV-2 infections to idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease patients. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	57
15709	How higher goals are constructed and collapse under stress: A hierarchical Bayesian control systems perspective. <i>Neuroscience and Biobehavioral Reviews</i> , 2021, 123, 257-285.	2.9	16
15710	Topological clustering of regulatory genes confers pathogenic tolerance to cassava brown streak virus (CBSV) in cassava. <i>Scientific Reports</i> , 2021, 11, 7872.	1.6	2
15711	mi-IsoNet: systems-scale microRNA landscape reveals rampant isoform-mediated gain of target interaction diversity and signaling specificity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
15712	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
15713	Comparative Perturbation-Based Modeling of the SARS-CoV-2 Spike Protein Binding with Host Receptor and Neutralizing Antibodies: Structurally Adaptable Allosteric Communication Hotspots Define Spike Sites Targeted by Global Circulating Mutations. <i>Biochemistry</i> , 2021, 60, 1459-1484.	1.2	62
15714	SARS-CoV-2 infection of human iPSC-derived cardiac cells reflects cytopathic features in hearts of patients with COVID-19. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	143
15715	Evolutionarily conserved hierarchical gene regulatory networks for plant salt stress response. <i>Nature Plants</i> , 2021, 7, 787-799.	4.7	45

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15716	Identifying the Potential Therapeutic Targets for Atopic Dermatitis Through the Immune Infiltration Analysis and Construction of a ceRNA Network. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2021, Volume 14, 437-453.	0.8	11
15719	Molecular Characterization of the Coat Protein Gene of Greek Apple Stem Pitting Virus Isolates: Evolution through Deletions, Insertions, and Recombination Events. <i>Plants</i> , 2021, 10, 917.	1.6	4
15720	LncRNA PART1 Promotes Proliferation and Migration, Is Associated with Cancer Stem Cells, and Alters the miRNA Landscape in Triple-Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 2644.	1.7	13
15721	<scp>Tenascinâ€C</scp> regulates migration of <scp>SOX10</scp> tendon stem cells via integrinâ€±9 for promoting patellar tendon remodeling. <i>BioFactors</i> , 2021, 47, 768-777.	2.6	8
15722	A novel diagnostic signature based on three circulating exosomal mircoRNAs for chronic obstructive pulmonary disease. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 717.	0.8	12
15723	Based on Plasma Metabonomics and Network Pharmacology Exploring the Therapeutic Mechanism of <i>Gynura procumbens</i> on Type 2 Diabetes. <i>Frontiers in Pharmacology</i> , 2021, 12, 674379.	1.6	3
15724	Auxiliary rapid identification of pathogenic and antagonistic microorganisms associated with <i>Coptis chinensis</i> root rot by high-throughput sequencing. <i>Scientific Reports</i> , 2021, 11, 11141.	1.6	8
15725	Construction of mRNA Regulatory Networks Reveals the Key Genes in Atrial Fibrillation. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	0.7	0
15726	Extremes of age are associated with differences in the expression of selected pattern recognition receptor genes and ACE2, the receptor for SARS-CoV-2: implications for the epidemiology of COVID-19 disease. <i>BMC Medical Genomics</i> , 2021, 14, 138.	0.7	12
15727	Differential Regulation of Maize and Sorghum Orthologs in Response to the Fungal Pathogen <i>Exserohilum turcicum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 675208.	1.7	6
15728	Molecular mechanisms, immune cell infiltration, and potential drugs for prostate cancer. <i>Cancer Biomarkers</i> , 2021, 31, 87-96.	0.8	8
15729	Molecular Networking Leveraging the Secondary Metabolomes Space of <i>Halophila stipulaceae</i> (Forsk.) Aschers. and <i>Thalassia hemprichii</i> (Ehrenb. ex Solms) Asch. in Tandem with Their Chemosystematics and Antidiabetic Potentials. <i>Marine Drugs</i> , 2021, 19, 279.	2.2	13
15731	Bioinformatics analysis and identification of genes and molecular pathways in steroid-induced osteonecrosis of the femoral head. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 327.	0.9	10
15733	Plasma Protein Biomarkers Associated with Higher Ovarian Cancer Risk in BRCA1/2 Carriers. <i>Cancers</i> , 2021, 13, 2300.	1.7	6
15734	Shifts in abundance and network complexity of coral bacteria in response to elevated ammonium stress. <i>Science of the Total Environment</i> , 2021, 768, 144631.	3.9	20
15735	Urothelial Cancer Associated 1 (UCA1) and miR-193 Are Two Non-coding RNAs Involved in Trophoblast Fusion and Placental Diseases. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 633937.	1.8	6
15736	Genome-Wide Identification of Tannase Genes and Their Function of Wound Response and Astringent Substances Accumulation in Juglandaceae. <i>Frontiers in Plant Science</i> , 2021, 12, 664470.	1.7	4
15737	Commonly and Specifically Activated Defense Responses in Maize Disease Lesion Mimic Mutants Revealed by Integrated Transcriptomics and Metabolomics Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 638792.	1.7	5

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15738	Weighted Gene Co-Expression Network Analysis Reveals Key Genes and Potential Drugs in Abdominal Aortic Aneurysm. <i>Biomedicines</i> , 2021, 9, 546.	1.4	6
15739	Do Autism Spectrum and Autoimmune Disorders Share Predisposition Gene Signature Due to mTOR Signaling Pathway Controlling Expression?. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5248.	1.8	7
15740	A miR-375/YAP axis regulates neuroendocrine differentiation and tumorigenesis in lung carcinoid cells. <i>Scientific Reports</i> , 2021, 11, 10455.	1.6	7
15741	Transcriptome and Metabolome Reveal Salt-Stress Responses of Leaf Tissues from <i>Dendrobium officinale</i> . <i>Biomolecules</i> , 2021, 11, 736.	1.8	32
15742	Modular Molecular Weaponry Plays a Key Role in Competition Within an Environmental <i>Vibrio cholerae</i> Population. <i>Frontiers in Microbiology</i> , 2021, 12, 671092.	1.5	15
15743	Development of an Immune-Related Prognostic Index Associated With Glioblastoma. <i>Frontiers in Neurology</i> , 2021, 12, 610797.	1.1	5
15744	Multiple cellular compartments engagement in <i>Nicotiana benthamiana</i> -peanut stunt virus-satRNA interactions revealed by systems biology approach. <i>Plant Cell Reports</i> , 2021, 40, 1247-1267.	2.8	4
15745	Immune-Related Gene <i>SERPINE1</i> Is a Novel Biomarker for Diffuse Lower-Grade Gliomas via Large-Scale Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 646060.	1.3	22
15746	A Seed Mucilage-Degrading Fungus From the Rhizosphere Strengthens the Plant-Soil-Microbe Continuum and Potentially Regulates Root Nutrients of a Cold Desert Shrub. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 538-546.	1.4	1
15748	Aberrant methylation modifications reflect specific drug responses in small cell lung cancer. <i>Genomics</i> , 2021, 113, 1114-1126.	1.3	4
15749	Quercetin for COVID-19 and DENGUE co-infection: a potential therapeutic strategy of targeting critical host signal pathways triggered by SARS-CoV-2 and DENV. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
15750	Increased Alpha-Band Connectivity During Tic Suppression in Children With Tourette Syndrome Revealed by Source Electroencephalography Analyses. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2021, , .	1.1	6
15751	Tomato fruit quality traits and metabolite content are affected by reciprocal crosses and heterosis. <i>Journal of Experimental Botany</i> , 2021, 72, 5407-5425.	2.4	10
15753	CWENA: gene co-expression networks analysis and extended modules characterization in a single Bioconductor package. <i>BMC Bioinformatics</i> , 2021, 22, 267.	1.2	20
15754	Genomic evidence supports an independent history of Levantine and Eurasian grapevines. <i>Plants People Planet</i> , 2021, 3, 414-427.	1.6	13
15755	Macrophage mediated recognition and clearance of <i>Borrelia burgdorferi</i> elicits MyD88-dependent and -independent phagosomal signals that contribute to phagocytosis and inflammation. <i>BMC Immunology</i> , 2021, 22, 32.	0.9	10
15756	Intersection of Syphilis and Human Immunodeficiency Virus (HIV) Networks to Identify Opportunities to Enhance HIV Prevention. <i>Clinical Infectious Diseases</i> , 2022, 74, 498-506.	2.9	2
15757	Quantitative proteomics analysis identifies salivary biomarkers for early detection of pregnancy loss in a Singaporean cohortâ€”A pilot study. <i>Proteomics - Clinical Applications</i> , 2021, 15, 2000068.	0.8	3



#	ARTICLE	IF	CITATIONS
15758	Multi-omics data integration and network-based analysis drives a multiplex drug repurposing approach to a shortlist of candidate drugs against COVID-19. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
15759	Continent-wide genomic signatures of adaptation to urbanisation in a songbird across Europe. <i>Nature Communications</i> , 2021, 12, 2983.	5.8	34
15760	Quantitative Analysis of Tyrosine Phosphorylation from FFPE Tissues Reveals Patient-Specific Signaling Networks. <i>Cancer Research</i> , 2021, 81, 3930-3941.	0.4	16
15761	Disentangling the aging gene expression network of termite queens. <i>BMC Genomics</i> , 2021, 22, 339.	1.2	10
15762	Diversity and distribution of viruses inhabiting the deepest ocean on Earth. <i>ISME Journal</i> , 2021, 15, 3094-3110.	4.4	55
15763	Genome wide analysis of <i>Mycobacterium leprae</i> for identification of putative microRNAs and their possible targets in human. <i>Biologia (Poland)</i> , 2021, 76, 2437-2454.	0.8	0
15764	â€œSomehow, I Wasnâ€™t Drawn into The Editorial Office of <i>Novyi Mir</i> â€ Digital Approaches to the Literary Environment of Late Socialist Journals. <i>Russian Literature</i> , 2021, 122-123, 163-191.	0.0	0
15765	In <i>Arabidopsis thaliana</i> Cd differentially impacts on hormone genetic pathways in the methylation defective <i>ddc</i> mutant compared to wild type. <i>Scientific Reports</i> , 2021, 11, 10965.	1.6	16
15766	Experimental and natural evidence of SARS-CoV-2-infection-induced activation of type I interferon responses. <i>IScience</i> , 2021, 24, 102477.	1.9	49
15767	Exploration of Crucial Mediators for Carotid Atherosclerosis Pathogenesis Through Integration of Microbiome, Metabolome, and Transcriptome. <i>Frontiers in Physiology</i> , 2021, 12, 645212.	1.3	11
15768	MIR-NATs repress MAPT translation and aid proteostasis in neurodegeneration. <i>Nature</i> , 2021, 594, 117-123.	13.7	29
15769	Differential Membrane Protein Profile in Bovine X- and Y-Sperm. <i>Journal of Proteome Research</i> , 2021, 20, 3031-3042.	1.8	7
15770	Transcriptional Analysis of Liver Tissue Identifies Distinct Phenotypes of Indeterminate Pediatric Acute Liver Failure. <i>Hepatology Communications</i> , 2021, 5, 1373-1384.	2.0	15
15771	Biosynthesis and Heterologous Production of Mycosporine-Like Amino Acid Palythines. <i>Journal of Organic Chemistry</i> , 2021, 86, 11160-11168.	1.7	15
15773	Genome-wide mapping of histone modifications during axenic growth in two species of <i>Leptosphaeria maculans</i> showing contrasting genomic organization. <i>Chromosome Research</i> , 2021, 29, 219-236.	1.0	17
15774	New insights into the function of the proteins <i>IsiC</i> and <i>IsiD</i> from <i>Synechocystis</i> sp. PCC 6803 under iron limitation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 4693-4707.	1.7	5
15775	Significances of viable synergistic autophagy-associated cathepsin B and cathepsin D (CTSB/CTSD) as potential biomarkers for sudden cardiac death. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 233.	0.7	15
15777	Understanding the differences in 2G ethanol fermentative scales through omics data integration. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	6

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15778	Small RNA and degradome deep sequencing reveals important roles of microRNAs in cotton ( <i>Gossypium hirsutum</i> L.) response to root-knot nematode <i>Meloidogyne incognita</i> infection. <i>Genomics</i> , 2021, 113, 1146-1156.	1.3	12
15779	Respiratory Co-Infections: Modulators of SARS-CoV-2 Patients' Clinical Sub-Phenotype. <i>Frontiers in Microbiology</i> , 2021, 12, 653399.	1.5	22
15780	Single-nucleus transcriptomic landscape of primate hippocampal aging. <i>Protein and Cell</i> , 2021, 12, 695-716.	4.8	49
15782	ncFANs v2.0: an integrative platform for functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, W459-W468.	6.5	18
15783	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. <i>Nature Communications</i> , 2021, 12, 3116.	5.8	19
15784	Identification of Diagnostic CpG Signatures in Patients with Gestational Diabetes Mellitus via Epigenome-Wide Association Study Integrated with Machine Learning. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	2
15785	Small in size, big on taste: Metabolomics analysis of flavor compounds from Philippine garlic. <i>PLoS ONE</i> , 2021, 16, e0247289.	1.1	2
15786	Integrated strategy of LC-MS and network pharmacology for predicting active constituents and pharmacological mechanisms of <i>Ranunculus japonicus</i> Thunb. for treating rheumatoid arthritis. <i>Journal of Ethnopharmacology</i> , 2021, 271, 113818.	2.0	16
15787	RNA Sequencing Reveals Key Metabolic Pathways Are Modified by Short-Term Whole Egg Consumption. <i>Frontiers in Nutrition</i> , 2021, 8, 652192.	1.6	0
15788	Host Response of Atlantic Salmon ( <i>Salmo salar</i> ) Re-Inoculated with <i>Paramoeba perurans</i> . <i>Microorganisms</i> , 2021, 9, 993.	1.6	1
15789	Unraveling Root Development Through Single-Cell Omics and Reconstruction of Gene Regulatory Networks. <i>Frontiers in Plant Science</i> , 2021, 12, 661361.	1.7	4
15790	Genetic network and gene set enrichment analyses identify MND1 as potential diagnostic and therapeutic target gene for lung adenocarcinoma. <i>Scientific Reports</i> , 2021, 11, 9430.	1.6	4
15792	Construction of circRNA-miRNA-mRNA network in the pathogenesis of recurrent implantation failure using integrated bioinformatics study. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 1853-1864.	1.6	10
15793	Identification of the conserved long non-coding RNAs in myogenesis. <i>BMC Genomics</i> , 2021, 22, 336.	1.2	0
15794	Discovering chemical reaction pathways using accelerated molecular dynamics simulations and network analysis tools – Application to oxidation induced decomposition of ethylene carbonate. <i>Chemical Physics Letters</i> , 2021, 770, 138439.	1.2	7
15796	Identification of collagen genes related to immune infiltration and epithelial-mesenchymal transition in glioma. <i>Cancer Cell International</i> , 2021, 21, 276.	1.8	31
15797	G-quadruplex motifs are functionally conserved in cis-regulatory regions of pathogenic bacteria: An in-silico evaluation. <i>Biochimie</i> , 2021, 184, 40-51.	1.3	13
15799	Comparative Transcriptomic Analysis of Spermatozoa From High- and Low-Fertile Crossbred Bulls: Implications for Fertility Prediction. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647717.	1.8	26

#	ARTICLE	IF	CITATIONS
15800	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. <i>Frontiers in Immunology</i> , 2021, 12, 616967.	2.2	13
15801	Bioinformatics-based Identification of Key Pathways and Hub Genes of Traumatic Brain Injury in a Rat Model. <i>Current Medical Science</i> , 2021, 41, 610-617.	0.7	2
15802	Proteome reprogramming of endometrial epithelial cells by human trophoctodermal small extracellular vesicles reveals key insights into embryo implantation. <i>Proteomics</i> , 2021, 21, e2000210.	1.3	18
15803	The human brain acetylome reveals that decreased acetylation of mitochondrial proteins associates with Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021, 158, 282-296.	2.1	11
15804	Analysis of Zika virus capsid-Aedes aegypti mosquito interactome reveals pro-viral host factors critical for establishing infection. <i>Nature Communications</i> , 2021, 12, 2766.	5.8	19
15805	The nucleoplasmic interactions among Lamin A/C-pRB-LAP2±-E2F1 are modulated by dexamethasone. <i>Scientific Reports</i> , 2021, 11, 10099.	1.6	3
15806	Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria. <i>BMC Genomics</i> , 2021, 22, 343.	1.2	11
15808	Hsa_circ_0000301 facilitates the progression of cervical cancer by targeting miR-1228-3p/IRF4 Axis. <i>BMC Cancer</i> , 2021, 21, 583.	1.1	9
15809	Network-based analysis of key regulatory genes implicated in Type 2 Diabetes Mellitus and Recurrent Miscarriages in Turner Syndrome. <i>Scientific Reports</i> , 2021, 11, 10662.	1.6	4
15810	Comparing Statistical Tests for Differential Network Analysis of Gene Modules. <i>Frontiers in Genetics</i> , 2021, 12, 630215.	1.1	4
15813	Epidermal Growth Factor Receptor Mutation Mechanisms in Nonsmall Cell Lung Cancer by Transcriptome Sequencing. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2022, 37, 560-568.	0.7	3
15815	Aloe djiboutiensis: Antioxidant Activity, Molecular Networking-Based Approach and In Vivo Toxicity of This Endemic Species in Djibouti. <i>Molecules</i> , 2021, 26, 3046.	1.7	3
15816	Identifying influential neighbors in social networks and venue affiliations among young MSM: a data science approach to predict HIV infection. <i>Aids</i> , 2021, 35, S65-S73.	1.0	6
15817	Lysosome-targeted photodynamic treatment induces primary keratinocyte differentiation. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2021, 218, 112183.	1.7	2
15818	ADAMTS12 acts as a tumor microenvironment related cancer promoter in gastric cancer. <i>Scientific Reports</i> , 2021, 11, 10996.	1.6	13
15819	Transcriptome analysis of potential candidate genes and molecular pathways in colitis-associated colorectal cancer of Mkp-1-deficient mice. <i>BMC Cancer</i> , 2021, 21, 607.	1.1	5
15820	A genome-wide analysis of NPF and NRT2 transporter gene families in bread wheat provides new insights into the distribution, function, regulation and evolution of nitrate transporters. <i>Plant and Soil</i> , 2021, 465, 47-63.	1.8	14
15821	Response to Anti-Î±4Î²7 Blockade in Patients With Ulcerative Colitis Is Associated With Distinct Mucosal Gene Expression Profiles at Baseline. <i>Inflammatory Bowel Diseases</i> , 2022, 28, 87-95.	0.9	6

#	ARTICLE	IF	CITATIONS
15822	Claudin-Low Breast Cancer Inflammatory Signatures Support Polarization of M1-Like Macrophages with Protumoral Activity. <i>Cancers</i> , 2021, 13, 2248.	1.7	7
15823	Visual exploration of large metabolic models. <i>Bioinformatics</i> , 2021, 37, 4460-4468.	1.8	4
15824	A Sigh on Single-Cell Transcriptomics in Plants Through the Prism of Cell-Based Computational Modeling Approaches: Benefits and Challenges for Data Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 652974.	1.1	7
15825	Genome-wide identification and expression pattern analysis of lipoxygenase gene family in banana. <i>Scientific Reports</i> , 2021, 11, 9948.	1.6	24
15826	Integrated analysis of ceRNA network and tumor-infiltrating immune cells in esophageal cancer. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
15828	Host-Parasite Interaction of Atlantic salmon ( <i>Salmo salar</i> ) and the Ectoparasite <i>Neoparamoeba perurans</i> in Amoebic Gill Disease. <i>Frontiers in Immunology</i> , 2021, 12, 672700.	2.2	22
15829	Microtubule Dynamics Plays a Vital Role in Plant Adaptation and Tolerance to Salt Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5957.	1.8	24
15830	Integrated bioinformatics analysis reveals novel key biomarkers and potential candidate small molecule drugs in gestational diabetes mellitus. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
15831	Underpinning the molecular programming attributing heat stress associated thermotolerance in tea ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Horticulture Research</i> , 2021, 8, 99.	2.9	19
15832	CmMLO17 and its partner CmKIC potentially support <i>Alternaria alternata</i> growth in <i>Chrysanthemum morifolium</i> . <i>Horticulture Research</i> , 2021, 8, 101.	2.9	13
15833	LncRNA Mrhl orchestrates differentiation programs in mouse embryonic stem cells through chromatin mediated regulation. <i>Stem Cell Research</i> , 2021, 53, 102250.	0.3	8
15834	Fusion protein EWS-FLI1 is incorporated into a protein granule in cells. <i>Rna</i> , 2021, 27, 920-932.	1.6	14
15835	IsoSplitter: identification and characterization of alternative splicing sites without a reference genome. <i>Rna</i> , 2021, 27, 868-875.	1.6	4
15836	Bioinformatics Analysis of a Prognostic miRNA Signature and Potential Key Genes in Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 641289.	1.3	16
15839	The Interaction between Rice Genotype and <i>Magnaporthe oryzae</i> Regulates the Assembly of Rice Root-Associated Microbiota. <i>Rice</i> , 2021, 14, 40.	1.7	6
15840	Siteng Fang Reverses Multidrug Resistance in Gastric Cancer: A Network Pharmacology and Molecular Docking Study. <i>Frontiers in Oncology</i> , 2021, 11, 671382.	1.3	5
15841	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from <i>Bacillus thuringiensis</i> sv. <i>andalousiensis</i> . <i>IScience</i> , 2021, 24, 102480.	1.9	18
15842	Single-cell transcriptomics trajectory and molecular convergence of clinically relevant mutations in Brugada syndrome. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2021, 320, H1935-H1948.	1.5	6

#	ARTICLE	IF	CITATIONS
15843	Overcoming false-positive gene-category enrichment in the analysis of spatially resolved transcriptomic brain atlas data. <i>Nature Communications</i> , 2021, 12, 2669.	5.8	74
15844	Assembly of abundant and rare bacterial and fungal sub-communities in different soil aggregate sizes in an apple orchard treated with cover crop and fertilizer. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108222.	4.2	76
15845	A resource to explore the discovery of rare diseases and their causative genes. <i>Scientific Data</i> , 2021, 8, 124.	2.4	11
15846	IDARE—Simultaneous Visualisation of Multiomics Data in Cytoscape. <i>Metabolites</i> , 2021, 11, 300.	1.3	2
15847	Integrated Pharmacological Analysis on the Mechanism of Fuyou Formula in Treating Precocious Puberty. <i>Frontiers in Pharmacology</i> , 2021, 12, 649732.	1.6	5
15848	Network pharmacology integrated with experimental validation revealed the anti-inflammatory effects of <i>Andrographis paniculata</i> . <i>Scientific Reports</i> , 2021, 11, 9752.	1.6	12
15849	Effects of Berberine on Circular RNA Expression Profiles in Human Gastric Cancer Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-16.	0.5	3
15850	Structural and mechanistic insights into the bifunctional HSN2 enzyme catalyzing the second and third steps of histidine biosynthesis in plants. <i>Scientific Reports</i> , 2021, 11, 9647.	1.6	5
15851	Constituents of <i>Chamaecrista diphylla</i> (L.) Greene Leaves with Potent Antioxidant Capacity: A Feature-Based Molecular Network Dereplication Approach. <i>Pharmaceutics</i> , 2021, 13, 681.	2.0	9
15852	Single-Cell scRNA Sequencing Reveals the Breadth of Osteoblast Heterogeneity. <i>JBMR Plus</i> , 2021, 5, e10496.	1.3	14
15853	Genotoxic effect induced by dried <i>Nicotiana tabacum</i> leaves from tobacco barns (kiln-houses) in chinese hamster lung fibroblast cells (V79). <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2021, 84, 689-701.	1.1	1
15854	Investigation of Anti-SARS, MERS, and COVID-19 Effect of Jinhua Qinggan Granules Based on a Network Pharmacology and Molecular Docking Approach. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110206.	0.2	2
15855	Exploration of Blood Lipoprotein and Lipid Fraction Profiles in Healthy Subjects through Integrated Univariate, Multivariate, and Network Analysis Reveals Association of Lipase Activity and Cholesterol Esterification with Sex and Age. <i>Metabolites</i> , 2021, 11, 326.	1.3	5
15856	A ten N <sup>6</sup> -methyladenosine-related long non-coding RNAs signature predicts prognosis of triple-negative breast cancer. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23779.	0.9	22
15857	Prognostic value of members of NFAT family for pan-cancer and a prediction model based on NFAT2 in bladder cancer. <i>Aging</i> , 2021, 13, 13876-13897.	1.4	5
15858	A Risk Signature with Autophagy-Related Long Noncoding RNAs for Predicting the Prognosis of Clear Cell Renal Cell Carcinoma: Based on the TCGA Database and Bioinformatics. <i>Disease Markers</i> , 2021, 2021, 1-18.	0.6	14
15859	Contrasting origins, expression patterns and functions of circRNAs between salt-sensitive and salt-tolerant poplars. <i>Environmental and Experimental Botany</i> , 2021, 185, 104403.	2.0	7
15861	The Relevance of a Physiological-Stage Approach Study of the Molecular and Environmental Factors Regulating Seed Germination in Wild Plants. <i>Plants</i> , 2021, 10, 1084.	1.6	2

#	ARTICLE	IF	CITATIONS
15862	Assessing the Contribution of Relative Macrophage Frequencies to Subcutaneous Adipose Tissue. <i>Frontiers in Nutrition</i> , 2021, 8, 675935.	1.6	2
15863	Fullerenol changes metabolite responses differently depending on the iron status of cucumber plants. <i>PLoS ONE</i> , 2021, 16, e0251396.	1.1	7
15864	GeneCaRNA: A Comprehensive Gene-centric Database of Human Non-coding RNAs in the GeneCards Suite. <i>Journal of Molecular Biology</i> , 2021, 433, 166913.	2.0	51
15865	CG6015 controls spermatogonia transit-amplifying divisions by epidermal growth factor receptor signaling in <i>Drosophila</i> testes. <i>Cell Death and Disease</i> , 2021, 12, 491.	2.7	8
15866	Comprehensive analysis of the lysine acetylome and succinylome in the hippocampus of gut microbiota-dysbiosis mice. <i>Journal of Advanced Research</i> , 2021, 30, 27-38.	4.4	26
15867	Identification of key genes in calcific aortic valve disease via weighted gene co-expression network analysis. <i>BMC Medical Genomics</i> , 2021, 14, 135.	0.7	8
15868	Genome-Wide Analysis of Coding and Non-coding RNA Reveals a Conserved miR164â€œNACâ€œ mRNA Regulatory Pathway for Disease Defense in <i>Populus</i> . <i>Frontiers in Genetics</i> , 2021, 12, 668940.	1.1	8
15869	Melatonin promotes <i>Arabidopsis</i> primary root growth in an IAA-dependent manner. <i>Journal of Experimental Botany</i> , 2021, 72, 5599-5611.	2.4	53
15870	The Gene Expression Profile of the Song Control Nucleus HVC Shows Sex Specificity, Hormone Responsiveness, and Species Specificity Among Songbirds. <i>Frontiers in Neuroscience</i> , 2021, 15, 680530.	1.4	10
15871	Transcriptome Profiling of Embryonic Retinal Pigment Epithelium Reprogramming. <i>Genes</i> , 2021, 12, 840.	1.0	9
15872	Learning from Embryogenesisâ€œA Comparative Expression Analysis in Melanoblast Differentiation and Tumorigenesis Reveals miRNAs Driving Melanoma Development. <i>Journal of Clinical Medicine</i> , 2021, 10, 2259.	1.0	5
15873	The gut microbiome in pancreatogenic diabetes differs from that of Type 1 and Type 2 diabetes. <i>Scientific Reports</i> , 2021, 11, 10978.	1.6	10
15874	Comprehensive Volatilome and Metabolome Signatures of Colorectal Cancer in Urine: A Systematic Review and Meta-Analysis. <i>Cancers</i> , 2021, 13, 2534.	1.7	19
15875	Gene Expression Profile of the Human Colorectal Carcinoma LoVo Cells Treated With Sporamin and Thapsigargin. <i>Frontiers in Oncology</i> , 2021, 11, 621462.	1.3	3
15877	MiRâ€œ193b deregulation is associated with Parkinson's disease. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 6348-6360.	1.6	15
15878	The paeonol target gene autophagy-related 5 has a potential therapeutic value in psoriasis treatment. <i>PeerJ</i> , 2021, 9, e11278.	0.9	4
15879	Transcriptome analysis of MBD5-associated neurodevelopmental disorder (MAND) neural progenitor cells reveals dysregulation of autism-associated genes. <i>Scientific Reports</i> , 2021, 11, 11295.	1.6	4
15880	Validation of the functions and prognostic values of synapse-associated proteins in lower-grade glioma. <i>Bioscience Reports</i> , 2021, 41, .	1.1	6



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15881	Molecular Targets and Biological Functions of cAMP Signaling in Arabidopsis. <i>Biomolecules</i> , 2021, 11, 688.	1.8	21
15882	Association of Gut Microbiota during Early Pregnancy with Risk of Incident Gestational Diabetes Mellitus. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e4128-e4141.	1.8	21
15884	A Machine Learning Bioinformatics Method to Predict Biological Activity from Biosynthetic Gene Clusters. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2560-2571.	2.5	38
15885	Specific microRNA/mRNA expression profiles and novel immune regulation mechanisms are induced in THP-1 macrophages by in vitro exposure to <i>Trichosporon asahii</i> . <i>Mycoses</i> , 2021, 64, 831-840.	1.8	2
15886	Construction of an immune-related signature with prognostic value for colon cancer. <i>PeerJ</i> , 2021, 9, e10812.	0.9	2
15887	Quantitative Proteomics Identifies Secreted Diagnostic Biomarkers as well as Tumor-Dependent Prognostic Targets for Clear Cell Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2022, 19, 1322-1337.	1.5	10
15888	Identification of viral-mediated pathogenic mechanisms in neurodegenerative diseases using network-based approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
15889	Identification of CDC20 as an immune infiltration-correlated prognostic biomarker in hepatocellular carcinoma. <i>Investigational New Drugs</i> , 2021, 39, 1439-1453.	1.2	11
15890	KEA3: improved kinase enrichment analysis via data integration. <i>Nucleic Acids Research</i> , 2021, 49, W304-W316.	6.5	55
15891	METTL13 inhibits progression of clear cell renal cell carcinoma with repression on PI3K/AKT/mTOR/HIF-1 $\alpha$ pathway and c-Myc expression. <i>Journal of Translational Medicine</i> , 2021, 19, 209.	1.8	14
15892	Identification of the EMT-Related Genes Signature for Predicting Occurrence and Progression in Thyroid Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3119-3131.	1.0	5
15894	Therapeutic Effects of Naringin in Rheumatoid Arthritis: Network Pharmacology and Experimental Validation. <i>Frontiers in Pharmacology</i> , 2021, 12, 672054.	1.6	48
15895	Systematic analysis of MYB gene family in <i>Acer rubrum</i> and functional characterization of ArMYB89 in regulating anthocyanin biosynthesis. <i>Journal of Experimental Botany</i> , 2021, 72, 6319-6335.	2.4	5
15896	Potential effect of Maxing Shigan decoction against coronavirus disease 2019 (COVID-19) revealed by network pharmacology and experimental verification. <i>Journal of Ethnopharmacology</i> , 2021, 271, 113854.	2.0	50
15897	Exposure to sevoflurane results in changes of transcription factor occupancy in sperm and inheritance of autism. <i>Biology of Reproduction</i> , 2021, 105, 705-719.	1.2	12
15898	Transcriptomic meta-analysis of disuse muscle atrophy vs. resistance exercise-induced hypertrophy in young and older humans. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 629-645.	2.9	15
15899	Genome-wide scan reveals genomic regions and candidate genes underlying direct and maternal effects of preweaning calf mortality in Nellore cattle. <i>Genomics</i> , 2021, 113, 1386-1395.	1.3	4
15900	scConnect: a method for exploratory analysis of cell-cell communication based on single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2021, 37, 3501-3508.	1.8	18

#	ARTICLE	IF	CITATIONS
15901	EGFR phosphorylates HDAC1 to regulate its expression and anti-apoptotic function. <i>Cell Death and Disease</i> , 2021, 12, 469.	2.7	6
15902	lncRNA Sequencing of Antler Mesenchymal Tissue Revealed that the Regulatory Network of Antler Cell Proliferation and Differentiation. <i>Animal Biotechnology</i> , 2021, , 1-10.	0.7	2
15903	Phenotypic and Multi-Omics Characterization of <i>Escherichia coli</i> K-12 Adapted to Chlorhexidine Identifies the Role of MlaA and Other Cell Envelope Alterations Regulated by Stress Inducible Pathways in CHX Resistance. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 659058.	1.6	8
15904	Integrated lncRNA and mRNA Transcriptome Analyses in the Ovary of <i>Cynoglossus semilaevis</i> Reveal Genes and Pathways Potentially Involved in Reproduction. <i>Frontiers in Genetics</i> , 2021, 12, 671729.	1.1	7
15905	Dysregulation of Transcription Factor Networks Unveils Different Pathways in Human Papillomavirus 16-Positive Squamous Cell Carcinoma and Adenocarcinoma of the Uterine Cervix. <i>Frontiers in Oncology</i> , 2021, 11, 626187.	1.3	10
15906	Integrative web-based analysis of omics data for study of drugs against SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 10763.	1.6	2
15907	Temporal Bacterial Community Diversity in the <i>Nicotiana tabacum</i> Rhizosphere Over Years of Continuous Monocropping. <i>Frontiers in Microbiology</i> , 2021, 12, 641643.	1.5	14
15908	Investigation of the Mechanism of Complement System in Diabetic Nephropathy via Bioinformatics Analysis. <i>Journal of Diabetes Research</i> , 2021, 2021, 1-14.	1.0	19
15909	Proteomic Comparison of Bone Marrow Derived Osteoblasts and Mesenchymal Stem Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5665.	1.8	15
15910	RAGE-mediated functional DNA methylated modification contributes to cigarette smoke-induced airway inflammation in mice. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
15912	Genome-wide DNA methylation and RNA-seq analyses identify genes and pathways associated with doxorubicin resistance in a canine diffuse large B-cell lymphoma cell line. <i>PLoS ONE</i> , 2021, 16, e0250013.	1.1	5
15913	Network Pharmacology and Molecular Docking Study on the Potential Mechanism of Yi-Qi-Huo-Xue-Tong-Luo Formula in Treating Diabetic Peripheral Neuropathy. <i>Journal of Diabetes Research</i> , 2021, 2021, 1-16.	1.0	15
15914	Single-cell profiling of tumor heterogeneity and the microenvironment in advanced non-small cell lung cancer. <i>Nature Communications</i> , 2021, 12, 2540.	5.8	295
15916	Dynamic Expression Profiles of Circular RNAs during Brown to White Adipose Tissue Transformation in Goats ( <i>Capra hircus</i> ). <i>Animals</i> , 2021, 11, 1351.	1.0	7
15917	Identification of MCM family as potential therapeutic and prognostic targets for hepatocellular carcinoma based on bioinformatics and experiments. <i>Life Sciences</i> , 2021, 272, 119227.	2.0	16
15918	Molecular signatures of labor and non-labor myometrium with parsimonious classification from two calcium transporter genes. <i>JCI Insight</i> , 2021, 6, .	2.3	2
15919	Comparative transcriptomic analysis reveals an association of gibel carp fatty liver with ferroptosis pathway. <i>BMC Genomics</i> , 2021, 22, 328.	1.2	7
15920	A prognostic model based on seven immune-related genes predicts the overall survival of patients with hepatocellular carcinoma. <i>BioData Mining</i> , 2021, 14, 29.	2.2	7

#	ARTICLE	IF	CITATIONS
15922	Potential treatment for chronic myeloid leukemia using microRNA: in silico comparison between plants and human microRNAs in targeting BCR-ABL1 gene. Egyptian Journal of Medical Human Genetics, 2021, 22, .	0.5	4
15923	Identification of prognostic and bone metastasis-related alternative splicing signatures in mesothelioma. Cancer Medicine, 2021, 10, 4478-4492.	1.3	1
15924	Minimized combinatorial CRISPR screens identify genetic interactions in autophagy. Nucleic Acids Research, 2021, 49, 5684-5704.	6.5	31
15925	Downregulation of USP18 reduces tumor-infiltrating activated dendritic cells in extranodal diffuse large B cell lymphoma patients. Aging, 2021, 13, 14131-14158.	1.4	6
15926	Integrative analysis identifies key mRNA biomarkers for diagnosis, prognosis, and therapeutic targets of HCV-associated hepatocellular carcinoma. Aging, 2021, 13, 12865-12895.	1.4	11
15927	Prunus persica plant endogenous peptides PpPep1 and PpPep2 cause PTI-like transcriptome reprogramming in peach and enhance resistance to Xanthomonas arboricola pv. pruni. BMC Genomics, 2021, 22, 360.	1.2	8
15928	Transcription Landscape of the Early Developmental Biology in Pigs. Animals, 2021, 11, 1443.	1.0	3
15930	Identification of a Prognostic Signature for Ovarian Cancer Based on the Microenvironment Genes. Frontiers in Genetics, 2021, 12, 680413.	1.1	12
15933	Microevolution in the pansecondary metabolome of <i>Aspergillus flavus</i> and its potential macroevolutionary implications for filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
15934	Comprehensive Analysis and Identification of Key Driver Genes for Distinguishing Between Esophageal Adenocarcinoma and Squamous Cell Carcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 676156.	1.8	8
15935	De Novo Transcriptome Meta-Assembly of the Mixotrophic Freshwater Microalga Euglena gracilis. Genes, 2021, 12, 842.	1.0	9
15937	A general non-self response as part of plant immunity. Nature Plants, 2021, 7, 696-705.	4.7	50
15938	Association of Extracellular Signal-Regulated Kinase Genes With Myopia: A Longitudinal Study of Chinese Children. Frontiers in Genetics, 2021, 12, 654869.	1.1	8
15940	Identification of Potential miRNA-mRNA Regulatory Network Contributing to Hypertrophic Cardiomyopathy (HCM). Frontiers in Cardiovascular Medicine, 2021, 8, 660372.	1.1	8
15941	Designing of Potential Polyvalent Vaccine Model for Respiratory Syncytial Virus by System Level Immunoinformatics Approaches. BioMed Research International, 2021, 2021, 1-18.	0.9	4
15942	Epigenetic control of region-specific transcriptional programs in mouse cerebellar and cortical astrocytes. Glia, 2021, 69, 2160-2177.	2.5	13
15944	Transcriptome and Metabolomic Analyses Reveal Regulatory Networks Controlling Maize Stomatal Development in Response to Blue Light. International Journal of Molecular Sciences, 2021, 22, 5393.	1.8	10
15945	Constitutive activation of CTNNB1 results in a loss of spermatogonial stem cell activity in mice. PLoS ONE, 2021, 16, e0251911.	1.1	14

#	ARTICLE	IF	CITATIONS
15946	ITGA2, LAMB3, and LAMC2 may be the potential therapeutic targets in pancreatic ductal adenocarcinoma: an integrated bioinformatics analysis. <i>Scientific Reports</i> , 2021, 11, 10563.	1.6	31
15947	Metabolomics bridging proteomics along metabolites/oncometabolites and protein modifications: Paving the way toward integrative multiomics. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 199, 114031.	1.4	8
15948	Comprehensive analysis of the competing endogenous circRNA-lncRNA-miRNA-mRNA network and identification of a novel potential biomarker for hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 15990-16008.	1.4	34
15949	Ecological and network analyses identify four microbial species with potential significance for the diagnosis/treatment of ulcerative colitis (UC). <i>BMC Microbiology</i> , 2021, 21, 138.	1.3	24
15950	Destabilization of EpCAM dimer is associated with increased susceptibility towards cleavage by TACE. <i>PeerJ</i> , 2021, 9, e11484.	0.9	3
15951	Circadian time series proteomics reveals daily dynamics in cartilage physiology. <i>Osteoarthritis and Cartilage</i> , 2021, 29, 739-749.	0.6	17
15952	TMT-based proteomic and bioinformatic analyses of human granulosa cells from obese and normal-weight female subjects. <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 75.	1.4	10
15954	Antifungal mechanism of <i>Bacillus amyloliquefaciens</i> strain GKT04 against <i>Fusarium</i> wilt revealed using genomic and transcriptomic analyses. <i>MicrobiologyOpen</i> , 2021, 10, e1192.	1.2	13
15955	Linking Coregulated Gene Modules with Polycyclic Aromatic Hydrocarbon-Related Cancer Risk in the 3D Human Bronchial Epithelium. <i>Chemical Research in Toxicology</i> , 2021, 34, 1445-1455.	1.7	10
15956	TIGIT and PD-1 Immune Checkpoint Pathways Are Associated With Patient Outcome and Anti-Tumor Immunity in Glioblastoma. <i>Frontiers in Immunology</i> , 2021, 12, 637146.	2.2	32
15957	Circular RNA ciRS-7 affects the propagation of <i>Cryptosporidium parvum</i> in HCT-8 cells by sponging miR-1270 to activate the NF- $\kappa$ B signaling pathway. <i>Parasites and Vectors</i> , 2021, 14, 238.	1.0	15
15958	The SAM domain-containing protein 1 (SAMD1) acts as a repressive chromatin regulator at unmethylated CpG islands. <i>Science Advances</i> , 2021, 7, .	4.7	22
15959	Identification of upregulated NF- $\kappa$ B inhibitor alpha and IRAK3 targeting lncRNA following intracranial aneurysm rupture-induced subarachnoid hemorrhage. <i>BMC Neurology</i> , 2021, 21, 197.	0.8	9
15960	Dysregulation of Glycerophosphocholines in the Cutaneous Lesion Caused by <i>Leishmania major</i> in Experimental Murine Models. <i>Pathogens</i> , 2021, 10, 593.	1.2	7
15961	Nicotinamide riboside attenuates age-associated metabolic and functional changes in hematopoietic stem cells. <i>Nature Communications</i> , 2021, 12, 2665.	5.8	45
15962	Cancer-Associated circRNA-miRNA-mRNA Regulatory Networks: A Meta-Analysis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 671309.	1.6	23
15963	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	5.8	43
15964	Metabolic Alterations in <i>Pisum sativum</i> Roots during Plant Growth and Arbuscular Mycorrhiza Development. <i>Plants</i> , 2021, 10, 1033.	1.6	13

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15965	Metabolism and Chronic Inflammation: The Links Between Chronic Heart Failure and Comorbidities. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 650278.	1.1	27
15966	Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. <i>Genetics Selection Evolution</i> , 2021, 53, 43.	1.2	4
15967	Network Pharmacology and Molecular Docking Combined to Analyze the Molecular and Pharmacological Mechanism of <i>Pinellia ternata</i> in the Treatment of Hypertension. <i>Current Issues in Molecular Biology</i> , 2021, 43, 65-78.	1.0	11
15968	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	1.7	39
15969	The Transcriptome of SH-SY5Y at Single-Cell Resolution: A CITE-Seq Data Analysis Workflow. <i>Methods and Protocols</i> , 2021, 4, 28.	0.9	2
15970	METTL14 Acts as a Potential Regulator of Tumor Immune and Progression in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 609174.	1.1	11
15971	The transcriptomic response to heat stress of a jujube ( <i>Ziziphus jujuba</i> Mill.) cultivar is featured with changed expression of long noncoding RNAs. <i>PLoS ONE</i> , 2021, 16, e0249663.	1.1	6
15972	Nuclear isoform of FGF13 regulates post-natal neurogenesis in the hippocampus through an epigenomic mechanism. <i>Cell Reports</i> , 2021, 35, 109127.	2.9	5
15974	MiMeNet: Exploring microbiome-metabolome relationships using neural networks. <i>PLoS Computational Biology</i> , 2021, 17, e1009021.	1.5	42
15975	Gut Microbial SNPs Induced by High-Fiber Diet Dominate Nutrition Metabolism and Environmental Adaption of <i>Faecalibacterium prausnitzii</i> in Obese Children. <i>Frontiers in Microbiology</i> , 2021, 12, 683714.	1.5	8
15976	Identifying Challenges and Solutions in Cultural Heritage Adaptive Reuse through the Historic Urban Landscape Approach in Amsterdam. <i>Sustainability</i> , 2021, 13, 5547.	1.6	14
15977	Computational Design of Novel Allosteric Inhibitors for <i>Plasmodium falciparum</i> DegP. <i>Molecules</i> , 2021, 26, 2742.	1.7	5
15978	Identification, evolution, expression analysis of phospholipase D (PLD) gene family in tea ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.4	10
15979	Genome stabilization by RAD51-stimulatory compound 1 enhances efficiency of somatic cell nuclear transfer-mediated reprogramming and full-term development of cloned mouse embryos. <i>Cell Proliferation</i> , 2021, 54, e13059.	2.4	7
15980	Adaptation to mitochondrial stress requires CHOP-directed tuning of ISR. <i>Science Advances</i> , 2021, 7, .	4.7	68
15981	<i>Schistosoma mansoni</i> Heterochromatin Protein 1 (HP1) nuclear interactome in cercariae. <i>Journal of Proteomics</i> , 2021, 239, 104170.	1.2	1
15982	Proteomic analysis of <i>Caenorhabditis elegans</i> wound model reveals novel molecular players involved in repair. <i>Journal of Proteomics</i> , 2021, 240, 104222.	1.2	1
15983	Large scale RNA-binding proteins/LncRNAs interaction analysis to uncover lncRNA nuclear localization mechanisms. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	19

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15984	The peripheral and core regions of virus-host network of COVID-19. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
15985	BENviewer: a gene interaction network visualization server based on graph embedding model. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	1
15986	Bioinformatic identification of hub genes and related transcription factors in low shear stress treated endothelial cells. <i>BMC Medical Genomics</i> , 2021, 14, 120.	0.7	2
15987	Tea polyphenols and Levofloxacin alleviate the lung injury of hepatopulmonary syndrome in common bile duct ligation rats through Endotoxin -TNF signaling. <i>Biomedicine and Pharmacotherapy</i> , 2021, 137, 111263.	2.5	8
15988	Nitrogen availability improves the physiological resilience of coral endosymbiont <i>Cladocodium goreaui</i> to high temperature. <i>Journal of Phycology</i> , 2021, 57, 1187-1198.	1.0	6
15989	Clump sequencing exposes the spatial expression programs of intestinal secretory cells. <i>Nature Communications</i> , 2021, 12, 3074.	5.8	43
15990	Signature RNAs and related regulatory roles in type 1 diabetes mellitus based on competing endogenous RNA regulatory network analysis. <i>BMC Medical Genomics</i> , 2021, 14, 133.	0.7	4
15991	An Integrated Analysis of Network Pharmacology, Molecular Docking, and Experiment Validation to Explore the New Candidate Active Component and Mechanism of Cuscutae Semen-Mori Fructus Coupled-Herbs in Treating Oligoasthenozoospermia. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15. 2059-2089.	2.0	7
15992	Characteristics of the AT-Hook Motif Containing Nuclear Localized (AHL) Genes in Carrot Provides Insight into Their Role in Plant Growth and Storage Root Development. <i>Genes</i> , 2021, 12, 764.	1.0	4
15994	The Value of Immune-Related Genes Signature in Osteosarcoma Based on Weighted Gene Co-expression Network Analysis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-17.	0.9	26
15995	Bone Marrow Soluble Mediator Signatures of Patients With Philadelphia Chromosome-Negative Myeloproliferative Neoplasms. <i>Frontiers in Oncology</i> , 2021, 11, 665037.	1.3	10
15996	Search and visualization of gene-drug-disease interactions for pharmacogenomics and precision medicine research using GeneDive. <i>Journal of Biomedical Informatics</i> , 2021, 117, 103732.	2.5	2
15997	Collateral Sensitivity to Î²-Lactam Drugs in Drug-Resistant Tuberculosis Is Driven by the Transcriptional Wiring of Blal Operon Genes. <i>MSphere</i> , 2021, 6, e0024521.	1.3	2
15999	Whole transcriptome RNA-seq reveals key regulatory factors involved in type 2 diabetes pathology in peripheral fat of Asian Indians. <i>Scientific Reports</i> , 2021, 11, 10632.	1.6	10
16000	Identification of Critical Genes and Signaling Pathways in Human Monocytes Following High-Intensity Exercise. <i>Healthcare (Switzerland)</i> , 2021, 9, 618.	1.0	2
16001	Altered Expression of Candidate Genes in Mayer-Rokitansky-Kuster-Hauser Syndrome May Influence Vaginal Keratinocytes Biology: A Focus on Protein Kinase X. <i>Biology</i> , 2021, 10, 450.	1.3	4
16002	Investigation of Early Supplementation of Nucleotides on the Intestinal Maturation of Weaned Piglets. <i>Animals</i> , 2021, 11, 1489.	1.0	3
16003	The Resistance Responses of Potato Plants to Potato Virus Y Are Associated with an Increased Cellular Methionine Content and an Altered SAM:SAH Methylation Index. <i>Viruses</i> , 2021, 13, 955.	1.5	9



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16004	Reconstruction and Dynamics of the Human Intestinal Microbiome Observed In Situ. <i>Engineering</i> , 2022, 15, 89-101.	3.2	9
16005	Transcriptome Analyses Implicate Endogenous Retroviruses Involved in the Host Antiviral Immune System through the Interferon Pathway. <i>Virologica Sinica</i> , 2021, 36, 1315-1326.	1.2	15
16006	Dynamic changes in gene-to-gene regulatory networks in response to SARS-CoV-2 infection. <i>Scientific Reports</i> , 2021, 11, 11241.	1.6	3
16007	Spatially visualized single-cell pathology of highly multiplexed protein profiles in health and disease. <i>Communications Biology</i> , 2021, 4, 632.	2.0	5
16008	The role of frontotemporal dementia associated genes in patients with Alzheimer's disease. <i>Neurobiology of Aging</i> , 2021, 107, 153-158.	1.5	8
16009	Oncogenic Landscape of Somatic Mutations Perturbing Pan-Cancer lncRNA-ceRNA Regulation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 658346.	1.8	14
16010	K-Domain Technology: Constitutive Expression of a Blueberry Keratin-Like Domain Mimics Expression of Multiple MADS-Box Genes in Enhancing Maize Grain Yield. <i>Frontiers in Plant Science</i> , 2021, 12, 664983.	1.7	5
16011	KIF4A as a novel prognostic biomarker in cholangiocarcinoma. <i>Medicine (United States)</i> , 2021, 100, e26130.	0.4	5
16012	IntAct App: a Cytoscape application for molecular interaction network visualization and analysis. <i>Bioinformatics</i> , 2021, 37, 3684-3685.	1.8	21
16013	JunB is a key regulator of multiple myeloma bone marrow angiogenesis. <i>Leukemia</i> , 2021, 35, 3509-3525.	3.3	19
16014	Cross-Model Comparison of Transcriptomic Dose-Response of Short-Chain Chlorinated Paraffins. <i>Environmental Science &amp; Technology</i> , 2021, 55, 8149-8158.	4.6	15
16015	Investigation of differentially expressed gene profile for cisplatin-treated lung cancer patients. <i>Anti-Cancer Drugs</i> , 2021, 32, 875-881.	0.7	1
16016	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. <i>Molecular Cell</i> , 2021, 81, 2201-2215.e9.	4.5	10
16017	Differential mass spectrometry-based proteome analyses unveil major regulatory hubs in rifamycin B production in <i>Amycolatopsis mediterranei</i> . <i>Journal of Proteomics</i> , 2021, 239, 104168.	1.2	6
16018	Mediterranean diet enriched in extra-virgin olive oil or nuts modulates circulating exosomal non-coding RNAs. <i>European Journal of Nutrition</i> , 2021, 60, 4279-4293.	1.8	21
16019	Insights into the taxonomic and functional characterization of agricultural crop core rhizobiomes and their potential microbial drivers. <i>Scientific Reports</i> , 2021, 11, 10068.	1.6	15
16020	High copy number variations, particular transcription factors, and low immunity contribute to the stemness of prostate cancer cells. <i>Journal of Translational Medicine</i> , 2021, 19, 206.	1.8	11
16021	Integrating Transcriptome and Coexpression Network Analyses to Characterize Salicylic Acid- and Jasmonic Acid-Related Genes in Tolerant Poplars Infected with Rust. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5001.	1.8	12

#	ARTICLE	IF	CITATIONS
16022	Genomic evolution of the class <i>Acidithiobacillia</i> : deep-branching Proteobacteria living in extreme acidic conditions. <i>ISME Journal</i> , 2021, 15, 3221-3238.	4.4	31
16023	Discovery of potential Q-marker of traditional Chinese medicine based on plant metabolomics and network pharmacology: <i>Periplocae Cortex</i> as an example. <i>Phytomedicine</i> , 2021, 85, 153535.	2.3	50
16024	Network Pharmacology-Based Systematic Analysis of Molecular Mechanisms of Dingji Fumai Decoction for Ventricular Arrhythmia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	9
16025	A Study to Decipher the Potential Effects of Butylphthalide against Central Nervous System Diseases Based on Network Pharmacology and Molecular Docking Integration Strategy. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	2
16028	Contrasting Patterns of the Resident and Active Rhizosphere Bacterial Communities of <i>Phragmites Australis</i> . <i>Microbial Ecology</i> , 2022, 83, 314-327.	1.4	3
16029	Comprehensive analysis of the long non-coding RNA expression profile and functional roles in a contrast-induced acute kidney injury rat model. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 739.	0.8	2
16032	Transcriptomics analysis of differentially expressed genes in subcutaneous and perirenal adipose tissue of sheep as affected by their pre- and early postnatal malnutrition histories. <i>BMC Genomics</i> , 2021, 22, 338.	1.2	7
16034	Prognosis and Characterization of Immune Microenvironment in Acute Myeloid Leukemia Through Identification of an Autophagy-Related Signature. <i>Frontiers in Immunology</i> , 2021, 12, 695865.	2.2	24
16035	Filling in the Gaps in Metformin Biodegradation: a New Enzyme and a Metabolic Pathway for Guanylurea. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	17
16036	Leptin receptor is a key gene involved in the immunopathogenesis of thyroid-associated ophthalmopathy. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 5799-5810.	1.6	5
16037	Discovering unknown human and mouse transcription factor binding sites and their characteristics from ChIP-seq data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	6
16038	Identification of key pathways and genes in carotid atherosclerosis through bioinformatics analysis of RNA-seq data. <i>Aging</i> , 2021, 13, 12733-12747.	1.4	3
16039	Gene Coexpression Network Reveals Highly Conserved, Well-Regulated Anti-Ageing Mechanisms in Old Ant Queens. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
16040	Genome-Wide Identification of MATE Gene Family in Potato ( <i>Solanum tuberosum</i> L.) and Expression Analysis in Heavy Metal Stress. <i>Frontiers in Genetics</i> , 2021, 12, 650500.	1.1	17
16041	Functional genomics meta-analysis to identify gene set enrichment networks in cardiac hypertrophy. <i>Biological Chemistry</i> , 2021, 402, 953-972.	1.2	3
16042	Analysis of Ecological Networks in Multicomponent Communities of Microorganisms: Possibilities, Limitations, and Potential Errors. <i>Russian Journal of Ecology</i> , 2021, 52, 188-200.	0.3	1
16043	Mechanistic insights into the anti-depressant effect of emodin: an integrated systems pharmacology study and experimental validation. <i>Aging</i> , 2021, 13, 15078-15099.	1.4	9
16044	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to <i>Verticillium</i> wilt. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5634.	1.8	2

#	ARTICLE	IF	CITATIONS
16045	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021, 56, 1238-1252.e5.	3.1	29
16046	Identification of Key Genes for Hepatitis Delta Virus-Related Hepatocellular Carcinoma by Bioinformatics Analysis. <i>Turkish Journal of Gastroenterology</i> , 2021, 32, 169-177.	0.4	3
16047	Expression Analysis of Long Non-Coding RNAs Related With FOXM1, GATA3, FOXA1 and ESR1 in Breast Tissues. <i>Frontiers in Oncology</i> , 2021, 11, 671418.	1.3	5
16049	Small-RNA Sequencing Reveals Altered Skeletal Muscle microRNAs and snoRNAs Signatures in Weanling Male Offspring from Mouse Dams Fed a Low Protein Diet during Lactation. <i>Cells</i> , 2021, 10, 1166.	1.8	4
16050	dsRNA Molecules From the Tobacco Mosaic Virus p126 Gene Counteract TMV-Induced Proteome Changes at an Early Stage of Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 663707.	1.7	7
16051	Similarities and Differences in Gene Expression Networks Between the Breast Cancer Cell Line Michigan Cancer Foundation-7 and Invasive Human Breast Cancer Tissues. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 674370.	2.0	6
16052	Identifying an lncRNA-Related ceRNA Network to Reveal Novel Targets for a Cutaneous Squamous Cell Carcinoma. <i>Biology</i> , 2021, 10, 432.	1.3	7
16053	Integrated Analysis of ceRNA Network Reveals Prognostic and Metastasis Associated Biomarkers in Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 670138.	1.3	9
16054	Comparative transcriptome profiling and co-expression network analysis uncover the key genes associated with early-stage resistance to <i>Aspergillus flavus</i> in maize. <i>BMC Plant Biology</i> , 2021, 21, 216.	1.6	15
16055	Integrated DNA Methylation and Gene Expression Analysis Identified S100A8 and S100A9 in the Pathogenesis of Obesity. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 631650.	1.1	8
16056	Characterization of DNA Methylation and Screening of Epigenetic Markers in Polycystic Ovary Syndrome. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 664843.	1.8	15
16057	Stable Epigenetic Programming of Effector and Central Memory CD4 T Cells Occurs Within 7 Days of Antigen Exposure In Vivo. <i>Frontiers in Immunology</i> , 2021, 12, 642807.	2.2	4
16058	Comprehensive analysis of competitive endogenous RNA associated with immune infiltration in lung adenocarcinoma. <i>Scientific Reports</i> , 2021, 11, 11056.	1.6	5
16060	Weighted correlation network analysis identifies FN1, COL1A1 and SERPINE1 associated with the progression and prognosis of gastric cancer. <i>Cancer Biomarkers</i> , 2021, 31, 59-75.	0.8	8
16061	Modifying the catalytic preference of alpha-amylase toward n-alkanes for bioremediation purposes using in silico strategies. <i>Journal of Computational Chemistry</i> , 2021, 42, 1540-1551.	1.5	2
16062	Pharmacological Mechanisms Underlying the Therapeutic Effects of Danhong Injection on Cerebral Ischemia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-10.	0.5	2
16063	Microarray profile of circular RNAs identifies hsa_circ_000455 as a new circular RNA biomarker for deep vein thrombosis. <i>Vascular</i> , 2021, , 170853812110161.	0.4	2
16064	PD-1 Coexpression Gene Analysis and the Regulatory Network in Endometrial Cancer Based on Bioinformatics Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-7.	0.9	1

#	ARTICLE	IF	CITATIONS
16066	Cyclin B1 acts as a tumor microenvironment-related cancer promoter and prognostic biomarker in hepatocellular carcinoma. <i>Journal of International Medical Research</i> , 2021, 49, 030006052110162.	0.4	6
16067	A large-scale investigation into the role of classical HLA loci in multiple types of severe infections, with a focus on overlaps with autoimmune and mental disorders. <i>Journal of Translational Medicine</i> , 2021, 19, 230.	1.8	5
16069	Vaccine-induced ICOS+CD38+ circulating Tfh are sensitive biosensors of age-related changes in inflammatory pathways. <i>Cell Reports Medicine</i> , 2021, 2, 100262.	3.3	26
16071	FIBexDB: a new online transcriptome platform to analyze development of plant cellulosic fibers. <i>New Phytologist</i> , 2021, 231, 512-515.	3.5	6
16072	VB10, a new blood biomarker for differential diagnosis and recovery monitoring of acute viral and bacterial infections. <i>EBioMedicine</i> , 2021, 67, 103352.	2.7	15
16073	Transcriptional regulation of wound suberin deposition in potato cultivars with differential wound healing capacity. <i>Plant Journal</i> , 2021, 107, 77-99.	2.8	21
16074	Esomeprazole attenuates inflammatory and fibrotic response in lung cells through the MAPK/Nrf2/HO1 pathway. <i>Journal of Inflammation</i> , 2021, 18, 17.	1.5	9
16075	Genotypic Variability on Grain Yield and Grain Nutritional Quality Characteristics of Wheat Grown under Elevated CO <sub>2</sub> and High Temperature. <i>Plants</i> , 2021, 10, 1043.	1.6	13
16076	Interdependencies between Toll-like receptors in <i>Leishmania</i> infection. <i>Immunology</i> , 2021, 164, 173-189.	2.0	10
16077	Single-cell RNA sequencing reveals the sustained immune cell dysfunction in the pathogenesis of sepsis secondary to bacterial pneumonia. <i>Genomics</i> , 2021, 113, 1219-1233.	1.3	29
16078	Perspectives in systems nephrology. <i>Cell and Tissue Research</i> , 2021, 385, 475-488.	1.5	7
16079	Constraint-based models for dominating protein interaction networks. <i>IET Systems Biology</i> , 2021, 15, 148-162.	0.8	3
16081	Mining Indonesian Microbial Biodiversity for Novel Natural Compounds by a Combined Genome Mining and Molecular Networking Approach. <i>Marine Drugs</i> , 2021, 19, 316.	2.2	14
16082	Adenosine A2A receptor null chondrocyte transcriptome resembles that of human osteoarthritic chondrocytes. <i>Purinergic Signalling</i> , 2021, 17, 439-448.	1.1	3
16083	Comparative Transcriptomics of IBD Patients Indicates Induction of Type 2 Immunity Irrespective of the Disease Ideotype. <i>Frontiers in Medicine</i> , 2021, 8, 664045.	1.2	3
16085	Identification of significant genes as prognostic markers and potential tumor suppressors in lung adenocarcinoma via bioinformatical analysis. <i>BMC Cancer</i> , 2021, 21, 616.	1.1	17
16087	A non-genetic, cell cycle-dependent mechanism of platinum resistance in lung adenocarcinoma. <i>ELife</i> , 2021, 10, .	2.8	14
16088	Coordination of microbe-host homeostasis by crosstalk with plant innate immunity. <i>Nature Plants</i> , 2021, 7, 814-825.	4.7	95

#	ARTICLE	IF	CITATIONS
16089	Apoptotic vesicles restore liver macrophage homeostasis to counteract type 2 diabetes. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12109.	5.5	90
16090	Changes of gut microbiota in pregnant sows induced by 5-Aminolevulinic acid. <i>Research in Veterinary Science</i> , 2021, 136, 57-65.	0.9	5
16091	Neuronal ApoE upregulates MHC-I expression to drive selective neurodegeneration in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 786-798.	7.1	91
16093	Identification of diagnostic genes and vital microRNAs involved in rheumatoid arthritis: based on data mining and experimental verification. <i>PeerJ</i> , 2021, 9, e11427.	0.9	6
16094	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 3155.	5.8	93
16095	Solid-Phase Extraction Embedded Dialysis (SPEED), an Innovative Procedure for the Investigation of Microbial Specialized Metabolites. <i>Marine Drugs</i> , 2021, 19, 371.	2.2	3
16096	PAX2GRAPHML: a python library for large-scale regulation network analysis using BioPAX. <i>Bioinformatics</i> , 2021, 37, 4889-4891.	1.8	1
16097	Circular RNAs acting as ceRNAs mediated by miRNAs may be involved in the synthesis of soybean fatty acids. <i>Functional and Integrative Genomics</i> , 2021, 21, 435-450.	1.4	6
16098	The m <sup>6</sup> A-related gene signature for predicting the prognosis of breast cancer. <i>PeerJ</i> , 2021, 9, e11561.	0.9	8
16099	Co-occurrence of Protein Crotonylation and 2-Hydroxyisobutyrylation in the Proteome of End-Stage Renal Disease. <i>ACS Omega</i> , 2021, 6, 15782-15793.	1.6	7
16100	Specific metagenomic asset drives the spontaneous fermentation of Italian sausages. <i>Food Research International</i> , 2021, 144, 110379.	2.9	13
16102	Acaricidal Activity of Annonaceae Plants for <i>Dermanyssus gallinae</i> (Acari: Dermanyssidae) and Metabolomic Profile by HPLC-MS/MS. <i>Neotropical Entomology</i> , 2021, 50, 662-672.	0.5	5
16103	Comprehensive Analysis of Competing Endogenous RNA Network Focusing on Long Noncoding RNA Involved in Cirrhotic Hepatocellular Carcinoma. <i>Analytical Cellular Pathology</i> , 2021, 2021, 1-12.	0.7	3
16104	Molecular Characterisation of Uterine Endometrial Proteins during Early Stages of Pregnancy in Pigs by MALDI TOF/TOF. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6720.	1.8	7
16105	Elevated TYROBP expression predicts poor prognosis and high tumor immune infiltration in patients with low-grade glioma. <i>BMC Cancer</i> , 2021, 21, 723.	1.1	23
16109	Overexpression of DDIT4 and TPTEP1 are associated with metastasis and advanced stages in colorectal cancer patients: a study utilizing bioinformatics prediction and experimental validation. <i>Cancer Cell International</i> , 2021, 21, 303.	1.8	9
16110	Construction and Validation of a Macrophage-Associated Risk Model for Predicting the Prognosis of Osteosarcoma. <i>Journal of Oncology</i> , 2021, 2021, 1-18.	0.6	6
16111	Reconstruction of circRNA-miRNA-mRNA associated ceRNA networks reveal functional circRNAs in intracerebral hemorrhage. <i>Scientific Reports</i> , 2021, 11, 11584.	1.6	11

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16112	miR-340 Promotes Retinoblastoma Cell Proliferation, Migration and Invasion Through Targeting WIF1. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3635-3648.	1.0	5
16113	Transcriptomic landscape of early age onset of colorectal cancer identifies novel genes and pathways in Indian CRC patients. <i>Scientific Reports</i> , 2021, 11, 11765.	1.6	16
16114	Identification of Ten Mitosis Genes Associated with Tamoxifen Resistance in Breast Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3611-3624.	1.0	1
16115	Fucoidan induces ROS-dependent epigenetic modulation in cervical cancer HeLa cell. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 180-192.	3.6	20
16116	An Arabidopsis expression predictor enables inference of transcriptional regulators for gene modules. <i>Plant Journal</i> , 2021, 107, 597-612.	2.8	11
16118	Multi-target pharmacological mechanisms of <i>Salvia miltiorrhiza</i> against oral submucous fibrosis: A network pharmacology approach. <i>Archives of Oral Biology</i> , 2021, 126, 105131.	0.8	5
16119	Genome-Wide Differential Expression Profiling of Pulmonary circRNAs Associated With Immune Reaction to <i>Pasteurella multocida</i> in Goats. <i>Frontiers in Veterinary Science</i> , 2021, 8, 615405.	0.9	7
16120	Cell cycle dysregulation with overexpression of KIF2C/MCAK is a critical event in nasopharyngeal carcinoma. <i>Genes and Diseases</i> , 2023, 10, 212-227.	1.5	3
16122	Identification of key genes in the tumor microenvironment of lung adenocarcinoma. <i>Medical Oncology</i> , 2021, 38, 83.	1.2	7
16123	Exploring polyps to colon carcinoma voyage: can blocking the crossroad halt the sequence?. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 2199-2207.	1.2	5
16124	SWATH-MS and MRM: Quantification of Ras-related proteins in HIV-1 infected and methamphetamine-exposed human monocyte-derived macrophages (hMDM). <i>Proteomics</i> , 2021, 21, e2100005.	1.3	4
16125	Differential methylation of G-protein coupled receptor signaling genes in gastrointestinal neuroendocrine tumors. <i>Scientific Reports</i> , 2021, 11, 12303.	1.6	7
16126	Hyaluronan-mediated motility receptor expression functions as a prognostic biomarker in uterine carcinosarcoma based on bioinformatics analysis. <i>Journal of International Medical Research</i> , 2021, 49, 030006052110210.	0.4	3
16127	Genome-wide analysis of long non-coding RNAs (lncRNAs) in two contrasting soybean genotypes subjected to phosphate starvation. <i>BMC Genomics</i> , 2021, 22, 433.	1.2	7
16128	Low nitrogen availability inhibits the phosphorus starvation response in maize ( <i>Zea mays</i> ssp. <i>mays</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 259.	1.6	16
16129	A Network Pharmacology Approach to Reveal the Underlying Mechanisms of Zuogui Yin in the Treatment of Male Infertility. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 803-813.	0.6	2
16130	Ex vivo and in vivo chemoprotective activity and potential mechanism of Martynoside against 5-fluorouracil-induced bone marrow cytotoxicity. <i>Biomedicine and Pharmacotherapy</i> , 2021, 138, 111501.	2.5	7
16131	A comparative genome-wide analysis of the ABC transporter gene family among three <i>Gossypium</i> species. <i>Crop Science</i> , 2021, 61, 2489-2509.	0.8	1



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16132	Transcriptomic studies revealed pathophysiological impact of COVID-19 to predominant health conditions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
16133	Identification of Common Driver Gene Modules and Associations between Cancers through Integrated Network Analysis. <i>Global Challenges</i> , 2021, 5, 2100006.	1.8	2
16135	Expression and prognostic relevance of long noncoding RNAs CRNDE and AOX2P in adult acute myeloid leukemia. <i>International Journal of Laboratory Hematology</i> , 2021, 43, 732-742.	0.7	7
16136	Global proteomic analyses of human cytotrophoblast differentiation/invasion. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	5
16137	Jejunal mucosa proteomics unravel metabolic adaptive processes to mild chronic heat stress in dairy cows. <i>Scientific Reports</i> , 2021, 11, 12484.	1.6	14
16138	Exploration of the Key Proteins in the Normal-Adenoma-Carcinoma Sequence of Colorectal Cancer Evolution Using In-Depth Quantitative Proteomics. <i>Journal of Oncology</i> , 2021, 2021, 1-19.	0.6	2
16139	Integrative Analysis of Selected Metabolites and the Fungal Transcriptome during the Developmental Cycle of <i>Ganoderma lucidum</i> Strain G0119 Correlates Lignocellulose Degradation with Carbohydrate and Triterpenoid Metabolism. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0053321.	1.4	9
16140	Systems pharmacogenomics identifies novel targets and clinically actionable therapeutics for medulloblastoma. <i>Genome Medicine</i> , 2021, 13, 103.	3.6	10
16141	Expression Profiles of Circular RNAs in Human Papillary Thyroid Carcinoma Based on RNA Deep Sequencing. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3821-3832.	1.0	8
16142	Dynamic residue interaction network analysis of the oseltamivir binding site of N1 neuraminidase and its H274Y mutation site conferring drug resistance in influenza A virus. <i>PeerJ</i> , 2021, 9, e11552.	0.9	8
16144	Identification of IL-6 as a potential mediator of the myocardial fibrosis that occurs in response to surgery with cardiopulmonary bypass in children with Tetralogy of Fallot. <i>Cardiology in the Young</i> , 2022, 32, 223-229.	0.4	2
16145	hsa_circ_0060975 is highly expressed and predicts a poor prognosis in gastric cancer. <i>Oncology Letters</i> , 2021, 22, 619.	0.8	3
16146	netgsa: Fast computation and interactive visualization for topology-based pathway enrichment analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1008979.	1.5	8
16147	Transcriptome analysis during early regeneration of <i>Lumbriculus variegatus</i> . <i>Gene Reports</i> , 2021, 23, 101050.	0.4	7
16148	Depletion of acetate-producing bacteria from the gut microbiota facilitates cognitive impairment through the gut-brain neural mechanism in diabetic mice. <i>Microbiome</i> , 2021, 9, 145.	4.9	56
16149	Cannabinoid Receptor 1 associates to different molecular complexes during GABAergic neuron maturation. <i>Journal of Neurochemistry</i> , 2021, 158, 640-656.	2.1	2
16150	On the Use of Topological Features of Metabolic Networks for the Classification of Cancer Samples. <i>Current Genomics</i> , 2021, 22, 88-97.	0.7	0
16151	Identification of Clinically Relevant Subgroups of Chronic Lymphocytic Leukemia Through Discovery of Abnormal Molecular Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 627964.	1.1	2

#	ARTICLE	IF	CITATIONS
16152	Identification of genes associated with sudden cardiac death: a network- and pathway-based approach. <i>Journal of Thoracic Disease</i> , 2021, 13, 3610-3627.	0.6	0
16153	Identification of G-protein signaling modulator 2 as a diagnostic and prognostic biomarker of pancreatic adenocarcinoma: an exploration of its regulatory mechanisms. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 1164-1179.	0.6	3
16154	Resistance to different anthracycline chemotherapeutics elicits distinct and actionable primary metabolic dependencies in breast cancer. <i>ELife</i> , 2021, 10, .	2.8	23
16155	Sequence-Function Relationships in Phage-Encoded Bacterial Cell Wall Lytic Enzymes and Their Implications for Phage-Derived Product Design. <i>Journal of Virology</i> , 2021, 95, e0032121.	1.5	19
16156	Identification of differentially expressed genes-related prognostic risk model for survival prediction in breast carcinoma patients. <i>Aging</i> , 2021, 13, 16577-16599.	1.4	0
16157	TCR repertoire diversity in Multiple Sclerosis: High-dimensional bioinformatics analysis of sequences from brain, cerebrospinal fluid and peripheral blood. <i>EBioMedicine</i> , 2021, 68, 103429.	2.7	18
16159	Age-related changes in metabolites in young donor livers and old recipient sera after liver transplantation from young to old rats. <i>Aging Cell</i> , 2021, 20, e13425.	3.0	13
16160	Identification of differently expressed mRNAs by peripheral blood mononuclear cells in Vogt-Koyanagi-Harada disease. <i>Genes and Diseases</i> , 2022, 9, 1378-1388.	1.5	4
16161	Bioinformatic analysis of the human brain extracellular matrix proteome in neurodegenerative disorders. <i>European Journal of Neuroscience</i> , 2021, 53, 4016-4033.	1.2	14
16163	Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. <i>Molecular Cell</i> , 2021, 81, 2549-2565.e8.	4.5	47
16164	Proteome dataset of chili pepper plant ( <i>Capsicum frutescens</i> ) infested by broad mite ( <i>Polyphagotarsonemus latus</i> ). <i>Data in Brief</i> , 2021, 36, 107095.	0.5	0
16165	Comprehensive Scanning of Prophages in <i>Lactobacillus</i> : Distribution, Diversity, Antibiotic Resistance Genes, and Linkages with CRISPR-Cas Systems. <i>MSystems</i> , 2021, 6, e0121120.	1.7	34
16166	Connecting COPD GWAS Genes: FAM13A Controls TGF $\beta$ 2 Secretion by Modulating AP-3 Transport. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 65, 532-543.	1.4	4
16167	Changes and relationship of N6-methyladenosine modification and long non-coding RNAs in oxidative damage induced by cadmium in pancreatic $\beta$ -cells. <i>Toxicology Letters</i> , 2021, 343, 56-66.	0.4	19
16168	Time trajectories in the transcriptomic response to exercise - a meta-analysis. <i>Nature Communications</i> , 2021, 12, 3471.	5.8	48
16169	Dissecting Disease-Suppressive Rhizosphere Microbiomes by Functional Amplicon Sequencing and 10 $\times$ Metagenomics. <i>MSystems</i> , 2021, 6, e0111620.	1.7	27
16170	Rapid proliferation due to better metabolic adaptation results in full virulence of a filament-deficient <i>Candida albicans</i> strain. <i>Nature Communications</i> , 2021, 12, 3899.	5.8	31
16171	Construction of a Myc-associated ceRNA network reveals a prognostic signature in hepatocellular carcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 1033-1050.	2.3	13

#	ARTICLE	IF	CITATIONS
16172	KnowSeq R-Bioc package: The automatic smart gene expression tool for retrieving relevant biological knowledge. <i>Computers in Biology and Medicine</i> , 2021, 133, 104387.	3.9	16
16173	A meta-analysis of transcriptomic profiles of Huntington's disease patients. <i>PLoS ONE</i> , 2021, 16, e0253037.	1.1	17
16174	Identification of Full-Length Wild-Type and Mutant Huntingtin Interacting Proteins by Crosslinking Immunoprecipitation in Mice Brain Cortex. <i>Journal of Huntington's Disease</i> , 2021, 10, 335-347.	0.9	11
16175	A network-based analysis and experimental validation of traditional Chinese medicine Yuanhu Zhitong Formula in treating neuropathic pain. <i>Journal of Ethnopharmacology</i> , 2021, 274, 114037.	2.0	7
16176	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021, 184, 3333-3348.e19.	13.5	48
16178	Successive plant growth amplifies genotype-specific assembly of the tomato rhizosphere microbiome. <i>Science of the Total Environment</i> , 2021, 772, 144825.	3.9	38
16179	NORMA: The Network Makeup Artist – A Web Tool for Network Annotation Visualization. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 578-586.	3.0	8
16180	Arhgef2 regulates neural differentiation in the cerebral cortex through mRNA m6A-methylation of Npdc1 and Cend1. <i>iScience</i> , 2021, 24, 102645.	1.9	4
16181	Conspiracy of Corporate Networks in Corruption Scandals. <i>Frontiers in Physics</i> , 2021, 9, .	1.0	8
16182	A chromosome-level <i>Camptotheca acuminata</i> genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 3531.	5.8	66
16183	Expression Profiling and Functional Analysis of Circular RNAs in Inner Mongolian Cashmere Goat Hair Follicles. <i>Frontiers in Genetics</i> , 2021, 12, 678825.	1.1	19
16184	Genome-Wide Identification and Genetic Variations of the Starch Synthase Gene Family in Rice. <i>Plants</i> , 2021, 10, 1154.	1.6	12
16186	Gene Expression Profile and Co-Expression Network of Pearl Gentian Grouper under Cold Stress by Integrating Illumina and PacBio Sequences. <i>Animals</i> , 2021, 11, 1745.	1.0	12
16187	Mass spectrometry and machine learning for the accurate diagnosis of benzylpenicillin and multidrug resistance of <i>Staphylococcus aureus</i> in bovine mastitis. <i>PLoS Computational Biology</i> , 2021, 17, e1009108.	1.5	8
16188	Spatial Virome Analysis of <i>Zanthoxylum armatum</i> Trees Affected With the Flower Yellowing Disease. <i>Frontiers in Microbiology</i> , 2021, 12, 702210.	1.5	5
16189	Exosomal ncRNAs profiling of mycobacterial infection identified miRNA-185-5p as a novel biomarker for tuberculosis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	23
16190	RNA-seq analysis of laser microdissected <i>Arabidopsis thaliana</i> leaf epidermis, mesophyll and vasculature defines tissue-specific transcriptional responses to multiple stress treatments. <i>Plant Journal</i> , 2021, 107, 938-955.	2.8	31
16191	Protein Biomarkers of Bovine Defective Meats at a Glance: Gel-Free Hybrid Quadrupole-Orbitrap Analysis for Rapid Screening. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 7478-7487.	2.4	9

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16192	MicroRNA profiles in five pairs of early gastric cancer tissues and adjacent non-cancerous tissues. <i>Oncology Letters</i> , 2021, 22, 595.	0.8	9
16193	Effective Generation of Glucosylpericidins with Selective Cytotoxicities and Insights into Their Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0029421.	1.4	5
16195	Identification of Novel Alternative Splicing Events Associated With Tumorigenesis, Protein Modification, and Immune Microenvironment in Early-Onset Gastric Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 640272.	1.3	4
16196	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and GRAS gene expression analysis in Chinese white pear ( <i>Pyrus bretschneideri</i> Rehder). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2022, 50, 303-325.	0.7	5
16197	O-GlcNAcylation Prediction: An Unattained Objective. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2021, Volume 14, 87-102.	1.6	5
16198	Identification of Susceptible Genes for Chronic Obstructive Pulmonary Disease with Lung Adenocarcinoma by Weighted Gene Co-Expression Network Analysis. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3625-3634.	1.0	2
16199	Analysis of the Role of FRMD5 in the Biology of Papillary Thyroid Carcinoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6726.	1.8	5
16200	Functionality of the Crosswise Model for Assessing Sensitive or Transgressive Behavior: A Systematic Review and Meta-Analysis. <i>Frontiers in Psychology</i> , 2021, 12, 655592.	1.1	11
16201	A Systems-Based Key Innovation-Driven Approach Infers Co-option of Jaw Developmental Programs During Cancer Progression. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 682619.	1.8	3
16203	A network pharmacology approach to determine the underlying mechanisms of action of Yishen Tongluo formula for the treatment of oligoasthenozoospermia. <i>PLoS ONE</i> , 2021, 16, e0252906.	1.1	4
16204	Genome-wide identification and expression analysis of Raffinose synthetase family in cotton. <i>BMC Bioinformatics</i> , 2021, 22, 356.	1.2	7
16205	Single-cell RNA sequencing of human femoral head in vivo. <i>Aging</i> , 2021, 13, 15595-15619.	1.4	13
16206	Transcriptomic Analysis of Changes in Gene Expression During Flowering Induction in Sugarcane Under Controlled Photoperiodic Conditions. <i>Frontiers in Plant Science</i> , 2021, 12, 635784.	1.7	13
16207	VAL genes regulate vegetative phase change via miR156-dependent and independent mechanisms. <i>PLoS Genetics</i> , 2021, 17, e1009626.	1.5	18
16208	Inhibition of Polyamine Biosynthesis Using Difluoromethylornithine Acts as a Potent Immune Modulator and Displays Therapeutic Synergy With PD-1-blockade. <i>Journal of Immunotherapy</i> , 2021, 44, 283-291.	1.2	6
16209	A network pharmacology approach to explore the mechanism of HuangZhi YiShen Capsule for treatment of diabetic kidney disease. <i>Journal of Translational Internal Medicine</i> , 2021, 9, 98-113.	1.0	14
16210	Responses of juvenile fathead minnow ( <i>Pimephales promelas</i> ) gut microbiome to a chronic dietary exposure of benzo[a]pyrene. <i>Environmental Pollution</i> , 2021, 278, 116821.	3.7	12
16212	Application of Molecular Nanoprobes in the Analysis of Differentially Expressed Genes and Prognostic Models of Primary Hepatocellular Carcinoma. <i>Journal of Biomedical Nanotechnology</i> , 2021, 17, 1020-1033.	0.5	4

#	ARTICLE	IF	CITATIONS
16213	Angelica Dahurica Regulated the Polarization of Macrophages and Accelerated Wound Healing in Diabetes: A Network Pharmacology Study and In Vivo Experimental Validation. <i>Frontiers in Pharmacology</i> , 2021, 12, 678713.	1.6	11
16214	Viromes in marine ecosystems reveal remarkable invertebrate RNA virus diversity. <i>Science China Life Sciences</i> , 2022, 65, 426-437.	2.3	22
16215	Screening and identification of key genes in EBV-associated gastric carcinoma based on bioinformatics analysis. <i>Pathology Research and Practice</i> , 2021, 222, 153439.	1.0	4
16216	Emergent "core communities" of microbes, meiofauna and macrofauna at hydrothermal vents. <i>ISME Communications</i> , 2021, 1, .	1.7	9
16218	Study on the Molecular Mechanism of the Herbal Couple Sparganii Rhizoma-Curcumae Rhizoma in the Treatment of Lung Cancer Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	5
16219	An integrative transcriptome study reveals Ddit4/Redd1 as a key regulator of cancer cachexia in rodent models. <i>Cell Death and Disease</i> , 2021, 12, 652.	2.7	16
16222	Reciprocal priming between receptor tyrosine kinases at recycling endosomes orchestrates cellular signalling outputs. <i>EMBO Journal</i> , 2021, 40, e107182.	3.5	12
16223	Differential analysis revealing APOC1 to be a diagnostic and prognostic marker for liver metastases of colorectal cancer. <i>World Journal of Clinical Cases</i> , 2021, 9, 3880-3894.	0.3	3
16224	In silico analysis and prediction of transcription factors of the proteins interacting with astrocyte elevated gene-1. <i>Computational Biology and Chemistry</i> , 2021, 92, 107478.	1.1	3
16225	Metabolomics and Network Pharmacology-Based Investigation into the Mechanisms Underlying the Therapeutic Effect of a New Chinese Traditional Medicine (Cui Nai Ling) on Bromocriptine-Induced Hypogalactia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	2
16226	Naturally circulating pertactin-deficient <i>Bordetella pertussis</i> strains induce distinct gene expression and inflammatory signatures in human dendritic cells. <i>Emerging Microbes and Infections</i> , 2021, 10, 1358-1368.	3.0	5
16227	Network Pharmacology Analysis of the Effects of <i>Achyranthis Bidentatae Radix</i> Plus <i>Semen Vaccariae</i> on Migraine-induced Erectile Dysfunction. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 1474-1487.	0.6	1
16228	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021, 6, e0053721.	1.7	8
16231	Bioinformatics analysis of differentially expressed genes and pathways in the development of cervical cancer. <i>BMC Cancer</i> , 2021, 21, 733.	1.1	11
16232	Assessment of Evolutionary Relationships for Prioritization of Myxobacteria for Natural Product Discovery. <i>Microorganisms</i> , 2021, 9, 1376.	1.6	7
16233	Pangenomics reveals alternative environmental lifestyles among chlamydiae. <i>Nature Communications</i> , 2021, 12, 4021.	5.8	29
16234	Identification of Diagnostic Markers for Major Depressive Disorder Using Machine Learning Methods. <i>Frontiers in Neuroscience</i> , 2021, 15, 645998.	1.4	17
16235	Assessing Biosynthetic Gene Cluster Diversity of Specialized Metabolites in the Conserved Gut Symbionts of Herbivorous Turtle Ants. <i>Frontiers in Microbiology</i> , 2021, 12, 678100.	1.5	10

#	ARTICLE	IF	CITATIONS
16236	Systemic lupus erythematosus overlapping dermatomyositis owing to a heterozygous TREX1 Asp130Asn missense mutation. <i>Clinical Immunology</i> , 2021, 227, 108732.	1.4	3
16237	Untargeted Metabolomics Approach for the Discovery of Environment-Related Pyran-2-Ones Chemodiversity in a Marine-Sourced <i>Penicillium restrictum</i> . <i>Marine Drugs</i> , 2021, 19, 378.	2.2	6
16239	Identification of Critical Host Targets for HCV Infection: A Systems Biology Approach. , 2021, 6, 755-763.		1
16240	Expression profiles of radio-resistant genes in colorectal cancer cells. <i>Radiation Medicine and Protection</i> , 2021, 2, 48-54.	0.4	0
16241	Integrated regulatory network based on lncRNA-miRNA-mRNA-TF reveals key genes and sub-networks associated with dilated cardiomyopathy. <i>Computational Biology and Chemistry</i> , 2021, 92, 107500.	1.1	4
16242	Clinicopathological-Associated Regulatory Network of Deregulated circRNAs in Hepatocellular Carcinoma. <i>Cancers</i> , 2021, 13, 2772.	1.7	7
16244	Identification of Novel Cancer Stem Cell Markers in Glioblastoma by Comparing Tumor Cells with Stem-cell-like Cell Lines. <i>Revista GEINTEC</i> , 2021, 11, 1567-1583.	0.2	0
16245	Identification and analysis of genes associated with epithelial ovarian cancer by integrated bioinformatics methods. <i>PLoS ONE</i> , 2021, 16, e0253136.	1.1	7
16246	MecCog: a knowledge representation framework for genetic disease mechanism. <i>Bioinformatics</i> , 2021, 37, 4180-4186.	1.8	1
16247	scNetViz: from single cells to networks using Cytoscape. <i>F1000Research</i> , 2021, 10, 448.	0.8	1
16248	Stress Granules and Neurodegenerative Disorders: A Scoping Review. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 650740.	1.7	22
16249	Quantifying flexibility in thought: The resiliency of semantic networks differs across the lifespan. <i>Cognition</i> , 2021, 211, 104631.	1.1	40
16250	Systematic analysis of molecular characterization and clinical relevance of m6A regulators in digestive system pan-cancers. <i>Experimental Biology and Medicine</i> , 2021, 246, 2007-2018.	1.1	1
16251	DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in gastric cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 695-710.	2.3	25
16252	Morphologic and molecular correlates of EZH2 as a predictor of platinum resistance in high-grade ovarian serous carcinoma. <i>BMC Cancer</i> , 2021, 21, 714.	1.1	5
16253	Co-expression network analysis identifies novel molecular pathways associated with cadmium and pyriproxyfen testicular toxicity in <i>Gammarus fossarum</i> . <i>Aquatic Toxicology</i> , 2021, 235, 105816.	1.9	9
16254	In Vitro Characterization of the Innate Immune Pathways Engaged by Live and Inactivated Tick-Borne Encephalitis Virus. <i>Vaccines</i> , 2021, 9, 664.	2.1	3
16255	Pharmacoepigonomics circuits induced by a novel retinoid-polyamine conjugate in human immortalized keratinocytes. <i>Pharmacogenomics Journal</i> , 2021, 21, 638-648.	0.9	3



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16256	Transcriptomic and Metabolomic Data Reveal the Key Metabolic Pathways Affecting <i>Streltzoviella insularis</i> (Staudinger) (Lepidoptera: Cossidae) Larvae During Overwintering. <i>Frontiers in Physiology</i> , 2021, 12, 655059.	1.3	6
16257	Exploration of the Modulatory Property Mechanism of ELeng Capsule in the Treatment of Endometriosis Using Transcriptomics Combined With Systems Network Pharmacology. <i>Frontiers in Pharmacology</i> , 2021, 12, 674874.	1.6	6
16258	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	16.1	26
16259	The synergistic actions of hydrolytic genes reveal the mechanism of <i>Trichoderma harzianum</i> for cellulose degradation. <i>Journal of Biotechnology</i> , 2021, 334, 1-10.	1.9	14
16260	Identification of an EMT-Related Gene Signature for Predicting Overall Survival in Gastric Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 661306.	1.1	20
16261	Bioinformatics Analysis of Autophagy-related lncRNAs in Esophageal Carcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 1374-1384.	0.6	1
16262	Using Network-Based Machine Learning to Predict Transcription Factors Involved in Drought Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 652189.	1.1	15
16263	Rapid inÂvitro prototyping of O-methyltransferases for pathway applications in <i>Escherichia coli</i> . <i>Cell Chemical Biology</i> , 2021, 28, 876-886.e4.	2.5	12
16265	Bioactive constituents and the molecular mechanism of <i>Curcumae Rhizoma</i> in the treatment of primary dysmenorrhea based on network pharmacology and molecular docking. <i>Phytomedicine</i> , 2021, 86, 153558.	2.3	40
16266	Integrated analysis of ceRNA network in hepatocellular carcinoma using bioinformatics analysis. <i>Medicine (United States)</i> , 2021, 100, e26194.	0.4	4
16267	Reducing neutrophil exposure to oxygen allows their basal state maintenance. <i>Immunology and Cell Biology</i> , 2021, 99, 782-789.	1.0	6
16268	PRISMA and BioID disclose a motifs-based interactome of the intrinsically disordered transcription factor C/EBPÎ±. <i>IScience</i> , 2021, 24, 102686.	1.9	16
16269	Integrated SMRT Technology with UMI RNA-Seq Reveals the Hub Genes in Stamen Petalody in <i>Camellia oleifera</i> . <i>Forests</i> , 2021, 12, 749.	0.9	3
16270	Drug repurposing for hyperlipidemia associated disorders: An integrative network biology and machine learning approach. <i>Computational Biology and Chemistry</i> , 2021, 92, 107505.	1.1	4
16271	A Compendium of Age-Related PheWAS and GWAS Traits for Human Genetic Association Studies, Their Networks and Genetic Correlations. <i>Frontiers in Genetics</i> , 2021, 12, 680560.	1.1	3
16272	Meta-Analysis of Yield-Related and N-Responsive Genes Reveals Chromosomal Hotspots, Key Processes and Candidate Genes for Nitrogen-Use Efficiency in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 627955.	1.7	22
16273	Transcriptome in combination with experimental validation unveils hub immune-related genes in oriental river prawn <i>Macrobrachium nipponense</i> against <i>Spiroplasma eriocheiris</i> challenge. <i>Aquaculture</i> , 2021, 539, 736625.	1.7	4
16274	A defective interleukin-17 receptor A1 causes weight loss and intestinal metabolism-related gene downregulation in Japanese medaka, <i>Oryzias latipes</i> . <i>Scientific Reports</i> , 2021, 11, 12099.	1.6	4

#	ARTICLE	IF	CITATIONS
16275	Systems biology approach highlights mechanistic differences between Crohn's disease and ulcerative colitis. <i>Scientific Reports</i> , 2021, 11, 11519.	1.6	10
16277	Comprehensive transcriptome and metabolome profiling reveal metabolic mechanisms of <i>Nitraria sibirica</i> Pall. to salt stress. <i>Scientific Reports</i> , 2021, 11, 12878.	1.6	30
16278	Global Screening of LUBAC and OTULIN Interacting Proteins by Human Proteome Microarray. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 686395.	1.8	0
16279	Identifying a Serum Exosomal-Associated lncRNA/circRNA-miRNA-mRNA Network in Coronary Heart Disease. <i>Cardiology Research and Practice</i> , 2021, 2021, 1-10.	0.5	11
16280	Transcriptomic Analysis of Peripheral Monocytes upon Fingolimod Treatment in Relapsing Remitting Multiple Sclerosis Patients. <i>Molecular Neurobiology</i> , 2021, 58, 4816-4827.	1.9	7
16281	Genome-Wide Identification and Transcript Analysis of TCP Gene Family in Banana ( <i>Musa acuminata</i> L.). <i>Biochemical Genetics</i> , 2021, , 1.	0.8	10
16283	Brain Protein Expression Profile Confirms the Protective Effect of the ACTH(4-7)PGP Peptide (Semax) in a Rat Model of Cerebral Ischemia-Reperfusion. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6179.	1.8	10
16284	A Novel Autophagy-Related lncRNA Gene Signature to Improve the Prognosis of Patients with Melanoma. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	11
16285	Screening of cervical cancer-related hub genes based on comprehensive bioinformatics analysis. <i>Cancer Biomarkers</i> , 2021, 32, 1-13.	0.8	6
16286	Formation of autotriploid <i>Carassius auratus</i> and its fertility-related genes analysis. <i>BMC Genomics</i> , 2021, 22, 435.	1.2	3
16287	State-of-the-Art Biocatalysis. <i>ACS Central Science</i> , 2021, 7, 1105-1116.	5.3	59
16288	Interpreting the lipidome: bioinformatic approaches to embrace the complexity. <i>Metabolomics</i> , 2021, 17, 55.	1.4	7
16289	MicroRNAs expression analysis shows key affirmation of Synaptopodin-2 as a novel prognostic and therapeutic biomarker for colorectal and cervical cancers. <i>Heliyon</i> , 2021, 7, e07347.	1.4	4
16290	Alternative splicing perturbation landscape identifies RNA binding proteins as potential therapeutic targets in cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 792-806.	2.3	15
16291	Weighted Gene Co-Expression Network Analysis Identifies Five Hub Genes Associated with Metastasis in Synovial Sarcoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, .	0.6	1
16292	Preexisting hypertension and pregnancy-induced hypertension reveal molecular differences in placental proteome in rodents. <i>Physiological Genomics</i> , 2021, 53, 259-268.	1.0	3
16293	Temporal Changes of Virus-Like Particle Abundance and Metagenomic Comparison of Viral Communities in Cropland and Prairie Soils. <i>MSphere</i> , 2021, 6, e0116020.	1.3	12
16294	Systems Toxicology Approach for Assessing Developmental Neurotoxicity in Larval Zebrafish. <i>Frontiers in Genetics</i> , 2021, 12, 652632.	1.1	3

#	ARTICLE	IF	CITATIONS
16295	Protein residue network analysis reveals fundamental properties of the human coagulation factor VIII. <i>Scientific Reports</i> , 2021, 11, 12625.	1.6	6
16296	Buxuhuayu decoction accelerates angiogenesis by activating the PI3K-Akt-eNOS signalling pathway in a streptozotocin-induced diabetic ulcer rat model. <i>Journal of Ethnopharmacology</i> , 2021, 273, 113824.	2.0	14
16297	Prognostic Biomarkers on a Competitive Endogenous RNA Network Reveals Overall Survival in Triple-Negative Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 681946.	1.3	3
16298	Exploring microRNA target genes and identifying hub genes in bladder cancer based on bioinformatic analysis. <i>BMC Urology</i> , 2021, 21, 90.	0.6	2
16301	An Integrative Transcriptomic and Methylation Approach for Identifying Differentially Expressed Circular RNAs Associated with DNA Methylation Change. <i>Biomedicines</i> , 2021, 9, 657.	1.4	6
16302	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of <i>Kitasatospora</i> , a Genus Closely Related to <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 683814.	1.5	11
16303	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. <i>JCI Insight</i> , 2021, 6, .	2.3	14
16304	Quantitative Proteomics Reveals that Hsp90 Inhibition Dynamically Regulates Global Protein Synthesis in <i>Leishmania mexicana</i> . <i>MSystems</i> , 2021, 6, .	1.7	10
16305	Elucidating the Mechanism of Action of the Attributed Immunomodulatory Role of Eltrombopag in Primary Immune Thrombocytopenia: An In Silico Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6907.	1.8	10
16306	StrongestPath: a Cytoscape application for protein-protein interaction analysis. <i>BMC Bioinformatics</i> , 2021, 22, 352.	1.2	19
16308	Landscape-Based Mutational Sensitivity Cartography and Network Community Analysis of the SARS-CoV-2 Spike Protein Structures: Quantifying Functional Effects of the Circulating D614G Variant. <i>ACS Omega</i> , 2021, 6, 16216-16233.	1.6	10
16310	Insight into chemical basis of traditional Chinese medicine based on the state-of-the-art techniques of liquid chromatography-mass spectrometry. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1469-1492.	5.7	59
16311	Disruption of NEUROD2 causes a neurodevelopmental syndrome with autistic features via cell-autonomous defects in forebrain glutamatergic neurons. <i>Molecular Psychiatry</i> , 2021, 26, 6125-6148.	4.1	21
16312	Molecular signatures of silencing suppression degeneracy from a complex RNA virus. <i>PLoS Computational Biology</i> , 2021, 17, e1009166.	1.5	3
16313	Mapping the multiscale structure of biological systems. <i>Cell Systems</i> , 2021, 12, 622-635.	2.9	19
16314	Transcriptional drug repositioning and cheminformatics approach for differentiation therapy of leukaemia cells. <i>Scientific Reports</i> , 2021, 11, 12537.	1.6	6
16315	Systemic Blockade of Clever-1 Elicits Lymphocyte Activation Alongside Checkpoint Molecule Downregulation in Patients with Solid Tumors: Results from a Phase I/II Clinical Trial. <i>Clinical Cancer Research</i> , 2021, 27, 4205-4220.	3.2	29
16316	Tyr-Asp inhibition of glyceraldehyde 3-phosphate dehydrogenase affects plant redox metabolism. <i>EMBO Journal</i> , 2021, 40, e106800.	3.5	29

#	ARTICLE	IF	CITATIONS
16317	An integrated overview of the bacterial flora composition of <i>Hyalomma anatolicum</i> , the main vector of CCHF. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009480.	1.3	9
16318	In Silico and In Vivo Studies on the Mechanisms of Chinese Medicine Formula (Gegen Qinlian) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	19
16319	Therapeutic Interleukin-6 Trans-signaling Inhibition by Olamkicept (sgp130Fc) in Patients With Active Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2021, 160, 2354-2366.e11.	0.6	120
16320	Multi-Omics Approach Reveals the Potential Core Vaccine Targets for the Emerging Foodborne Pathogen <i>Campylobacter jejuni</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 665858.	1.5	7
16321	The Placental Response to Guinea Pig Cytomegalovirus Depends Upon the Timing of Maternal Infection. <i>Frontiers in Immunology</i> , 2021, 12, 686415.	2.2	2
16322	Identification and characterization of immune-related lncRNAs and lncRNA-miRNA-mRNA networks of <i>Paralichthys olivaceus</i> involved in <i>Vibrio anguillarum</i> infection. <i>BMC Genomics</i> , 2021, 22, 447.	1.2	17
16323	Oxysterols Modify NLRP2 in Epithelial Cells, Identifying a Mediator of Ozone-induced Inflammation. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 65, 500-512.	1.4	5
16324	Identification and prediction of common molecular culprits between psoriasis and melanoma via bioinformatical analysis. <i>Gene Reports</i> , 2021, 23, 101143.	0.4	0
16325	A network-based approach to identify key genes between follicular thyroid cancer and follicular thyroid adenoma. <i>Gene Reports</i> , 2021, 23, 101075.	0.4	1
16326	Integrated bioinformatics analysis and screening of hub genes in papillary thyroid carcinoma. <i>PLoS ONE</i> , 2021, 16, e0251962.	1.1	3
16327	Drug target gene-based analyses of drug repositionability in rare and intractable diseases. <i>Scientific Reports</i> , 2021, 11, 12338.	1.6	5
16328	Highly Sensitive Flow Cytometry Allows Monitoring of Changes in Circulating Immune Cells in Blood After Tdap Booster Vaccination. <i>Frontiers in Immunology</i> , 2021, 12, 666953.	2.2	17
16329	Identification of Lung and Blood Microbiota Implicated in COVID-19 Prognosis. <i>Cells</i> , 2021, 10, 1452.	1.8	10
16330	Glycyrrhizic Acid for COVID-19: Findings of Targeting Pivotal Inflammatory Pathways Triggered by SARS-CoV-2. <i>Frontiers in Pharmacology</i> , 2021, 12, 631206.	1.6	18
16331	MCM4 Is a Novel Biomarker Associated With Genomic Instability, BRCAness Phenotype, and Therapeutic Potentials in Soft-Tissue Sarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 666376.	1.8	3
16332	Engineering osteoarthritic cartilage model through differentiating senescent human mesenchymal stem cells for testing disease-modifying drugs. <i>Science China Life Sciences</i> , 2022, 65, 309-327.	2.3	9
16333	Root-associated (rhizosphere and endosphere) microbiomes of the <i>Miscanthus sinensis</i> and their response to the heavy metal contamination. <i>Journal of Environmental Sciences</i> , 2021, 104, 387-398.	3.2	53
16334	Study of mangal based naphthoquinone derivatives anticancer potential towards chemo-resistance related Never in mitosis gene A-related kinase 2-Insilico approach. <i>Molecular Simulation</i> , 2021, 47, 1078-1092.	0.9	3

#	ARTICLE	IF	CITATIONS
16335	Mapping Proximity Associations of Core Spindle Assembly Checkpoint Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 3414-3427.	1.8	10
16336	Transcription-associated topoisomerase 2 $\pm$ (TOP2A) activity is a major effector of cytotoxicity induced by G-quadruplex ligands. <i>ELife</i> , 2021, 10, .	2.8	46
16337	Utilizing MIKC-type MADS-box protein SOC1 for yield potential enhancement in maize. <i>Plant Cell Reports</i> , 2021, 40, 1679-1693.	2.8	12
16338	TCGA dataset screening for genes implicated in endometrial cancer using RNA-seq profiling. <i>Cancer Genetics</i> , 2021, 254-255, 40-47.	0.2	2
16339	Gene interaction network to unravel the role of gut bacterial species in cardiovascular diseases: E. coli O157:H7 host-bacterial interaction study. <i>Computers in Biology and Medicine</i> , 2021, 133, 104417.	3.9	14
16340	circPTPN22 as a novel biomarker and ceRNA in peripheral blood mononuclear cells of rheumatoid arthritis. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	16
16341	G-quadruplex binders as cytostatic modulators of innate immune genes in cancer cells. <i>Nucleic Acids Research</i> , 2021, 49, 6673-6686.	6.5	26
16342	Neuronal Graphs: A Graph Theory Primer for Microscopic, Functional Networks of Neurons Recorded by Calcium Imaging. <i>Frontiers in Neural Circuits</i> , 2021, 15, 662882.	1.4	10
16343	TNF blockade uncouples toxicity from antitumor efficacy induced with CD40 chemoimmunotherapy. <i>JCI Insight</i> , 2021, 6, .	2.3	6
16344	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 110.	3.0	108
16345	Changes in the Allostatic Response to Whole-Body Cryotherapy and Static-Stretching Exercises in Chronic Fatigue Syndrome Patients vs. Healthy Individuals. <i>Journal of Clinical Medicine</i> , 2021, 10, 2795.	1.0	2
16346	The DNA Sensor IFIX Drives Proteome Alterations To Mobilize Nuclear and Cytoplasmic Antiviral Responses, with Its Acetylation Acting as a Localization Toggle. <i>MSystems</i> , 2021, 6, e0039721.	1.7	8
16347	Systematic analysis of exonic germline and postzygotic de novo mutations in bipolar disorder. <i>Nature Communications</i> , 2021, 12, 3750.	5.8	15
16349	<i>Burkholderia</i> from Fungus Gardens of Fungus-Growing Ants Produces Antifungals That Inhibit the Specialized Parasite <i>Escovopsis</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0017821.	1.4	8
16350	Integrative Transcriptomic Analysis Reveals Distinctive Molecular Traits and Novel Subtypes of Collecting Duct Carcinoma. <i>Cancers</i> , 2021, 13, 2903.	1.7	7
16351	Transcriptomic landscape of circulating mononuclear phagocytes in Langerhans cell histiocytosis at the single-cell level. <i>Blood</i> , 2021, 138, 1237-1248.	0.6	13
16352	Proteomic analysis of chicken bone marrow-derived dendritic cells in response to an inactivated IBV $\Delta$ NDV poultry vaccine. <i>Scientific Reports</i> , 2021, 11, 12666.	1.6	4
16353	Proteomics Analysis Reveals Bacterial Antibiotics Resistance Mechanism Mediated by <i>ahslyA</i> Against Enoxacin in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 699415.	1.5	2

#	ARTICLE	IF	CITATIONS
16354	Comprehensive high-throughput meta-analysis of differentially expressed microRNAs in transcriptomic datasets reveals significant disruption of MAPK/JNK signal transduction pathway in Adult T-cell leukemia/lymphoma. <i>Infectious Agents and Cancer</i> , 2021, 16, 49.	1.2	5
16355	Comprehensive transcriptome analysis of peripheral blood unravels key lncRNAs implicated in ABPA and asthma. <i>PeerJ</i> , 2021, 9, e11453.	0.9	0
16356	Low-density lipoprotein receptor-related protein 1 (LRP1) is a novel receptor for apolipoprotein A4 (APOA4) in adipose tissue. <i>Scientific Reports</i> , 2021, 11, 13289.	1.6	16
16358	Atg7 deficiency in microglia drives an altered transcriptomic profile associated with an impaired neuroinflammatory response. <i>Molecular Brain</i> , 2021, 14, 87.	1.3	6
16359	Involvement of plasminogen activator inhibitor-1 and its related molecules in atrial fibrosis in patients with atrial fibrillation. <i>PeerJ</i> , 2021, 9, e11488.	0.9	3
16360	Antiproliferative activity of <i>Syzygium coriaceum</i> , an endemic plant of Mauritius, with its UPLC-MS metabolite fingerprint: A mechanistic study. <i>PLoS ONE</i> , 2021, 16, e0252276.	1.1	9
16361	Comparative transcriptome analysis reveals key genes associated with pigmentation in radish ( <i>Raphanus sativus</i> L.) skin and flesh. <i>Scientific Reports</i> , 2021, 11, 11434.	1.6	9
16362	Transcriptome and physiological analyses provide insights into the leaf epicuticular wax accumulation mechanism in yellowhorn. <i>Horticulture Research</i> , 2021, 8, 134.	2.9	14
16363	Global Proteomic Profiling of Pediatric AML: A Pilot Study. <i>Cancers</i> , 2021, 13, 3161.	1.7	6
16364	Integrating genome-wide association and transcriptome prediction model identifies novel target genes for osteoporosis. <i>Osteoporosis International</i> , 2021, 32, 2493-2503.	1.3	4
16365	Effect of Dietary Tryptophan on Growth, Intestinal Microbiota, and Intestinal Gene Expression in an Improved Triploid Crucian Carp. <i>Frontiers in Nutrition</i> , 2021, 8, 676035.	1.6	15
16366	Expression of a maize SOC1 gene enhances soybean yield potential through modulating plant growth and flowering. <i>Scientific Reports</i> , 2021, 11, 12758.	1.6	15
16367	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021, 81, 2533-2548.e9.	4.5	31
16368	Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021, 81, 2656-2668.e8.	4.5	137
16369	Genomic insights into the fast growth of paulownias and the formation of Paulownia witches' broom. <i>Molecular Plant</i> , 2021, 14, 1668-1682.	3.9	39
16370	SARS-CoV-2 exacerbates proinflammatory responses in myeloid cells through C-type lectin receptors and Tweety family member 2. <i>Immunity</i> , 2021, 54, 1304-1319.e9.	6.6	115
16371	Molecular Mechanisms of the Toll-Like Receptor, STING, MAVS, Inflammasome, and Interferon Pathways. <i>MSystems</i> , 2021, 6, e0033621.	1.7	9
16373	Development and Validation of Novel Biomarkers Related to M2 Macrophages Infiltration by Weighted Gene Co-Expression Network Analysis in Prostate Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 634075.	1.3	10



#	ARTICLE	IF	CITATIONS
16374	A proteomic investigation of isogenic radiation resistant prostate cancer cell lines. <i>Proteomics - Clinical Applications</i> , 2021, 15, 2100037.	0.8	4
16375	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021, 12, 3503.	5.8	97
16377	Nucleocytoplasmic transport of the RNA-binding protein CELF2 regulates neural stem cell fates. <i>Cell Reports</i> , 2021, 35, 109226.	2.9	16
16379	Measurement of Volatile Compounds for Real-Time Analysis of Soil Microbial Metabolic Response to Simulated Snowmelt. <i>Frontiers in Microbiology</i> , 2021, 12, 679671.	1.5	5
16380	Integrated network analysis identifying potential novel drug candidates and targets for Parkinson's disease. <i>Scientific Reports</i> , 2021, 11, 13154.	1.6	8
16381	A Combined Network Pharmacology and Molecular Docking Approach to Investigate Candidate Active Components and Multitarget Mechanisms of <i>Hemerocallis</i> Flowers on Antidepressant Effect. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	3
16382	±-Terpineol fumigation alleviates negative plant-soil feedbacks of <i>Panax notoginseng</i> via suppressing Ascomycota and enriching antagonistic bacteria. <i>Phytopathology Research</i> , 2021, 3, .	0.9	13
16383	Transcriptome Analysis of Microglia Reveals That the TLR2/IRF7 Signaling Axis Mediates Neuroinflammation After Subarachnoid Hemorrhage. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 645649.	1.7	7
16384	Identification of Atrial Fibrillation-Associated Genes ERBB2 and MYPN Using Genome-Wide Association and Transcriptome Expression Profile Data on Leftâ€”Right Atrial Appendages. <i>Frontiers in Genetics</i> , 2021, 12, 696591.	1.1	3
16385	Disruption of nucleocytoplasmic trafficking as a cellular senescence driver. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1092-1108.	3.2	19
16386	Identification and characterization of microRNAs in the immature stage of the beneficial predatory bug <i>Arma chinensis</i> Fallou (Hemiptera: Pentatomidae). <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21796.	0.6	3
16387	A MicroRNA-Based Network Provides Potential Predictive Signatures and Reveals the Crucial Role of PI3K/AKT Signaling for Hepatic Lineage Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 670059.	1.8	3
16388	Chamber-enriched gene expression profiles in failing human hearts with reduced ejection fraction. <i>Scientific Reports</i> , 2021, 11, 11839.	1.6	14
16390	Investigation of the antimony fractions and indigenous microbiota in aerobic and anaerobic rice paddies. <i>Science of the Total Environment</i> , 2021, 771, 145408.	3.9	17
16391	Screening and identification of potential biomarkers and therapeutic targets for systemic sclerosis-associated interstitial lung disease. <i>Archives of Rheumatology</i> , 2021, 36, 548-559.	0.3	0
16392	A few dominant bacteria and their genomic basis in mediating distinct ecosystem functions. <i>Environmental Microbiology</i> , 2021, 23, 4478-4488.	1.8	2
16393	A comparative genomic database of skeletogenesis genes: from fish to mammals. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100796.	0.4	2
16394	Green tea infusion prevents diabetic nephropathy aggravation in recent-onset type 1 diabetes regardless of glycemic control. <i>Journal of Ethnopharmacology</i> , 2021, 274, 114032.	2.0	8

#	ARTICLE	IF	CITATIONS
16395	Application of a High-Content Screening Assay Utilizing Primary Human Lung Fibroblasts to Identify Antifibrotic Drugs for Rapid Repurposing in COVID-19 Patients. <i>SLAS Discovery</i> , 2021, 26, 1091-1106.	1.4	3
16396	Optimising SARS-CoV-2 pooled testing strategies on social networks for low-resource settings. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2021, 54, 294002.	0.7	1
16397	The endogenous cellular protease inhibitor SPINT2 controls SARS-CoV-2 viral infection and is associated to disease severity. <i>PLoS Pathogens</i> , 2021, 17, e1009687.	2.1	4
16398	miRNAs generated from Meg3-Mirg locus are downregulated during aging. <i>Aging</i> , 2021, 13, 15875-15897.	1.4	2
16399	Ayurveda botanicals in COVID-19 management: An in silico multi-target approach. <i>PLoS ONE</i> , 2021, 16, e0248479.	1.1	60
16400	Neuronal Cytoskeleton in Intellectual Disability: From Systems Biology and Modeling to Therapeutic Opportunities. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6167.	1.8	13
16404	Potential biomarkers for lung adenocarcinoma identified by integrative transcriptomics analysis. <i>Tarla Bitkileri Merkez Arastirma Enstitusu</i> , 2021, 30, 33-42.	0.2	1
16405	A novel method to identify gene interaction patterns. <i>BMC Genomics</i> , 2021, 22, 436.	1.2	5
16407	Î2-elemene alleviates airway stenosis via the ILK/Akt pathway modulated by MIR143HG sponging miR-1275. <i>Cellular and Molecular Biology Letters</i> , 2021, 26, 28.	2.7	7
16408	N6-Methyladenosine RNA Methylation Regulator-Related Alternative Splicing (AS) Gene Signature Predicts Non-“Small Cell Lung Cancer Prognosis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 657087.	1.6	19
16409	Compositional and genetic alterations in Gravesâ€™ disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	4.4	30
16410	The landscape and biological relevance of aberrant alternative splicing events in esophageal squamous cell carcinoma. <i>Oncogene</i> , 2021, 40, 4184-4197.	2.6	8
16411	Identification of VEGFA-centric temporal hypoxia-responsive dynamic cardiopulmonary network biomarkers. <i>Life Sciences</i> , 2021, 281, 119718.	2.0	1
16413	Synaptic disruption and CREB-regulated transcription are restored by K <sup>+</sup> channel blockers in ALS. <i>EMBO Molecular Medicine</i> , 2021, 13, e13131.	3.3	22
16414	MicroRNA Sequences Modulated by Beta Cell Lipid Metabolism: Implications for Type 2 Diabetes Mellitus. <i>Biology</i> , 2021, 10, 534.	1.3	4
16415	Tankyrase regulates epithelial lumen formation via suppression of Rab11 GEFs. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	6
16416	Transplanting experiment and transcriptome sequencing reveal the potential ecological adaptation to plateau environments in the allopolyploid <i>Isoetes sinensis</i> . <i>Aquatic Botany</i> , 2021, 172, 103394.	0.8	5
16417	Integrated analysis of multiple microarray studies to identify potential pathogenic gene modules in preeclampsia. <i>Experimental and Molecular Pathology</i> , 2021, 120, 104631.	0.9	6

#	ARTICLE	IF	CITATIONS
16418	Identification of Key Gene Networks Associated With Cell Wall Components Leading to Flesh Firmness in Watermelon. <i>Frontiers in Plant Science</i> , 2021, 12, 630243.	1.7	14
16419	Co-occurrence of enzyme domains guides the discovery of an oxazolone synthetase. <i>Nature Chemical Biology</i> , 2021, 17, 794-799.	3.9	13
16420	Side effect prediction based on drug-induced gene expression profiles and random forest with iterative feature selection. <i>Pharmacogenomics Journal</i> , 2021, 21, 673-681.	0.9	14
16421	Yanghe Decoction Suppresses the Experimental Autoimmune Thyroiditis in Rats by Improving NLRP3 Inflammasome and Immune Dysregulation. <i>Frontiers in Pharmacology</i> , 2021, 12, 645354.	1.6	14
16422	Constrained G4 structures unveil topology specificity of known and new G4 binding proteins. <i>Scientific Reports</i> , 2021, 11, 13469.	1.6	15
16423	MicroRNA-142-3p suppresses cell proliferation, invasion and epithelial-to-mesenchymal transition via RAC1-ERK1/2 signaling in colorectal cancer. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	10
16424	Inhibition of biogenic amines accumulation during Yucha fermentation by autochthonous <i>Lactobacillus plantarum</i> strains. <i>Journal of Food Processing and Preservation</i> , 2021, 45, e15291.	0.9	6
16425	LPMO-oxidized cellulose oligosaccharides evoke immunity in <i>Arabidopsis</i> conferring resistance towards necrotrophic fungus <i>B. cinerea</i> . <i>Communications Biology</i> , 2021, 4, 727.	2.0	33
16426	Molecular networking-based chemical profiling and anti-influenza viral and neuroprotective effects of <i>Elaeocarpus hygrophilus</i> Kurz.. <i>Chemical Papers</i> , 2021, 75, 5323-5337.	1.0	2
16427	A catalog of the diversity and ubiquity of bacterial microcompartments. <i>Nature Communications</i> , 2021, 12, 3809.	5.8	55
16428	ALKBH1-8 and FTO: Potential Therapeutic Targets and Prognostic Biomarkers in Lung Adenocarcinoma Pathogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 633927.	1.8	13
16429	Joint contributions of the gut microbiota and host genetics to feed efficiency in chickens. <i>Microbiome</i> , 2021, 9, 126.	4.9	58
16430	The amino acid substitution affects cellular response to mistranslation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	10
16431	Tripartite Separation of Glomerular Cell Types and Proteomes from Reporter-Free Mice. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2175-2193.	3.0	16
16432	Dissecting the novel mechanism of reduning injection in treating Coronavirus Disease 2019 (COVID-19) based on network pharmacology and experimental verification. <i>Journal of Ethnopharmacology</i> , 2021, 273, 113871.	2.0	23
16433	Extensive remodeling of the extracellular matrix during aging contributes to age-dependent impairments of muscle stem cell functionality. <i>Cell Reports</i> , 2021, 35, 109223.	2.9	49
16434	Computational Identification of miRNAs and Temperature-Responsive lncRNAs From Mango ( <i>Mangifera</i> ) Tj ETQq0 0 0 rgBT /Qverlock 10	1.1	7
16435	Reduced mitochondrial DNA and OXPHOS protein content in skeletal muscle of children with cerebral palsy. <i>Developmental Medicine and Child Neurology</i> , 2021, 63, 1204-1212.	1.1	9

#	ARTICLE	IF	CITATIONS
16436	Asporin inhibits collagen matrix-mediated intercellular mechanocommunications between fibroblasts during keloid progression. <i>FASEB Journal</i> , 2021, 35, e21705.	0.2	12
16437	A proximity-dependent biotinylation map of a human cell. <i>Nature</i> , 2021, 595, 120-124.	13.7	263
16438	Identification of a Competing Endogenous RNA Network Related to Immune Signature in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 665555.	1.1	2
16439	A metabolic data-driven systems pharmacology strategy for decoding and validating the mechanism of Compound Kushen Injection against HCC. <i>Journal of Ethnopharmacology</i> , 2021, 274, 114043.	2.0	10
16440	KRT7 Overexpression is Associated with Poor Prognosis and Immune Cell Infiltration in Patients with Pancreatic Adenocarcinoma. <i>International Journal of General Medicine</i> , 2021, Volume 14, 2677-2694.	0.8	11
16441	Comparing the efficacy of $\hat{I}^3$ - and electron-irradiation of PBMCs to promote secretion of paracrine, regenerative factors. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 21, 14-27.	1.8	2
16442	Screening of Biological Target Molecules Related to Glucocorticoid-Induced Cataract (GIC) on the Basis of Constructing ceRNA Network. <i>Biochemical Genetics</i> , 2022, 60, 24-38.	0.8	0
16443	Investigating the active compounds and mechanism of HuaShi XuanFei formula for prevention and treatment of COVID-19 based on network pharmacology and molecular docking analysis. <i>Molecular Diversity</i> , 2022, 26, 1175-1190.	2.1	14
16444	Insights Into the Mechanisms Implicated in Pinus pinaster Resistance to Pinewood Nematode. <i>Frontiers in Plant Science</i> , 2021, 12, 690857.	1.7	15
16447	Identification of Dysregulated Complement Activation Pathways Driven by N-Glycosylation Alterations in T2D Patients. <i>Frontiers in Chemistry</i> , 2021, 9, 677621.	1.8	7
16448	Inhibition of the Human Hsc70 System by Small Ligands as a Potential Anticancer Approach. <i>Cancers</i> , 2021, 13, 2936.	1.7	7
16449	Pan-cancer characterization of long non-coding RNA and DNA methylation mediated transcriptional dysregulation. <i>EBioMedicine</i> , 2021, 68, 103399.	2.7	25
16450	Identification of Key Pathways and Genes in Obesity Using Bioinformatics Analysis and Molecular Docking Studies. <i>Frontiers in Endocrinology</i> , 2021, 12, 628907.	1.5	11
16451	A network-biology approach for identification of key genes and pathways involved in malignant peritoneal mesothelioma. <i>Genomics and Informatics</i> , 2021, 19, e16.	0.4	4
16452	Comparative transcriptome analysis reveals distinct gene expression profiles in <i>Brachypodium distachyon</i> infected by two fungal pathogens. <i>BMC Plant Biology</i> , 2021, 21, 304.	1.6	5
16453	A Comprehensive Analysis of the Downregulation of miRNA-1827 and Its Prognostic Significance by Targeting SPTBN2 and BCL2L1 in Ovarian Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 687576.	1.6	6
16454	Coordinated action of human papillomavirus type 16 E6 and E7 oncoproteins on competitive endogenous RNA (ceRNA) network members in primary human keratinocytes. <i>BMC Cancer</i> , 2021, 21, 673.	1.1	5
16455	Intrahepatic TLR3 and IFNL3 Expressions Are Associated with Stages of Fibrosis in Chronic Hepatitis C. <i>Viruses</i> , 2021, 13, 1103.	1.5	3

#	ARTICLE	IF	CITATIONS
16456	Tumor Microenvironment Subtypes and Immune-Related Signatures for the Prognosis of Breast Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	2
16457	Transcriptomic heterogeneity of driver gene mutations reveals novel mutual exclusivity and improves exploration of functional associations. <i>Cancer Medicine</i> , 2021, 10, 4977-4993.	1.3	1
16458	Pharmacophore based in silico study with laboratory verification—environmental explanation of prostate cancer recurrence. <i>Environmental Science and Pollution Research</i> , 2021, 28, 61581-61591.	2.7	17
16459	Revealing the Viral Community in the Hadal Sediment of the New Britain Trench. <i>Genes</i> , 2021, 12, 990.	1.0	2
16460	Overlapping Structures Detection in Protein-Protein Interaction Networks Using Community Detection Algorithm Based on Neighbor Clustering Coefficient. <i>Frontiers in Genetics</i> , 2021, 12, 689515.	1.1	1
16461	Transcriptome profiling of developing leaf and shoot apices to reveal the molecular mechanism and co-expression genes responsible for the wheat heading date. <i>BMC Genomics</i> , 2021, 22, 468.	1.2	11
16462	Combination of high-throughput microfluidics and FACS technologies to leverage the numbers game in natural product discovery. <i>Microbial Biotechnology</i> , 2022, 15, 415-430.	2.0	8
16463	hsp-90 and unc-45 depletion induce characteristic transcriptional signatures in coexpression cliques of <i>C. elegans</i> . <i>Scientific Reports</i> , 2021, 11, 12852.	1.6	2
16464	A computational approach for detecting physiological homogeneity in the midst of genetic heterogeneity. <i>American Journal of Human Genetics</i> , 2021, 108, 1012-1025.	2.6	6
16465	Genome reduction and relaxed selection is associated with the transition to symbiosis in the basidiomycete genus <i>Podaxis</i> . <i>iScience</i> , 2021, 24, 102680.	1.9	9
16466	Computational analysis of protein stability and allosteric interaction networks in distinct conformational forms of the SARS-CoV-2 spike D614G mutant: reconciling functional mechanisms through allosteric model of spike regulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 9724-9741.	2.0	11
16467	Prolonged exposure to traffic-related particulate matter and gaseous pollutants implicate distinct molecular mechanisms of lung injury in rats. <i>Particle and Fibre Toxicology</i> , 2021, 18, 24.	2.8	14
16468	The relationship between lncRNAs and lung adenocarcinoma as well as their ceRNA network. <i>Cancer Biomarkers</i> , 2021, 31, 165-176.	0.8	6
16469	Transcriptome Analyses Provide Insights into the Aggressive Behavior toward Conspecific and Heterospecific in <i>Thitarodes xiaojinensis</i> (Lepidoptera: Hepialidae). <i>Insects</i> , 2021, 12, 577.	1.0	1
16471	Identification of Early Diagnostic and Prognostic Biomarkers via WGCNA in Stomach Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 636461.	1.3	23
16472	Dysregulation of core circadian genes, <i>BMAL1</i> and <i>CLOCK</i> , in colorectal cancer. <i>Biological Rhythm Research</i> , 0, , 1-14.	0.4	1
16473	Translational Proteomics Analysis of Anthracycline-Induced Cardiotoxicity From Cardiac Microtissues to Human Heart Biopsies. <i>Frontiers in Genetics</i> , 2021, 12, 695625.	1.1	12
16474	Identifying Hypoxia Characteristics to Stratify Prognosis and Assess the Tumor Immune Microenvironment in Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 606816.	1.1	8

#	ARTICLE	IF	CITATIONS
16475	Construction of Two Alternative Polyadenylation Signatures to Predict the Prognosis of Sarcoma Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 595331.	1.8	5
16477	Sec62 promotes pro-angiogenesis of hepatocellular carcinoma cells under hypoxia. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 747-755.	0.9	10
16478	An efficient marker recycling system for sequential gene deletion in a deep sea-derived fungus <i>Acremonium</i> sp. HDN16-126. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 127-133.	1.8	4
16479	Legumes as Functional Food for Cardiovascular Disease. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 5475.	1.3	15
16480	Novel loci and potential mechanisms of major depressive disorder, bipolar disorder, and schizophrenia. <i>Science China Life Sciences</i> , 2022, 65, 167-183.	2.3	9
16481	Rapid Repurposing of Novel Combination Drugs for the Treatment of Heart Failure via a Computationally Guided Network Screening Approach. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 5223-5232.	2.5	6
16482	Quantitative Proteomics Reveals Knockdown of CD44 Promotes Proliferation and Migration in Claudin-Low MDA-MB-231 and Hs 578T Breast Cancer Cell Lines. <i>Journal of Proteome Research</i> , 2021, 20, 3720-3733.	1.8	4
16483	CROsBAR: comprehensive resource of biomedical relations with knowledge graph representations. <i>Nucleic Acids Research</i> , 2021, 49, e96-e96.	6.5	19
16484	Dietary phosphorus and calcium in feed affects miRNA profiles and their mRNA targets in jejunum of two strains of laying hens. <i>Scientific Reports</i> , 2021, 11, 13534.	1.6	5
16485	Spatial and temporal distribution of aerobic anoxygenic phototrophic bacteria: key functional groups in biological soil crusts. <i>Environmental Microbiology</i> , 2021, 23, 3554-3567.	1.8	10
16487	Integrated analysis on transcriptome and behaviors defines HTT repeat-dependent network modules in Huntington's disease. <i>Genes and Diseases</i> , 2022, 9, 479-493.	1.5	9
16488	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. <i>MSystems</i> , 2021, 6, .	1.7	27
16489	Site-Specific and Common Prostate Cancer Metastasis Genes as Suggested by Meta-Analysis of Gene Expression Data. <i>Life</i> , 2021, 11, 636.	1.1	7
16490	Multi-target mode of action of silver against <i>Staphylococcus aureus</i> endows it with capability to combat antibiotic resistance. <i>Nature Communications</i> , 2021, 12, 3331.	5.8	80
16491	Dynamic Host Immune and Transcriptomic Responses to Respiratory Syncytial Virus Infection in a Vaccination-Challenge Mouse Model. <i>Virologica Sinica</i> , 2021, 36, 1327-1340.	1.2	3
16492	A comprehensive review of integrative pharmacology-based investigation: A paradigm shift in traditional Chinese medicine. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1379-1399.	5.7	61
16493	Identification of genes predicting unfavorable prognosis in hepatitis B virus-associated hepatocellular carcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 975-975.	0.7	5
16494	Exposure to hypoxia causes stress erythropoiesis and downregulates immune response genes in spleen of mice. <i>BMC Genomics</i> , 2021, 22, 413.	1.2	15



#	ARTICLE	IF	CITATIONS
16495	Efficient conversion of organic nitrogenous wastewater to nitrate solution driven by comammox Nitrospira. <i>Water Research</i> , 2021, 197, 117088.	5.3	19
16496	Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. <i>Nature Communications</i> , 2021, 12, 3832.	5.8	119
16497	Acquisition of antibiotic resistance genes on human skin after swimming in the ocean. <i>Environmental Research</i> , 2021, 197, 110978.	3.7	9
16498	Integration of enzyme constraints in a genome-scale metabolic model of <i>Aspergillus niger</i> improves phenotype predictions. <i>Microbial Cell Factories</i> , 2021, 20, 125.	1.9	17
16499	Mortalin/glucose-regulated protein 75 promotes the cisplatin-resistance of gastric cancer via regulating anti-oxidation/apoptosis and metabolic reprogramming. <i>Cell Death Discovery</i> , 2021, 7, 140.	2.0	8
16500	Identification of novel hub genes associated with gastric cancer using integrated bioinformatics analysis. <i>BMC Cancer</i> , 2021, 21, 697.	1.1	18
16501	Assessing conservation of alternative splicing with evolutionary splicing graphs. <i>Genome Research</i> , 2021, 31, 1462-1473.	2.4	8
16502	Multimiomics analyses reveal the roles of the ASR1 transcription factor in tomato fruits. <i>Journal of Experimental Botany</i> , 2021, 72, 6490-6509.	2.4	4
16503	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	7.7	62
16505	Transcriptomic Analysis Exploring the Molecular Mechanisms of Hanchuan Zupa Granules in Alleviating Asthma in Rat. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	2
16506	A single-cell type transcriptomics map of human tissues. <i>Science Advances</i> , 2021, 7, .	4.7	632
16507	Microbiota continuum along the chicken oviduct and its association with host genetics and egg formation. <i>Poultry Science</i> , 2021, 100, 101104.	1.5	20
16508	Classical and Variant Merkel Cell Carcinoma Cell Lines Display Different Degrees of Neuroendocrine Differentiation and Epithelial-Mesenchymal Transition. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1675-1686.e4.	0.3	13
16509	Bioinformatics study on genes related to a high-risk postoperative recurrence of lung adenocarcinoma. <i>Science Progress</i> , 2021, 104, 003685042110180.	1.0	5
16510	Highlighting the Biotechnological Potential of Deep Oceanic Crust Fungi through the Prism of Their Antimicrobial Activity. <i>Marine Drugs</i> , 2021, 19, 411.	2.2	5
16511	Identification of COVID-19 and Dengue Host Factor Interaction Networks Based on Integrative Bioinformatics Analyses. <i>Frontiers in Immunology</i> , 2021, 12, 707287.	2.2	11
16512	A Novel Ferroptosis-Related Pathway for Regulating Immune Checkpoints in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 678694.	1.3	6
16513	Multiregional profiling of the brain transmembrane proteome uncovers novel regulators of depression. <i>Science Advances</i> , 2021, 7, .	4.7	13

#	ARTICLE	IF	CITATIONS
16514	Identification of differential key biomarkers in the synovial tissue between rheumatoid arthritis and osteoarthritis using bioinformatics analysis. <i>Clinical Rheumatology</i> , 2021, 40, 5103-5110.	1.0	7
16515	Metatranscriptomic analysis of colonic microbiota's functional response to different dietary fibers in growing pigs. <i>Animal Microbiome</i> , 2021, 3, 45.	1.5	12
16516	Identification of potential biomarkers for pathogenesis of Alzheimer's disease. <i>Hereditas</i> , 2021, 158, 23.	0.5	13
16517	Endophytic <i>Bacillus subtilis</i> TR21 Improves Banana Plant Resistance to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> and Promotes Root Growth by Upregulating the Jasmonate and Brassinosteroid Biosynthesis Pathways. <i>Phytopathology</i> , 2022, 112, 219-231.	1.1	14
16518	BacAnt: A Combination Annotation Server for Bacterial DNA Sequences to Identify Antibiotic Resistance Genes, Integrons, and Transposable Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 649969.	1.5	38
16519	Genome-wide transcriptional analysis unveils the molecular basis of organ-specific expression of isosteroidal alkaloids biosynthesis in critically endangered <i>Fritillaria roylei</i> Hook. <i>Phytochemistry</i> , 2021, 187, 112772.	1.4	20
16521	Genomic Surveillance and Phylodynamic Analyses Reveal the Emergence of Novel Mutations and Co-mutation Patterns Within SARS-CoV-2 Variants Prevalent in India. <i>Frontiers in Microbiology</i> , 2021, 12, 703933.	1.5	5
16522	Integrating transcriptomics, proteomics, glycomics and glycoproteomics to characterize paclitaxel resistance in breast cancer cells. <i>Journal of Proteomics</i> , 2021, 243, 104266.	1.2	14
16523	Network pharmacology-based evaluation of natural compounds with paclitaxel for the treatment of metastatic breast cancer. <i>Toxicology and Applied Pharmacology</i> , 2021, 423, 115576.	1.3	4
16524	The site of breast cancer metastases dictates their clonal composition and reversible transcriptomic profile. <i>Science Advances</i> , 2021, 7, .	4.7	23
16525	Conserved features of the <i>MlaD</i> domain aid the trafficking of hydrophobic molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1473-1488.	1.5	1
16526	Signals of pseudo-starvation unveil the amino acid transporter SLC7A11 as key determinant in the control of Treg cell proliferative potential. <i>Immunity</i> , 2021, 54, 1543-1560.e6.	6.6	42
16527	Comparative transcriptomic analysis reveals conserved programmes underpinning organogenesis and reproduction in land plants. <i>Nature Plants</i> , 2021, 7, 1143-1159.	4.7	61
16528	In silico-driven analysis of the <i>Glossina morsitans morsitans</i> antennae transcriptome in response to repellent or attractant compounds. <i>PeerJ</i> , 2021, 9, e11691.	0.9	2
16529	Advances in protein-protein interaction network analysis for Parkinson's disease. <i>Neurobiology of Disease</i> , 2021, 155, 105395.	2.1	31
16530	Assessing the relationship between the rumen microbiota and feed efficiency in Nellore steers. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 79.	2.1	37
16531	Comparative Transcriptome and Weighted Gene Co-expression Network Analysis Identify Key Transcription Factors of <i>Rosa chinensis</i> 'Old Blush' After Exposure to a Gradual Drought Stress Followed by Recovery. <i>Frontiers in Genetics</i> , 2021, 12, 690264.	1.1	7
16532	Integrative Bioinformatics Study of Tangeretin Potential Targets for Preventing Metastatic Breast Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	7

#	ARTICLE	IF	CITATIONS
16533	Disruption of a 24 nucleotide small RNA pathway elevates DNA damage responses in <i>Tetrahymena thermophila</i> . <i>Molecular Biology of the Cell</i> , 2021, 32, 1335-1346.	0.9	4
16534	Cigarette Smoke Specifically Affects Small Airway Epithelial Cell Populations and Triggers the Expansion of Inflammatory and Squamous Differentiation Associated Basal Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7646.	1.8	16
16535	A Hypoxia Gene-Based Signature to Predict the Survival and Affect the Tumor Immune Microenvironment of Osteosarcoma in Children. <i>Journal of Immunology Research</i> , 2021, 2021, 1-13.	0.9	21
16536	Exploring the Impact of Cerebrovascular Disease and Major Depression on Non-diseased Human Tissue Transcriptomes. <i>Frontiers in Genetics</i> , 2021, 12, 696836.	1.1	2
16537	Risk Score Based on Two microRNAs as a Prognostic Marker of Hepatocellular Carcinoma and the Corresponding Competitive Endogenous RNA Network. <i>International Journal of General Medicine</i> , 2021, Volume 14, 3377-3385.	0.8	2
16538	The BBX gene family in Moso bamboo ( <i>Phyllostachys edulis</i> ): identification, characterization and expression profiles. <i>BMC Genomics</i> , 2021, 22, 533.	1.2	20
16539	miRNA regulation of G protein-coupled receptor mediated angiogenic pathways in cancer. <i>Nucleus (India)</i> , 0, , 1.	0.9	4
16541	Host habitat is the major determinant of the gut microbiome of fish. <i>Microbiome</i> , 2021, 9, 166.	4.9	100
16542	Ziziphus joazeiro Stem Bark Extract as a Green Corrosion Inhibitor for Mild Steel in Acid Medium. <i>Processes</i> , 2021, 9, 1323.	1.3	10
16543	Effects of Cancer Presence and Therapy on the Platelet Proteome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8236.	1.8	8
16544	Identification of serum prognostic marker miRNAs and construction of microRNA-mRNA networks of esophageal cancer. <i>PLoS ONE</i> , 2021, 16, e0255479.	1.1	2
16545	Single-cell atlas of domestic pig cerebral cortex and hypothalamus. <i>Science Bulletin</i> , 2021, 66, 1448-1461.	4.3	20
16546	Cell-intrinsic glial pathology is conserved across human and murine models of Huntington's disease. <i>Cell Reports</i> , 2021, 36, 109308.	2.9	28
16547	Analysis of Hub Genes and the Mechanism of Immune Infiltration in Stanford Type a Aortic Dissection. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 680065.	1.1	14
16549	Integrated microRNA and mRNA signatures associated with overall survival in epithelial ovarian cancer. <i>PLoS ONE</i> , 2021, 16, e0255142.	1.1	4
16550	Unraveling the molecular crosstalk between Atherosclerosis and COVID-19 comorbidity. <i>Computers in Biology and Medicine</i> , 2021, 134, 104459.	3.9	18
16551	Integrated miRNA-mRNA analysis provides potential biomarkers for selective breeding in bay scallop ( <i>Argopecten irradians</i> ). <i>Genomics</i> , 2021, 113, 2744-2755.	1.3	3
16552	Variability of multi-omics profiles in a population-based child cohort. <i>BMC Medicine</i> , 2021, 19, 166.	2.3	23

#	ARTICLE	IF	CITATIONS
16553	A novel platform for discovery of differentially expressed microRNAs in patients with repeated implantation failure. <i>Fertility and Sterility</i> , 2021, 116, 181-188.	0.5	20
16554	Chromosome-level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. <i>Molecular Ecology Resources</i> , 2021, 21, 2533-2545.	2.2	30
16555	A novel RNA binding protein-associated prognostic model to predict overall survival in hepatocellular carcinoma patients. <i>Medicine (United States)</i> , 2021, 100, e26491.	0.4	3
16556	Correlation between targeted RNAseq signature of breast cancer CTCs and onset of bone-only metastases. <i>British Journal of Cancer</i> , 2022, 126, 419-429.	2.9	10
16557	Screening of the HBx transactivation domain interacting proteins and the function of interactor Pin1 in HBV replication. <i>Scientific Reports</i> , 2021, 11, 14176.	1.6	9
16558	A generative network model of neurodevelopmental diversity in structural brain organization. <i>Nature Communications</i> , 2021, 12, 4216.	5.8	34
16559	Transcriptomic diversity in longissimus thoracis muscles of Barbari and Changthangi goat breeds of India. <i>Genomics</i> , 2021, 113, 1639-1646.	1.3	10
16560	Loss of Setd2 associates with aberrant microRNA expression and contributes to inflammatory bowel disease progression in mice. <i>Genomics</i> , 2021, 113, 2441-2454.	1.3	2
16561	Proteomics analysis reveals the importance of transcriptional regulator slyA in regulation of several physiological functions in <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2021, 244, 104275.	1.2	4
16562	LncRNA RCAT1 promotes tumor progression and metastasis via miR-214-5p/E2F2 axis in renal cell carcinoma. <i>Cell Death and Disease</i> , 2021, 12, 689.	2.7	26
16563	Monitoring Cyanobacterial Blooms during the COVID-19 Pandemic in Campania, Italy: The Case of Lake Avernus. <i>Toxins</i> , 2021, 13, 471.	1.5	10
16564	Transcriptome Analysis of Kidney Grafts Subjected to Normothermic Ex Vivo Perfusion Demonstrates an Enrichment of Mitochondrial Metabolism Genes. <i>Transplantation Direct</i> , 2021, 7, e719.	0.8	7
16565	Associations Among Parental Caregiving Quality, Cannabinoid Receptor 1 Expression-Based Polygenic Scores, and Infant-Parent Attachment: Evidence for Differential Genetic Susceptibility?. <i>Frontiers in Neuroscience</i> , 2021, 15, 704392.	1.4	3
16566	Analysis of Ferroptosis-Mediated Modification Patterns and Tumor Immune Microenvironment Characterization in Uveal Melanoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 685120.	1.8	20
16567	A panel of miRNAs as prognostic markers for African-American patients with triple negative breast cancer. <i>BMC Cancer</i> , 2021, 21, 861.	1.1	8
16569	Genetic basis and network underlying synergistic roots and shoots biomass accumulation revealed by genome-wide association studies in rice. <i>Scientific Reports</i> , 2021, 11, 13769.	1.6	4
16570	Genome-Wide Comparative Analysis of Flowering-Time Genes; Insights on the Gene Family Expansion and Evolutionary Perspective. <i>Frontiers in Plant Science</i> , 2021, 12, 702243.	1.7	8
16571	Integrative analysis of ceRNA network reveals functional lncRNAs associated with independent recurrent prognosis in colon adenocarcinoma. <i>Cancer Cell International</i> , 2021, 21, 352.	1.8	11

#	ARTICLE	IF	CITATIONS
16572	Characteristics and metabolic patterns of soil methanogenic archaea communities in the high-latitude natural forested wetlands of China. <i>Ecology and Evolution</i> , 2021, 11, 10396-10408.	0.8	5
16574	Comparative Transcriptome and Endophytic Bacterial Community Analysis of <i>Morchella conica</i> SH. <i>Frontiers in Microbiology</i> , 2021, 12, 682356.	1.5	3
16575	Organelle Crosstalk Regulators Are Regulated in Diseases, Tumors, and Regulatory T Cells: Novel Classification of Organelle Crosstalk Regulators. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 713170.	1.1	11
16576	Metabolism and transcriptome profiling provides insight into the genes and transcription factors involved in monoterpene biosynthesis of borneol chemotype of <i>Cinnamomum camphora</i> induced by mechanical damage. <i>PeerJ</i> , 2021, 9, e11465.	0.9	11
16577	A Causal Web between Chronotype and Metabolic Health Traits. <i>Genes</i> , 2021, 12, 1029.	1.0	4
16578	Bioinformatics integrated analysis to investigate candidate biomarkers and associated metabolites in osteosarcoma. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 432.	0.9	3
16579	Transcriptional profiling reveals multiple defense responses in downy mildew-resistant transgenic grapevine expressing a TIR-NBS-LRR gene located at the MrRUN1/MrRPV1 locus. <i>Horticulture Research</i> , 2021, 8, 161.	2.9	6
16580	Evolution of Toll, Spatzle and MyD88 in insects: the problem of the Diptera bias. <i>BMC Genomics</i> , 2021, 22, 562.	1.2	13
16581	Identification of CXCL13 as an Immune-Related Biomarker Associated with Tumorigenesis and Prognosis in Cutaneous Melanoma Patients. <i>Medical Science Monitor</i> , 2021, 27, e932052.	0.5	7
16583	Comparative transcriptome analysis reveals regulatory network and regulators associated with proanthocyanidin accumulation in persimmon. <i>BMC Plant Biology</i> , 2021, 21, 356.	1.6	13
16584	Ebola vaccine-induced protection in nonhuman primates correlates with antibody specificity and Fc-mediated effects. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	22
16585	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. <i>Pharmacogenomics</i> , 2021, 22, 603-618.	0.6	7
16586	Weighted gene co-expression network analysis identifies specific modules and hub genes related to Parkinson's disease. <i>NeuroReport</i> , 2021, 32, 1073-1081.	0.6	4
16587	RNA Sequencing Reveals Dynamic Carbohydrate Metabolism and Phytohormone Signaling Accompanying Post-mowing Regeneration of Forage Winter Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 664933.	1.7	3
16589	A review on network pharmacology based phytotherapy in treating diabetes- An environmental perspective. <i>Environmental Research</i> , 2021, 202, 111656.	3.7	10
16590	Identification of Key Biomarkers and Immune Infiltration in Systemic Juvenile Idiopathic Arthritis by Integrated Bioinformatic Analysis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 681526.	1.6	2
16591	Identification of consistent post-translational regulatory triplets related to oncogenic and tumour suppressive modulators in childhood acute lymphoblastic leukemia. <i>PeerJ</i> , 2021, 9, e11803.	0.9	0
16592	Stability and similarity in financial networks—How do they change in times of turbulence?. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2021, 574, 126016.	1.2	8

#	ARTICLE	IF	CITATIONS
16593	The Differential Growth Inhibition of <i>Phytophthora</i> spp. Caused by the Rare Sugar Tagatose Is Associated With Species-Specific Metabolic and Transcriptional Changes. <i>Frontiers in Microbiology</i> , 2021, 12, 711545.	1.5	9
16594	â€œMolecular Anatomyâ€: a new multi-dimensional hierarchical scaffold analysis tool. <i>Journal of Cheminformatics</i> , 2021, 13, 54.	2.8	12
16595	Unraveling negative biotic interactions determining soil microbial community assembly and functioning. <i>ISME Journal</i> , 2022, 16, 296-306.	4.4	80
16596	Expression and prognostic potential of PLEK2 in head and neck squamous cell carcinoma based on bioinformatics analysis. <i>Cancer Medicine</i> , 2021, 10, 6515-6533.	1.3	10
16597	A first perturbome of <i>Pseudomonas aeruginosa</i> : Identification of core genes related to multiple perturbations by a machine learning approach. <i>BioSystems</i> , 2021, 205, 104411.	0.9	6
16598	Comprehensive analysis of diabetic nephropathy expression profile based on weighted gene co-expression network analysis algorithm. <i>BMC Nephrology</i> , 2021, 22, 245.	0.8	19
16599	The methylome of the model arbuscular mycorrhizal fungus, <i>Rhizophagus irregularis</i> , shares characteristics with early diverging fungi and Dikarya. <i>Communications Biology</i> , 2021, 4, 901.	2.0	17
16600	Exploration of Long-Chain Vitamin E Metabolites for the Discovery of a Highly Potent, Orally Effective, and Metabolically Stable 5-LOX Inhibitor that Limits Inflammation. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 11496-11526.	2.9	7
16601	Characterization of the Heat-Stable Proteome during Seed Germination in <i>Arabidopsis</i> with Special Focus on LEA Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8172.	1.8	12
16602	Assessing the Toxicity of 17 $\beta$ -Ethinylestradiol in Rainbow Trout Using a 4-Day Transcriptomics Benchmark Dose (BMD) Embryo Assay. <i>Environmental Science &amp; Technology</i> , 2021, 55, 10608-10618.	4.6	14
16603	Insights into heat response mechanisms in <i>Clematis</i> species: physiological analysis, expression profiles and function verification. <i>Plant Molecular Biology</i> , 2021, 106, 569-587.	2.0	0
16606	SARS-CoV-2 Infected Pediatric Cerebral Cortical Neurons: Transcriptomic Analysis and Potential Role of Toll-like Receptors in Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8059.	1.8	10
16607	Oncogenic enhancers drive esophageal squamous cell carcinogenesis and metastasis. <i>Nature Communications</i> , 2021, 12, 4457.	5.8	27
16609	Transcriptome-Based WGCNA Analysis Reveals Regulated Metabolite Fluxes between Floral Color and Scent in <i>Narcissus tazetta</i> Flower. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8249.	1.8	25
16610	Network pharmacology dissection of multiscale mechanisms for jiaoqi powder in treating ulcerative colitis. <i>Journal of Ethnopharmacology</i> , 2021, 275, 114109.	2.0	7
16611	Identification of Candidate Blood mRNA Biomarkers in Intracerebral Hemorrhage Using Integrated Microarray and Weighted Gene Co-expression Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 707713.	1.1	4
16612	Baicalin Rescues Cognitive Dysfunction, Mitigates Neurodegeneration, and Exerts Anti-Epileptic Effects Through Activating TLR4/MYD88/Caspase-3 Pathway in Rats. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 3163-3180.	2.0	11
16613	Adenosine deaminase modulates metabolic remodeling and orchestrates joint destruction in rheumatoid arthritis. <i>Scientific Reports</i> , 2021, 11, 15129.	1.6	21



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16614	Mechanisms of Impaired Lung Development and Ciliation in Mannosidase-1-Alpha-2 (Man1a2) Mutants. <i>Frontiers in Physiology</i> , 2021, 12, 658518.	1.3	2
16615	Analysis of Immune-Related Signatures Related to CD4+ T Cell Infiltration With Gene Co-Expression Network in Pancreatic Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 674897.	1.3	3
16616	Application and Perspectives of MALDI-TOF Mass Spectrometry in Clinical Microbiology Laboratories. <i>Microorganisms</i> , 2021, 9, 1539.	1.6	60
16618	Prediction of Disease Genes Based on Stage-Specific Gene Regulatory Networks in Breast Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 717557.	1.1	3
16619	Decoding the molecular mechanism of parthenocarpy in <i>Musa</i> spp. through protein-protein interaction network. <i>Scientific Reports</i> , 2021, 11, 14592.	1.6	10
16620	Complex Networks of Prion-Like Proteins Reveal Cross Talk Between Stress and Memory Pathways in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 707286.	1.7	13
16621	neoDL: a novel neoantigen intrinsic feature-based deep learning model identifies IDH wild-type glioblastomas with the longest survival. <i>BMC Bioinformatics</i> , 2021, 22, 382.	1.2	3
16622	The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. <i>Cell</i> , 2021, 184, 3915-3935.e21.	13.5	133
16623	Recent ultra-rare inherited variants implicate new autism candidate risk genes. <i>Nature Genetics</i> , 2021, 53, 1125-1134.	9.4	68
16624	Mechanism of Growth Regulation of Yeast Involving Hydrogen Sulfide From S-Propargyl-Cysteine Catalyzed by Cystathionine-β-Lyase. <i>Frontiers in Microbiology</i> , 2021, 12, 679563.	1.5	1
16625	Endosomal cAMP production broadly impacts the cellular phosphoproteome. <i>Journal of Biological Chemistry</i> , 2021, 297, 100907.	1.6	36
16626	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021, 184, 3774-3793.e25.	13.5	34
16627	Network analysis and the impact of Aflibercept on specific mediators of angiogenesis in HUVEC cells. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 8285-8299.	1.6	8
16628	Systematic Bioinformatic Analyses of Nutrigenomic Modifications by Polyphenols Associated with Cardiometabolic Health in Humans—Evidence from Targeted Nutrigenomic Studies. <i>Nutrients</i> , 2021, 13, 2326.	1.7	15
16629	Uncovering Potential lncRNAs and mRNAs in the Progression From Acute Myocardial Infarction to Myocardial Fibrosis to Heart Failure. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 664044.	1.1	10
16630	Plastic film mulch changes the microbial community in maize root-associated compartments. <i>Plant and Soil</i> , 2022, 470, 5-20.	1.8	20
16631	Lnc-STYK1-2 regulates bladder cancer cell proliferation, migration, and invasion by targeting miR-146b-5p expression and AKT/STAT3/NF-κB signaling. <i>Cancer Cell International</i> , 2021, 21, 408.	1.8	12
16632	De novo generation of macrophage from placenta-derived hemogenic endothelium. <i>Developmental Cell</i> , 2021, 56, 2121-2133.e6.	3.1	25

#	ARTICLE	IF	CITATIONS
16633	DIA-Based Quantitative Proteomics Reveals the Protein Regulatory Networks of Floral Thermogenesis in <i>Nelumbo nucifera</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 8251.	1.8	6
16634	Identification of Potential Key Genes and Regulatory Markers in Essential Thrombocythemia Through Integrated Bioinformatics Analysis and Clinical Validation. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 767-784.	0.4	5
16635	Identification and Characterization of lncRNA and mRNA in Testes of Landrace and Hezuo Boars. <i>Animals</i> , 2021, 11, 2263.	1.0	7
16636	Insights into the Variation in Bioactivities of Closely Related <i>Streptomyces</i> Strains from Marine Sediments of the Visayan Sea against ESKAPE and Ovarian Cancer. <i>Marine Drugs</i> , 2021, 19, 441.	2.2	10
16637	Profiling NSD3-dependent neural crest gene expression reveals known and novel candidate regulatory factors. <i>Developmental Biology</i> , 2021, 475, 118-130.	0.9	7
16638	Integrated global analysis reveals a vitamin E-vitamin K1 sub-network, downstream of COLD1, underlying rice chilling tolerance divergence. <i>Cell Reports</i> , 2021, 36, 109397.	2.9	22
16639	Maintenance of Metabolic Plasticity despite Relaxed Selection in a Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>American Naturalist</i> , 2021, 198, 93-112.	1.0	10
16640	A network pharmacology approach to uncover the key ingredients in <i>Ginkgo Folium</i> and their anti-Alzheimer's disease mechanisms. <i>Aging</i> , 2021, 13, 18993-19012.	1.4	12
16641	Impact of human rhinoviruses on gene expression in pediatric patients with severe acute respiratory infection. <i>Virus Research</i> , 2021, 300, 198408.	1.1	5
16643	Alteration of protein expression and spliceosome pathway activity during Barrett's carcinogenesis. <i>Journal of Gastroenterology</i> , 2021, 56, 791-807.	2.3	1
16644	Profiling Basal Forebrain Cholinergic Neurons Reveals a Molecular Basis for Vulnerability Within the Ts65Dn Model of Down Syndrome and Alzheimer's Disease. <i>Molecular Neurobiology</i> , 2021, 58, 5141-5162.	1.9	12
16645	Circular DNA viruses identified in short-finned pilot whale and orca tissue samples. <i>Virology</i> , 2021, 559, 156-164.	1.1	4
16646	Transcriptome landscape of double negative T cells by single-cell RNA sequencing. <i>Journal of Autoimmunity</i> , 2021, 121, 102653.	3.0	20
16647	Systems pharmacology dissection of action mechanisms for herbs in osteoporosis treatment. <i>Chinese Herbal Medicines</i> , 2021, 13, 313-331.	1.2	4
16648	Orthogonal Degron System for Controlled Protein Degradation in Cyanobacteria. <i>ACS Synthetic Biology</i> , 2021, 10, 1667-1681.	1.9	13
16649	Tomato Cultivars With Variable Tolerances to Water Deficit Differentially Modulate the Composition and Interaction Patterns of Their Rhizosphere Microbial Communities. <i>Frontiers in Plant Science</i> , 2021, 12, 688533.	1.7	10
16651	Temporal transcriptomic profiling reveals dynamic changes in gene expression of <i>Xenopus</i> animal cap upon activin treatment. <i>Scientific Reports</i> , 2021, 11, 14537.	1.6	3
16652	ACE2-lentiviral transduction enables mouse SARS-CoV-2 infection and mapping of receptor interactions. <i>PLoS Pathogens</i> , 2021, 17, e1009723.	2.1	28

#	ARTICLE	IF	CITATIONS
16653	mRNA Inventory of Extracellular Vesicles from <i>Ustilago maydis</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 562.	1.5	21
16654	Exploring the Mechanism of <i>Scutellaria baicalensis</i> Georgi Efficacy against Oral Squamous Cell Carcinoma Based on Network Pharmacology and Molecular Docking Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	4
16655	FAIRSCAPE: a Framework for FAIR and Reproducible Biomedical Analytics. <i>Neuroinformatics</i> , 2022, 20, 187-202.	1.5	4
16656	Long noncoding RNA HOTAIR interacts with Y-Box Protein-1 (YBX1) to regulate cell proliferation. <i>Life Science Alliance</i> , 2021, 4, e202101139.	1.3	16
16657	Screening of Atherosclerotic Druggable Targets from the Proteome Network of Differentially Expressed Genes. <i>Assay and Drug Development Technologies</i> , 2021, 19, 290-299.	0.6	0
16658	SLC1A5 co-expression with TALDO1 associates with endocrine therapy failure in estrogen receptor-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 189, 317-331.	1.1	5
16659	Statin Treatment Induced a Lipogenic Expression Hierarchical Network Centered by SREBF2 in the Liver. <i>Frontiers in Endocrinology</i> , 2021, 12, 573824.	1.5	1
16660	Analysis of Bioactive Components in the Fruit, Roots, and Leaves of <i>Alpinia oxyphylla</i> by UPLC-MS/MS. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-11.	0.5	7
16663	A diagnostic miRNA signature for pulmonary arterial hypertension using a consensus machine learning approach. <i>EBioMedicine</i> , 2021, 69, 103444.	2.7	30
16666	Filtering of Data-Driven Gene Regulatory Networks Using <i>Drosophila melanogaster</i> as a Case Study. <i>Frontiers in Genetics</i> , 2021, 12, 649764.	1.1	2
16667	Resequencing 250 Soybean Accessions: New Insights into Genes Associated with Agronomic Traits and Genetic Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 29-41.	3.0	21
16668	Transcriptomic analysis to reveal the differentially expressed miRNA targets and their miRNAs in response to <i>Ralstonia solanacearum</i> in ginger species. <i>BMC Plant Biology</i> , 2021, 21, 355.	1.6	11
16669	Prediction of well-being and insight into work-life integration among physicians using machine learning approach. <i>PLoS ONE</i> , 2021, 16, e0254795.	1.1	4
16670	Comprehensive Analysis of the Value of SMYD Family Members in the Prognosis and Immune Infiltration of Malignant Digestive System Tumors. <i>Frontiers in Genetics</i> , 2021, 12, 699910.	1.1	4
16673	Microbial Profiles of Retail Pacific Oysters ( <i>Crassostrea gigas</i> ) From Guangdong Province, China. <i>Frontiers in Microbiology</i> , 2021, 12, 689520.	1.5	8
16674	Biomarker Categorization in Transcriptomic Meta-Analysis by Concordant Patterns With Application to Pan-Cancer Studies. <i>Frontiers in Genetics</i> , 2021, 12, 651546.	1.1	5
16676	In Vitro Metabolism Study of Seongsanamide A in Human Liver Microsomes Using Non-Targeted Metabolomics and Feature-Based Molecular Networking. <i>Pharmaceutics</i> , 2021, 13, 1031.	2.0	1
16677	New candidate blood biomarkers potentially associated with white matter hyperintensities progression. <i>Scientific Reports</i> , 2021, 11, 14324.	1.6	4

#	ARTICLE	IF	CITATIONS
16678	Age-Related miRNA-Mediated Regulatory Networks Orchestrating Chronological Development of Meristems in <i>Larix Kaempferi</i> . <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2305-2318.	2.8	2
16679	Developmental Alcohol Exposure in <i>Drosophila</i> : Effects on Adult Phenotypes and Gene Expression in the Brain. <i>Frontiers in Psychiatry</i> , 2021, 12, 699033.	1.3	13
16680	Correlation between vascular endothelial growth factor pathway and immune microenvironment in head and neck squamous cell carcinoma. <i>BMC Cancer</i> , 2021, 21, 836.	1.1	5
16681	Identification of Hub Genes Associated with Diabetes Mellitus and Tuberculosis Using Bioinformatic Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 4061-4072.	0.8	7
16683	Prognostic Prediction, Immune Microenvironment, and Drug Resistance Value of Collagen Type I Alpha 1 Chain: From Gastrointestinal Cancers to Pan-Cancer Analysis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 692120.	1.6	6
16684	Examination of the Global Regulon of CsrA in <i>Xanthomonas citri</i> subsp. <i>citri</i> Using Quantitative Proteomics and Other Approaches. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1236-1249.	1.4	3
16685	Genomic insights into molecular adaptation to intertidal environments in the mangrove <i>Aegiceras corniculatum</i> . <i>New Phytologist</i> , 2021, 231, 2346-2358.	3.5	32
16686	Integration of segmented regression analysis with weighted gene correlation network analysis identifies genes whose expression is remodeled throughout physiological aging in mouse tissues. <i>Aging</i> , 2021, 13, 18150-18190.	1.4	9
16687	Molecular Determinants of the Cardiometabolic Improvements of Dietary Flavanols Identified by an Integrative Analysis of Nutrigenomic Data from a Systematic Review of Animal Studies. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2100227.	1.5	9
16688	A chromosome-scale genome sequence of pitaya ( <i>Hylocereus undatus</i> ) provides novel insights into the genome evolution and regulation of betalain biosynthesis. <i>Horticulture Research</i> , 2021, 8, 164.	2.9	44
16689	Effect of dapagliflozin on diabetic patients with cardiovascular disease via MAPK signalling pathway. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7500-7512.	1.6	7
16690	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	1.5	23
16691	RNA-Seq analysis and WGCNA reveal dynamic molecular responses to air exposure in the hard clam <i>Mercenaria mercenaria</i> . <i>Genomics</i> , 2021, 113, 2847-2859.	1.3	18
16692	On the Trail of the German Purity Law: Distinguishing the Metabolic Signatures of Wheat, Corn and Rice in Beer. <i>Frontiers in Chemistry</i> , 2021, 9, 715372.	1.8	9
16693	Quick-start infrastructure for untargeted metabolomics analysis in GNPS. <i>Nature Metabolism</i> , 2021, 3, 880-882.	5.1	11
16695	Trehalose in pine wood nematode participates in DJ3 formation and confers resistance to low-temperature stress. <i>BMC Genomics</i> , 2021, 22, 524.	1.2	6
16696	Identification of Underlying Hub Genes Associated with Hypertrophic Cardiomyopathy by Integrated Bioinformatics Analysis. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 823-837.	0.4	5
16698	CSNK1A1, KDM2A, and LTB4R2 Are New Druggable Vulnerabilities in Lung Cancer. <i>Cancers</i> , 2021, 13, 3477.	1.7	4

#	ARTICLE	IF	CITATIONS
16699	Construction of Adipogenic ceRNA Network Based on lncRNA Expression Profile of Adipogenic Differentiation of Human MSC Cells. <i>Biochemical Genetics</i> , 2021, , 1.	0.8	1
16700	Identification of an RNA-Binding-Protein-Based Prognostic Model for Ewing Sarcoma. <i>Cancers</i> , 2021, 13, 3736.	1.7	7
16701	The Mechanism Underlying of Long-Term Stable Indigo Reduction State in Indigo Fermentation Using Sukumo (Composted <i>Polygonum tinctorium</i> Leaves). <i>Frontiers in Microbiology</i> , 2021, 12, 698674.	1.5	6
16702	Identification of Biomarkers for Predicting Allograft Rejection following Kidney Transplantation Based on the Weighted Gene Coexpression Network Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	3
16703	Combined bioinformatics technology to explore pivot genes and related clinical prognosis in the development of gastric cancer. <i>Scientific Reports</i> , 2021, 11, 15412.	1.6	4
16704	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 42-59.	3.0	18
16705	Identification of Indicators for Preterm Birth Using Retinoid Metabolites. <i>Metabolites</i> , 2021, 11, 443.	1.3	7
16706	Impact of anthropogenic activities on changes of ichthyofauna in the middle and lower Xiang River. <i>Aquaculture and Fisheries</i> , 2022, 7, 693-702.	1.2	10
16707	Study on the potential active components and molecular mechanism of Xiao Huoluo Pills in the treatment of cartilage degeneration of knee osteoarthritis based on bioinformatics analysis and molecular docking technology. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 460.	0.9	15
16708	Crosslink: An R Package for Network Visualization of Grouped Nodes. <i>Frontiers in Genetics</i> , 2021, 12, 706854.	1.1	2
16709	Comparative transcriptomics and network analysis define gene coexpression modules that control maize aleurone development and auxin signaling. <i>Plant Genome</i> , 2021, 14, e20126.	1.6	3
16710	Characterization of metabolic fate of phellodendrine and its potential pharmacological mechanism against diabetes mellitus by ultra-high-performance liquid chromatography-coupled time-of-flight mass spectrometry and network pharmacology. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e9157.	0.7	4
16711	Interleukin-2 inducible T-cell kinase: a potential prognostic biomarker and tumor microenvironment remodeling indicator for hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 18620-18644.	1.4	2
16713	The nasal microbiome, nasal transcriptome, and pet sensitization. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 244-249.e4.	1.5	8
16714	Differential expression analysis in ovarian cancer: A functional genomics and systems biology approach. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 4069-4081.	1.8	14
16715	The trans-omics landscape of COVID-19. <i>Nature Communications</i> , 2021, 12, 4543.	5.8	75
16716	Co-expression network and comparative transcriptome analysis for fiber initiation and elongation reveal genetic differences in two lines from upland cotton CCR170 RIL population. <i>PeerJ</i> , 2021, 9, e11812.	0.9	9
16717	Genome-wide identification and analysis of the YABBY gene family in Moso Bamboo ( <i>Phyllostachys</i> ) TJ ETQq1 1 0.784314 rgBT /Overl	0.9	9

#	ARTICLE	IF	CITATIONS
16718	Single-cell spatial transcriptomic analysis reveals common and divergent features of developing postnatal granule cerebellar cells and medulloblastoma. <i>BMC Biology</i> , 2021, 19, 135.	1.7	20
16719	Identification of Potential Signatures and Their Functions for Acute Lymphoblastic Leukemia: A Study Based on the Cancer Genome Atlas. <i>Frontiers in Genetics</i> , 2021, 12, 656042.	1.1	12
16720	Juvenile Huntington's Disease and Other PolyQ Diseases, Update on Neurodevelopmental Character and Comparative Bioinformatic Review of Transcriptomic and Proteomic Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 642773.	1.8	8
16721	A system biology approach based on metabolic biomarkers and protein-protein interactions for identifying pathways underlying schizophrenia and bipolar disorder. <i>Scientific Reports</i> , 2021, 11, 14450.	1.6	4
16722	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1128-1142.	1.4	6
16723	Integrated Analysis of lncRNAs, mRNAs, and TFs to Identify Regulatory Networks Underlying MAP Infection in Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 668448.	1.1	6
16724	Single-Cell Transcriptome Analysis in Melanoma Using Network Embedding. <i>Frontiers in Genetics</i> , 2021, 12, 700036.	1.1	0
16725	Identification of tumor microenvironment-related prognostic genes in colorectal cancer based on bioinformatic methods. <i>Scientific Reports</i> , 2021, 11, 15040.	1.6	17
16726	Dental biofilm and its ecological interrelationships in ovine periodontitis. <i>Journal of Medical Microbiology</i> , 2021, 70, .	0.7	11
16727	SLIDE's Novel Approach to Apocrine Sweat Sampling for Lipid Profiling in Healthy Individuals. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8054.	1.8	4
16728	Early Transcriptional Liver Signatures in Experimental Visceral Leishmaniasis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7161.	1.8	4
16730	Identification of candidate biomarkers and therapeutic agents for heart failure by bioinformatics analysis. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 329.	0.7	28
16731	Identification and characterization of prognosis-related genes in the tumor microenvironment of esophageal squamous cell carcinoma. <i>International Immunopharmacology</i> , 2021, 96, 107616.	1.7	5
16732	Microbiome diversity and host immune functions influence survivorship of sponge holobionts under future ocean conditions. <i>ISME Journal</i> , 2022, 16, 58-67.	4.4	27
16733	Molecular Networking of High-Resolution Tandem Ion Mobility Spectra: A Structurally Relevant Way of Organizing Data in Glycomics?. <i>Analytical Chemistry</i> , 2021, 93, 10871-10878.	3.2	10
16734	Molecular characterization of projection neuron subtypes in the mouse olfactory bulb. <i>ELife</i> , 2021, 10, .	2.8	22
16735	Is there a relationship between psoriasis and hepatitis C? A meta-analysis and bioinformatics investigation. <i>Virology Journal</i> , 2021, 18, 135.	1.4	1
16736	Profiles and interrelationships of functional soil microbiomes involved in phosphorus cycling in diversified agricultural land-use systems. <i>Food and Energy Security</i> , 2021, 10, e315.	2.0	2



#	ARTICLE	IF	CITATIONS
16737	Crosstalks between NOD1 and Histone H2A Contribute to Host Defense against <i>Streptococcus agalactiae</i> Infection in Zebrafish. <i>Antibiotics</i> , 2021, 10, 861.	1.5	3
16739	Identification of the Prognostic Signatures of Glioma With Different PTEN Status. <i>Frontiers in Oncology</i> , 2021, 11, 633357.	1.3	15
16740	A Deep-Learning Model With the Attention Mechanism Could Rigorously Predict Survivals in Neuroblastoma. <i>Frontiers in Oncology</i> , 2021, 11, 653863.	1.3	3
16741	Investigation into the effect of mannan-rich fraction supplementation on the metagenome of broiler chickens. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
16742	Identification and validation of an immune-related prognostic signature and key gene in papillary thyroid carcinoma. <i>Cancer Cell International</i> , 2021, 21, 378.	1.8	15
16743	Identification and expression analysis of lncRNA in seven organs of <i>Rhinopithecus roxellana</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 543-555.	1.4	2
16744	Grazing accelerates labile and recalcitrant soil carbon loss driving by rare microbial taxa in a desert steppe. <i>Land Degradation and Development</i> , 2021, 32, 4241-4253.	1.8	13
16745	Short-term response of pelagic planktonic communities after inoculation with the mass cultured dinoflagellate <i>Alexandrium affine</i> in a large-scale mesocosm experiment. <i>Journal of Applied Phycology</i> , 2021, 33, 3123-3137.	1.5	3
16747	Molecular Networking-Guided Isolation of New Etzionin-Type Diketopiperazine Hydroxamates from the Persian Gulf Sponge <i>Cliona celata</i> . <i>Marine Drugs</i> , 2021, 19, 439.	2.2	7
16749	Nuclear Transfer Arrest Embryos Show Massive Dysregulation of Genes Involved in Transcription Pathways. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8187.	1.8	3
16750	Differential gene expression in liver of colored broiler chicken divergently selected for residual feed intake. <i>Tropical Animal Health and Production</i> , 2021, 53, 403.	0.5	5
16751	The Orchid Bee Fauna (Hymenoptera: Apidae: Euglossini) of a Neotropical Savanna: an Efficient Protocol to Assess Bee Community and Diversity Along Elevational and Habitat Complexity Gradients. <i>Neotropical Entomology</i> , 2021, 50, 748-758.	0.5	3
16752	An Azo Coupling-Based Chemoproteomic Approach to Systematically Profile the Tyrosine Reactivity in the Human Proteome. <i>Analytical Chemistry</i> , 2021, 93, 10334-10342.	3.2	11
16753	Genome-wide identification of cyclin-dependent kinase (CDK) genes affecting adipocyte differentiation in cattle. <i>BMC Genomics</i> , 2021, 22, 532.	1.2	14
16754	Wastewater effluents cause microbial community shifts and change trophic status. <i>Water Research</i> , 2021, 200, 117206.	5.3	53
16755	Integrated multiplex network based approach for hub gene identification in oral cancer. <i>Heliyon</i> , 2021, 7, e07418.	1.4	9
16756	The Antioxidative Role of Natural Compounds from a Green Coconut Mesocarp Undeniably Contributes to Control Diabetic Complications as Evidenced by the Associated Genes and Biochemical Indexes. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-22.	1.9	11
16757	p53 mitigates the effects of oncogenic HRAS in urothelial cells via the repression of MCOLN1. <i>IScience</i> , 2021, 24, 102701.	1.9	5

#	ARTICLE	IF	CITATIONS
16758	In silico analysis of the potential mechanism of a preventive Chinese medicine formula on coronavirus disease 2019. <i>Journal of Ethnopharmacology</i> , 2021, 275, 114098.	2.0	13
16759	Identification of 3D motifs based on sequences and structures for binding to CFIâ€400945, and deep screeningâ€based design of new lead molecules for PLKâ€4. <i>Chemical Biology and Drug Design</i> , 2021, 98, 522-538.	1.5	2
16760	Impacts of biochar-based fertilization on soil arbuscular mycorrhizal fungal community structure in a karst mountainous area. <i>Environmental Science and Pollution Research</i> , 2021, 28, 66420-66434.	2.7	13
16761	Soil microbes drive the effect of plant species and genotypic diversity interaction on productivity.. <i>Plant and Soil</i> , 2021, 467, 165.	1.8	7
16764	Significant Diagnostic and Prognostic Value of FLAD1 and Related MicroRNAs in Breast Cancer after a Pan-Cancer Analysis. <i>Disease Markers</i> , 2021, 2021, 1-21.	0.6	3
16765	Multi-Omics Integrative Bioinformatics Analyses Reveal Long Non-coding RNA Modulates Genomic Integrity via Competing Endogenous RNA Mechanism and Serves as Novel Biomarkers for Overall Survival in Lung Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 691540.	1.8	4
16767	Integration of transcriptomic data identifies key hallmark genes in hypertrophic cardiomyopathy. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 330.	0.7	4
16768	Single-Cell Sequencing to Identify Six Heat Shock Protein (HSP) Genes-Mediated Progression Subtypes of Clear Cell Renal Cell Carcinoma. <i>International Journal of General Medicine</i> , 2021, Volume 14, 3761-3773.	0.8	3
16769	Glycolysis Define Two Prognostic Subgroups of Lung Adenocarcinoma With Different Mutation Characteristics and Immune Infiltration Signatures. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645482.	1.8	3
16770	Comprehensive analysis of DNA methylation and gene expression profiles in gestational diabetes mellitus. <i>Medicine (United States)</i> , 2021, 100, e26497.	0.4	3
16771	Construction and Analysis of Coexpression Network to Understand Biological Responses in Chickens Infected by <i>Eimeria tenella</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 688684.	0.9	3
16772	Generalist Taxa Shape Fungal Community Structure in Cropping Ecosystems. <i>Frontiers in Microbiology</i> , 2021, 12, 678290.	1.5	6
16773	MALBoost: a web-based application for gene regulatory network analysis in <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2021, 20, 317.	0.8	0
16774	Molecular mechanism of reproductive toxicity induced by <i>Tripterygium Wilfordii</i> based on network pharmacology. <i>Medicine (United States)</i> , 2021, 100, e26197.	0.4	9
16775	Global identification of phospho-dependent SCF substrates reveals a FBXO22 phosphodegron and an ERK-FBXO22-BAG3 axis in tumorigenesis. <i>Cell Death and Differentiation</i> , 2022, 29, 1-13.	5.0	22
16776	High expression of DNA damage-inducible transcript 4 (DDIT4) is associated with advanced pathological features in the patients with colorectal cancer. <i>Scientific Reports</i> , 2021, 11, 13626.	1.6	15
16777	Neurotranscriptomic changes associated with chick-directed parental care in adult non-reproductive Japanese quail. <i>Scientific Reports</i> , 2021, 11, 15481.	1.6	6
16778	Dysregulation of Synaptic Signaling Genes Is Involved in Biology of Uterine Leiomyoma. <i>Genes</i> , 2021, 12, 1179.	1.0	2

#	ARTICLE	IF	CITATIONS
16779	iTRAQ-based proteomic analysis of sperm reveals candidate proteins that affect the quality of spermatozoa from boars on plateaus. <i>Proteome Science</i> , 2021, 19, 9.	0.7	7
16780	Identification of m6A-Related Biomarkers Associated with Prognosis of Colorectal Cancer. <i>Medical Science Monitor</i> , 2021, 27, e932370.	0.5	9
16781	Aurora kinase A (AURKA) promotes the progression and imatinib resistance of advanced gastrointestinal stromal tumors. <i>Cancer Cell International</i> , 2021, 21, 407.	1.8	2
16783	Purine metabolite-based machine learning models for risk prediction, prognosis, and diagnosis of coronary artery disease. <i>Biomedicine and Pharmacotherapy</i> , 2021, 139, 111621.	2.5	9
16784	Molecular Commerce on Coral Reefs: Using Metabolomics to Reveal Biochemical Exchanges Underlying Holobiont Biology and the Ecology of Coastal Ecosystems. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	12
16785	Baicalein ameliorates osteoporosis via AKT/FOXO1 signaling. <i>Aging</i> , 2021, 13, 17370-17379.	1.4	14
16786	Identification and characterization of long non-coding RNA and their response against citrus bark cracking viroid infection in <i>Humulus lupulus</i> . <i>Genomics</i> , 2021, 113, 2350-2364.	1.3	6
16787	Non-functional <i>GoFLA19s</i> are responsible for the male sterility caused by hybrid breakdown in cotton ( <i>Gossypium</i> spp.). <i>Plant Journal</i> , 2021, 107, 1198-1212.	2.8	8
16788	Chondrocyte protein co-synthesis network analysis links ECM mechanosensing to metabolic adaptation in osteoarthritis. <i>Expert Review of Proteomics</i> , 2021, 18, 623-635.	1.3	1
16789	Screening of hub genes and evaluation of the growth regulatory role of CD44 in metastatic prostate cancer. <i>Oncology Reports</i> , 2021, 46, .	1.2	2
16790	Nicotinic Acetylcholine Receptor Partial Antagonist Polyamides from Tunicates and Their Predatory Sea Slugs. <i>ACS Chemical Neuroscience</i> , 2021, 12, 2693-2704.	1.7	4
16792	Bacterial RF3 senses chaperone function in co-translational folding. <i>Molecular Cell</i> , 2021, 81, 2914-2928.e7.	4.5	9
16793	Network and co-expression analysis of airway smooth muscle cell transcriptome delineates potential gene signatures in asthma. <i>Scientific Reports</i> , 2021, 11, 14386.	1.6	14
16794	Analysis of Immune Associated Co-Expression Networks Reveals Immune-Related Long Non-Coding RNAs during MI in the Presence and Absence of HDC. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7401.	1.8	2
16795	Transcriptional Insights into Key Genes and Pathways Underlying Muscovy Duck Subcutaneous Fat Deposition at Different Developmental Stages. <i>Animals</i> , 2021, 11, 2099.	1.0	6
16796	Evolution and Characterization of Acetyl Coenzyme A: Diacylglycerol Acyltransferase Genes in Cotton Identify the Roles of GhDGAT3D in Oil Biosynthesis and Fatty Acid Composition. <i>Genes</i> , 2021, 12, 1045.	1.0	11
16799	Exploring Microbial Resource of Different Rhizocompartments of Dominant Plants Along the Salinity Gradient Around the Hypersaline Lake Ejinur. <i>Frontiers in Microbiology</i> , 2021, 12, 698479.	1.5	14
16800	COVID-19 Candidate Genes and Pathways Potentially Share the Association with Lung Cancer. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 2463-2472.	0.6	4

#	ARTICLE	IF	CITATIONS
16801	Improved immobilization of soil cadmium by regulating soil characteristics and microbial community through reductive soil disinfestation. <i>Science of the Total Environment</i> , 2021, 778, 146222.	3.9	20
16802	Discovery of the Class I Antimicrobial Lasso Peptide Arcumycin. <i>ChemBioChem</i> , 2021, 22, 2632-2640.	1.3	10
16803	Single-oocyte transcriptome analysis reveals aging-associated effects influenced by life stage and calorie restriction. <i>Aging Cell</i> , 2021, 20, e13428.	3.0	22
16804	Curcumin and Biochemical Parameters in Metabolic-Associated Fatty Liver Disease (MAFLD) – A Review. <i>Nutrients</i> , 2021, 13, 2654.	1.7	12
16806	Synergistic role of retinoic acid signaling and Gata3 during primitive choanae formation. <i>Human Molecular Genetics</i> , 2021, 30, 2383-2392.	1.4	4
16807	A systems-based framework to computationally describe putative transcription factors and signaling pathways regulating glycan biosynthesis. <i>Beilstein Journal of Organic Chemistry</i> , 2021, 17, 1712-1724.	1.3	7
16808	Using food network analysis to understand meal patterns in pregnant women with high and low diet quality. <i>International Journal of Behavioral Nutrition and Physical Activity</i> , 2021, 18, 101.	2.0	2
16809	Network Pharmacology-Based Analysis and Experimental Exploration of Antidiabetic Mechanisms of Gegen Qinlian Decoction. <i>Frontiers in Pharmacology</i> , 2021, 12, 649606.	1.6	6
16811	Gene Expression Profile of Human Mesenchymal Stromal Cells Exposed to Hypoxic and Pseudohypoxic Preconditioning – An Analysis by RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8160.	1.8	4
16812	Plasma-Derived Exosomal hsa-miR-4488 and hsa-miR-1228-5p: Novel Biomarkers for Dermatomyositis-Associated Interstitial Lung Disease with Anti-Melanoma Differentiation-Associated Protein 5 Antibody-Positive Subset. <i>BioMed Research International</i> , 2021, 2021, 1-16.	0.9	13
16813	GWAS and WGCNA uncover hub genes controlling salt tolerance in maize ( <i>Zea mays</i> L.) seedlings. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3305-3318.	1.8	54
16814	Genomic and pleiotropic analyses of resting QT interval identifies novel loci and overlap with atrial electrical disorders. <i>Human Molecular Genetics</i> , 2021, 30, 2513-2523.	1.4	5
16815	<i>Syzygium aromaticum</i> (clove) essential oil: An alternative for the sanitization of citrus fruit in packinghouses. <i>Journal of Food Processing and Preservation</i> , 2021, 45, e15496.	0.9	3
16816	Increase in sedimentary organic carbon with a change from hypoxic to oxic conditions. <i>Marine Pollution Bulletin</i> , 2021, 168, 112397.	2.3	2
16817	Feature-based molecular networking for identification of organic micropollutants including metabolites by non-target analysis applied to riverbank filtration. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 5291-5300.	1.9	15
16818	The Gut Microbiota of Naturally Occurring and Laboratory Aquaculture <i>Lytechinus variegatus</i> Revealed Differences in the Community Composition, Taxonomic Co-Occurrence, and Predicted Functional Attributes. <i>Applied Microbiology</i> , 2021, 1, 201-224.	0.7	2
16819	E-type prostanoid receptor 4 drives resolution of intestinal inflammation by blocking epithelial necroptosis. <i>Nature Cell Biology</i> , 2021, 23, 796-807.	4.6	38
16820	Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. <i>Molecular Cell</i> , 2021, 81, 2944-2959.e10.	4.5	19

#	ARTICLE	IF	CITATIONS
16821	Identification of Key Candidate Genes Related to Inflammatory Osteolysis Associated with Vitamin E-Blended UHMWPE Debris of Orthopedic Implants by Integrated Bioinformatics Analysis and Experimental Confirmation. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 3537-3554.	1.6	14
16823	Development of a four-gene prognostic model for clear cell renal cell carcinoma based on transcriptome analysis. <i>Genomics</i> , 2021, 113, 1816-1827.	1.3	12
16824	Mitochondrial Proteostasis Requires Genes Encoded in a Neurodevelopmental Syndrome Locus. <i>Journal of Neuroscience</i> , 2021, 41, 6596-6616.	1.7	18
16825	Profile of protein lysine propionylation in <i>Aeromonas hydrophila</i> and its role in enzymatic regulation. <i>Biochemical and Biophysical Research Communications</i> , 2021, 562, 1-8.	1.0	2
16826	Integration of Transcriptome and Metabolome Reveals the Genes and Metabolites Involved in <i>Bifidobacterium bifidum</i> Biofilm Formation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7596.	1.8	20
16827	Genome-Wide Investigation of Spliceosomal SM/LSM Genes in Wheat ( <i>Triticum aestivum</i> L.) and Its Progenitors. <i>Agronomy</i> , 2021, 11, 1429.	1.3	0
16828	Vertical Stratification of Dissolved Organic Matter Linked to Distinct Microbial Communities in Subtropic Estuarine Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 697860.	1.5	12
16829	Characterization of the Impact of Density Gradient Centrifugation on the Profile of the Pig Sperm Transcriptome by RNA-Seq. <i>Frontiers in Veterinary Science</i> , 2021, 8, 668158.	0.9	4
16830	Compatibility of Distinct Label-Free Proteomic Workflows in Absolute Quantification of Proteins Linked to the Oocyte Quality in Human Follicular Fluid. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7415.	1.8	5
16831	Inference of kinase-signaling networks in human myeloid cell line models by Phosphoproteomics using kinase activity enrichment analysis (KAEA). <i>BMC Cancer</i> , 2021, 21, 789.	1.1	2
16832	RNA sequencing reveals potential interacting networks between the altered transcriptome and ncRNome in the skeletal muscle of diabetic mice. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
16833	Viromics unveils extraordinary genetic diversity of the family <i>Closteroviridae</i> in wild citrus. <i>PLoS Pathogens</i> , 2021, 17, e1009751.	2.1	17
16834	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7266.	1.8	14
16835	Motor Stereotypic Behavior Was Associated With Immune Response in Macaques: Insight From Transcriptome and Gut Microbiota Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 644540.	1.5	3
16836	The Identification of Childhood Asthma Progression-Related lncRNAs and mRNAs Suitable as Biomarkers Using Weighted Gene Coexpression Network Analysis. <i>Genetical Research</i> , 2021, 2021, 1-10.	0.3	5
16837	Autophagy-Related Genes in Atherosclerosis. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	6
16839	Characterization of DNA Methylomic Signatures in Induced Pluripotent Stem Cells During Neuronal Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647981.	1.8	7
16840	Development of a Novel Immune Infiltration-Related ceRNA Network and Prognostic Model for Sarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 652300.	1.8	2

#	ARTICLE	IF	CITATIONS
16841	Shared and tailored common bean transcriptomic responses to combined fusarium wilt and water deficit. <i>Horticulture Research</i> , 2021, 8, 149.	2.9	10
16842	Altered expression of genes controlling metabolism characterizes the tissue response to immune injury in lupus. <i>Scientific Reports</i> , 2021, 11, 14789.	1.6	22
16843	Prediction of chemoresistance trait of cancer cell lines using machine learning algorithms and systems biology analysis. <i>Journal of Big Data</i> , 2021, 8, .	6.9	4
16844	Bioinformatics analysis of differentially expressed genes and identification of an miRNA-mRNA network associated with entorhinal cortex and hippocampus in Alzheimer's disease. <i>Hereditas</i> , 2021, 158, 25.	0.5	6
16845	Comparative transcriptomics of leaves of five mulberry accessions and cataloguing structural and expression variants for future prospects. <i>PLoS ONE</i> , 2021, 16, e0252246.	1.1	3
16846	Omics Multi-Layers Networks Provide Novel Mechanistic and Functional Insights Into Fat Storage and Lipid Metabolism in Poultry. <i>Frontiers in Genetics</i> , 2021, 12, 646297.	1.1	9
16848	Antimetastatic Effects of Ganoderma lucidum Polysaccharide Peptide on B16-F10-luc-G5 Melanoma Mice With Sleep Fragmentation. <i>Frontiers in Pharmacology</i> , 2021, 12, 650216.	1.6	14
16849	Radiosensitivity of herbaceous plants to chronic radiation exposure: Field study in the Chernobyl exclusion zone. <i>Science of the Total Environment</i> , 2021, 777, 146206.	3.9	16
16850	Exploring PIF4's contribution to early flowering in plants under daily variable temperature and its tissue-specific flowering gene network. <i>Plant Direct</i> , 2021, 5, e339.	0.8	8
16851	Persistence and reversibility of arsenic-induced gut microbiome and metabolome shifts in male rats after 30-days recovery duration. <i>Science of the Total Environment</i> , 2021, 776, 145972.	3.9	16
16852	The Construction and Comprehensive Analysis of Inflammation-Related ceRNA Networks and Tissue-Infiltrating Immune Cells in Ulcerative Colitis Progression. <i>BioMed Research International</i> , 2021, 2021, 1-20.	0.9	12
16853	Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. <i>Ecological Applications</i> , 2021, 31, e02379.	1.8	23
16854	Network-Based Analysis of Fatal Comorbidities of COVID-19 and Potential Therapeutics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1271-1280.	1.9	23
16855	Blue Biotechnology: Computational Screening of Sarcophyton Cembranoid Diterpenes for SARS-CoV-2 Main Protease Inhibition. <i>Marine Drugs</i> , 2021, 19, 391.	2.2	22
16856	Bruceine A induces cell growth inhibition and apoptosis through PFKFB4/GSK3 $\beta$ signaling in pancreatic cancer. <i>Pharmacological Research</i> , 2021, 169, 105658.	3.1	15
16857	LGALS3BP: A Potential Plasma Biomarker Associated with Diagnosis and Prognosis in Patients with Sepsis. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 2863-2871.	1.1	5
16859	Lipidomics of Environmental Microbial Communities. II: Characterization Using Molecular Networking and Information Theory. <i>Frontiers in Microbiology</i> , 2021, 12, 659315.	1.5	11
16861	AKT3 and related molecules as potential biomarkers responsible for cryptorchidism and cryptorchidism-induced azoospermia. <i>Translational Pediatrics</i> , 2021, 10, 1805-1817.	0.5	6



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16862	Elevated plasma succinate levels are linked to higher cardiovascular disease risk factors in young adults. <i>Cardiovascular Diabetology</i> , 2021, 20, 151.	2.7	36
16863	Capturing the transcription factor interactome in response to sub-lethal insecticide exposure. <i>Current Research in Insect Science</i> , 2021, 1, 100018.	0.8	4
16864	Lytic archaeal viruses infect abundant primary producers in Earth's crust. <i>Nature Communications</i> , 2021, 12, 4642.	5.8	28
16865	GC-TOF/MS-based metabolomics analysis to investigate the changes driven by N-Acetylcysteine in the plant-pathogen <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>Scientific Reports</i> , 2021, 11, 15558.	1.6	3
16866	Rhamnolipid Enhances the Nitrogen Fixation Activity of <i>Azotobacter chroococcum</i> by Influencing Lysine Succinylation. <i>Frontiers in Microbiology</i> , 2021, 12, 697963.	1.5	4
16868	Identification of novel genes and pathways regulated by the orphan nuclear receptor COUP-TFII in mouse MA-10 Leydig cells. <i>Biology of Reproduction</i> , 2021, 105, 1283-1306.	1.2	7
16869	Genetic alterations and functional networks of m6A RNA methylation regulators in pancreatic cancer based on data mining. <i>Journal of Translational Medicine</i> , 2021, 19, 323.	1.8	3
16870	Structure-based molecular networking for the target discovery of novel germicidin derivatives from the sponge-associated streptomyces sp. 18A01. <i>Journal of Antibiotics</i> , 2021, 74, 799-806.	1.0	3
16871	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , 2021, 10, .	2.8	7
16873	Identification of JAK2 and FOXM1 expression as novel candidate biomarkers for predicting the benefit of immunotherapy in lung squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 1081-1081.	0.7	1
16874	A new family of globally distributed lytic roseophages with unusual deoxythymidine to deoxyuridine substitution. <i>Current Biology</i> , 2021, 31, 3199-3206.e4.	1.8	13
16875	Genome-wide identification and comparative analysis of the WRKY gene family in aquatic plants and their response to abiotic stresses in giant duckweed ( <i>Spirodela polyrhiza</i> ). <i>Genomics</i> , 2021, 113, 1761-1777.	1.3	19
16876	Complex analysis of the personalized pharmacotherapy in the management of COVID-19 patients and suggestions for applications of predictive, preventive, and personalized medicine attitude. <i>EPMA Journal</i> , 2021, 12, 307-324.	3.3	11
16877	Microarray-based selection of a serum biomarker panel that can discriminate between latent and active pulmonary TB. <i>Scientific Reports</i> , 2021, 11, 14516.	1.6	7
16878	Milk and serum proteomes in subclinical and clinical mastitis in Simmental cows. <i>Journal of Proteomics</i> , 2021, 244, 104277.	1.2	25
16879	The association between social and spatial closeness with PrEP conversations among Latino men who have sex with men. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2021, Publish Ahead of Print, 366-375.	0.9	4
16881	Local clustering via approximate heat kernel PageRank with subgraph sampling. <i>Scientific Reports</i> , 2021, 11, 15786.	1.6	0
16882	Network Pharmacology Approach for Predicting Targets of Zishen Yutai Pills on Premature Ovarian Insufficiency. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	9

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16883	Dual Transcriptomic Analyses Unveil Host-Pathogen Interactions Between <i>Salmonella enterica</i> Serovar Enteritidis and Laying Ducks ( <i>Anas platyrhynchos</i> ). <i>Frontiers in Microbiology</i> , 2021, 12, 705712.	1.5	1
16884	Genome Analysis of <i>Streptomyces nojiriensis</i> JCM 3382 and Distribution of Gene Clusters for Three Antibiotics and an Azasugar across the Genus <i>Streptomyces</i> . <i>Microorganisms</i> , 2021, 9, 1802.	1.6	5
16885	The expression and potential mechanism of EGFR and EZH2 in breast cancer. <i>Gland Surgery</i> , 2021, 10, 2535-2545.	0.5	2
16887	<i>In silico</i> predictions of protein interactions between Zika virus and human host. <i>PeerJ</i> , 2021, 9, e11770.	0.9	3
16888	Phytate and Microbial Suspension Amendments Increased Soybean Growth and Shifted Microbial Community Structure. <i>Microorganisms</i> , 2021, 9, 1803.	1.6	6
16889	Inflammatory gene expression profiling in peripheral blood from patients with Alzheimer's disease reveals key pathways and hub genes with potential diagnostic utility: a preliminary study. <i>PeerJ</i> , 2021, 9, e12016.	0.9	1
16891	Is platelet responsiveness to clopidogrel attenuated in overweight or obese patients and why? A reverse translational study in mice. <i>British Journal of Pharmacology</i> , 2022, 179, 46-64.	2.7	4
16892	Identification of the Mouse T Cell ADP-Ribosylome Uncovers ARTC2.2 Mediated Regulation of CD73 by ADP-Ribosylation. <i>Frontiers in Immunology</i> , 2021, 12, 703719.	2.2	3
16893	LinkedImm: a linked data graph database for integrating immunological data. <i>BMC Bioinformatics</i> , 2021, 22, 105.	1.2	4
16894	Exploring the Pharmacological Mechanisms of <i>Tripterygium wilfordii</i> Hook F against Cardiovascular Disease Using Network Pharmacology and Molecular Docking. <i>BioMed Research International</i> , 2021, 1-11.	0.9	3
16895	Comprehensive Analysis of the Systemic Transcriptomic Alternations and Inflammatory Response during the Occurrence and Progress of COVID-19. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-17.	1.9	13
16896	The Synergistic Effect of Ginkgo biloba Extract 50 and Aspirin Against Platelet Aggregation. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 3543-3560.	2.0	19
16897	Construction of Potential Gene Expression and Regulation Networks in Prostate Cancer Using Bioinformatics Tools. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-11.	1.9	6
16898	Gut Microbiome Structure and Association with Host Factors in a Korean Population. <i>MSystems</i> , 2021, 6, e0017921.	1.7	14
16899	Comparative Analysis of Structural and Dynamical Features of Ribosome Upon Association With mRNA Reveals Potential Role of Ribosomal Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 654164.	1.6	4
16900	Spliceosomal component PRP-40 is a central regulator of microexon splicing. <i>Cell Reports</i> , 2021, 36, 109464.	2.9	16
16901	The pentose phosphate pathway constitutes a major metabolic hub in pathogenic <i>Francisella</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009326.	2.1	16
16902	Angiogenic gene networks are dysregulated in opioid use disorder: evidence from multi-omics and imaging of postmortem human brain. <i>Molecular Psychiatry</i> , 2021, 26, 7803-7812.	4.1	31

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16903	Identification of COVID-19 prognostic markers and therapeutic targets through meta-analysis and validation of Omics data from nasopharyngeal samples. <i>EBioMedicine</i> , 2021, 70, 103525.	2.7	27
16904	Network-Based Integration of Multi-Omics Data Identifies the Determinants of miR-491-5p Effects. <i>Cancers</i> , 2021, 13, 3970.	1.7	1
16905	Non-targeted screening of trace organic contaminants in surface waters by a multi-tool approach based on combinatorial analysis of tandem mass spectra and open access databases. <i>Talanta</i> , 2021, 230, 122293.	2.9	18
16906	Key radioresistance regulation models and marker genes identified by integrated transcriptome analysis in nasopharyngeal carcinoma. <i>Cancer Medicine</i> , 2021, 10, 7404-7417.	1.3	10
16907	CANVS: an easy-to-use application for the analysis and visualization of mass spectrometry-based protein-protein interaction/association data. <i>Molecular Biology of the Cell</i> , 2021, 32, br9.	0.9	0
16908	Identification of key molecules in recurrent miscarriage based on bioinformatics analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, .	0.6	0
16909	Pathways Related to the Anti-Cancer Effects of Metabolites Derived from Cerrado Biome Native Plants: An Update and Bioinformatics Analysis on Oral Squamous Cell Carcinoma. <i>Protein and Peptide Letters</i> , 2021, 28, 735-749.	0.4	4
16910	Impact and mechanism of sulphur-deficiency on modern wheat farming nitrogen-related sustainability and gliadin content. <i>Communications Biology</i> , 2021, 4, 945.	2.0	29
16911	Deciphering the Therapeutic Mechanisms of Wuzi Ershen Decoction in Treating Oligoasthenozoospermia through the Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	2
16912	Structure characterization and potential role of soybean phospholipases A multigene family in response to multiple abiotic stress uncovered by CRISPR/Cas9 technology. <i>Environmental and Experimental Botany</i> , 2021, 188, 104521.	2.0	14
16913	Identification of Potential Genomic Alterations and the circRNA-miRNA-mRNA Regulatory Network in Primary and Recurrent Synovial Sarcomas. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 707151.	1.6	9
16914	High-Throughput In Vitro Gene Expression Profile to Screen of Natural Herbals for Breast Cancer Treatment. <i>Frontiers in Oncology</i> , 2021, 11, 684351.	1.3	4
16915	Construction of a Novel Gene-Based Model for Survival Prediction of Hepatitis B Virus Carriers With HCC Development. <i>Frontiers in Genetics</i> , 2021, 12, 720888.	1.1	2
16916	Unraveling the Genetic Basis of Fertility Restoration for Cytoplasmic Male Sterile Line WNJ01A Originated From <i>Brassica juncea</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 721980.	1.7	4
16917	Elevated circRNAs circ_0000745, circ_0001531 and circ_0001640 in human whole blood: Potential novel diagnostic biomarkers for breast cancer. <i>Experimental and Molecular Pathology</i> , 2021, 121, 104661.	0.9	10
16918	Expression profiling of TRIM gene family reveals potential diagnostic biomarkers for rifampicin-resistant tuberculosis. <i>Microbial Pathogenesis</i> , 2021, 157, 104916.	1.3	1
16919	Meta-analysis of genome-wide association studies and gene networks analysis for milk production traits in Holstein cows. <i>Livestock Science</i> , 2021, 250, 104605.	0.6	4
16920	Beauty and Wellness in the Semantic Memory of the Beholder. <i>Frontiers in Psychology</i> , 2021, 12, 696507.	1.1	5

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16921	Diverse energy metabolism patterns in females in <i>Neodon fuscus</i> , <i>Lasiopodomys brandtii</i> , and <i>Mus musculus</i> revealed by comparative transcriptomics under hypoxic conditions. <i>Science of the Total Environment</i> , 2021, 783, 147130.	3.9	9
16922	The exon-junction complex helicase eIF4A3 controls cell fate via coordinated regulation of ribosome biogenesis and translational output. <i>Science Advances</i> , 2021, 7, .	4.7	25
16923	CD86 Molecule Might Be a Novel Immune-Related Prognostic Biomarker for Patients With Bladder Cancer by Bioinformatics and Experimental Assays. <i>Frontiers in Oncology</i> , 2021, 11, 679851.	1.3	4
16924	Evidence for miRNAs involved in the high-altitude responses of sainfoin ( <i>Onobrychis viciifolia</i> ) grown in the Qinghai-Tibetan plateau. <i>Journal of Plant Biochemistry and Biotechnology</i> , 0, , 1.	0.9	0
16925	Identification of Core Genes and Key Pathways in Gastric Cancer using Bioinformatics Analysis. <i>Russian Journal of Genetics</i> , 2021, 57, 963-971.	0.2	0
16926	Transcriptome Atlas of 16 Donkey Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 682734.	1.1	8
16927	Pro-inflammatory $\hat{I}^2$ cell small extracellular vesicles induce $\hat{I}^2$ cell failure through activation of the CXCL10/CXCR3 axis in diabetes. <i>Cell Reports</i> , 2021, 36, 109613.	2.9	25
16928	High-throughput analysis of the interactions between viral proteins and host cell RNAs. <i>Computers in Biology and Medicine</i> , 2021, 135, 104611.	3.9	9
16929	Metabolic, structural, and proteomic changes in <i>Candida albicans</i> cells induced by the protein-carbohydrate fraction of <i>Dendrobaena veneta</i> coelomic fluid. <i>Scientific Reports</i> , 2021, 11, 16711.	1.6	8
16930	Cadherin and Wnt signaling pathways as key regulators in diabetic nephropathy. <i>PLoS ONE</i> , 2021, 16, e0255728.	1.1	2
16931	A primary cell wall cellulose-dependent defense mechanism against vascular pathogens revealed by time-resolved dual transcriptomics. <i>BMC Biology</i> , 2021, 19, 161.	1.7	26
16932	Correcting for sparsity and interdependence in glycomics by accounting for glycan biosynthesis. <i>Nature Communications</i> , 2021, 12, 4988.	5.8	22
16933	Marine-Derived Xyloketal Compound Ameliorates MPP <sup>+</sup> -Induced Neuronal Injury through Regulating of the IRE1/XBP1 Signaling Pathway. <i>ACS Chemical Neuroscience</i> , 2021, 12, 3101-3111.	1.7	4
16934	Long-term acclimation to cadmium exposure reveals extensive phenotypic plasticity in <i>Chlamydomonas</i> . <i>Plant Physiology</i> , 2021, 187, 1653-1678.	2.3	7
16935	Phosphoproteomics Identifies Significant Biomarkers Associated with the Proliferation and Metastasis of Prostate Cancer. <i>Toxins</i> , 2021, 13, 554.	1.5	0
16936	Arabidopsis-Based Dual-Layered Biological Network Analysis Elucidates Fully Modulated Pathways Related to Sugarcane Resistance on Biotrophic Pathogen Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 707904.	1.7	0
16937	A global map of associations between types of protein posttranslational modifications and human genetic diseases. <i>IScience</i> , 2021, 24, 102917.	1.9	7
16938	Tracing colonic embryonic transcriptional profiles and their reactivation upon intestinal damage. <i>Cell Reports</i> , 2021, 36, 109484.	2.9	18

#	ARTICLE	IF	CITATIONS
16939	Expanding Urinary Metabolite Annotation through Integrated Mass Spectral Similarity Networking. <i>Analytical Chemistry</i> , 2021, 93, 12001-12010.	3.2	22
16940	Genomic and molecular evidence reveals novel pathways associated with cell surface polysaccharides in bacteria. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	1
16941	Proteomic analysis of ubiquitination substrates reveals a CTLH E3 ligase complexâ€dependent regulation of glycolysis. <i>FASEB Journal</i> , 2021, 35, e21825.	0.2	19
16942	In vivo and in vitro $\hat{\pm}$ -amanitin metabolism studies using molecular networking. <i>Toxicology Letters</i> , 2021, 346, 1-6.	0.4	17
16943	Comparative transcriptomic analysis of the brain in Takifugu rubripes shows its tolerance to acute hypoxia. <i>Fish Physiology and Biochemistry</i> , 2021, 47, 1669-1685.	0.9	10
16944	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. <i>Nature Neuroscience</i> , 2021, 24, 1367-1376.	7.1	137
16945	The rice foot rot pathogen <i>Dickeya zeae</i> alters the inâ€field plant microbiome. <i>Environmental Microbiology</i> , 2021, 23, 7671-7687.	1.8	14
16946	Soil mesoâ€fauna community composition predicts ecosystem multifunctionality along a coastalâ€inland gradient of the Bohai Bay. <i>Land Degradation and Development</i> , 2021, 32, 4574-4582.	1.8	3
16947	Multilevel systems biology analysis of lung transcriptomics data identifies key miRNAs and potential miRNA target genes for SARS-CoV-2 infection. <i>Computers in Biology and Medicine</i> , 2021, 135, 104570.	3.9	31
16948	Gene expression profiling reveals candidate genes for defining spider silk gland types. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 135, 103594.	1.2	9
16949	A toxicity pathway-based approach for modeling the mode of action framework of lead-induced neurotoxicity. <i>Environmental Research</i> , 2021, 199, 111328.	3.7	9
16950	Distinct Persistence Fate of Mycobacterium tuberculosis in Various Types of Cells. <i>MSystems</i> , 2021, 6, e0078321.	1.7	4
16951	Identification and Characterization of Rice Circular RNAs Responding to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Invasion. <i>Phytopathology</i> , 2022, 112, 492-500.	1.1	2
16952	Bacterial Diversity in Calcium Carbonate Paleo Accretions ( <i>Tosca</i> ) in the Southern Pampas, Argentina. <i>Geomicrobiology Journal</i> , 2021, 38, 869-878.	1.0	1
16953	High Resolution Analysis of Proteome Dynamics during <i>Bacillus subtilis</i> Sporulation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9345.	1.8	8
16954	Proteomic Analysis Reveals Key Proteins in Extracellular Vesicles Cargo Associated with Idiopathic Pulmonary Fibrosis In Vitro. <i>Biomedicines</i> , 2021, 9, 1058.	1.4	18
16955	Identification of hub genes and functional modules in colon adenocarcinoma based on public databases by bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 1613-1624.	0.6	2
16956	The Spleen as a Target to Characterize Immunomodulatory Effects of Down-Stream Processed <i>Cyberlindnera jadinii</i> Yeasts in Atlantic Salmon Exposed to a Dietary Soybean Meal Challenge. <i>Frontiers in Immunology</i> , 2021, 12, 708747.	2.2	11

#	ARTICLE	IF	CITATIONS
16957	The pesticide chlorpyrifos promotes obesity by inhibiting diet-induced thermogenesis in brown adipose tissue. <i>Nature Communications</i> , 2021, 12, 5163.	5.8	47
16958	Global mapping of <i>Salmonella enterica</i> -host protein-protein interactions during infection. <i>Cell Host and Microbe</i> , 2021, 29, 1316-1332.e12.	5.1	39
16960	<i>Prevotella copri</i> increases fat accumulation in pigs fed with formula diets. <i>Microbiome</i> , 2021, 9, 175.	4.9	100
16961	Genome-wide study of copy number variation implicates multiple novel loci for schizophrenia risk in Han Chinese family trios. <i>IScience</i> , 2021, 24, 102894.	1.9	5
16962	Employing bioinformatics analysis to identify hub genes and microRNAs involved in colorectal cancer. <i>Medical Oncology</i> , 2021, 38, 114.	1.2	11
16963	Clinical Genetic Risk Variants Inform a Functional Protein Interaction Network for Tetralogy of Fallot. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003410.	1.6	15
16964	Cardiac risk stratification in cancer patients: A longitudinal patient network analysis. <i>PLoS Medicine</i> , 2021, 18, e1003736.	3.9	19
16965	Ten simple rules for creating reusable pathway models for computational analysis and visualization. <i>PLoS Computational Biology</i> , 2021, 17, e1009226.	1.5	13
16966	A Biological Insight into the Susceptibility to Influenza Infection in Junior Rats by Comprehensive Analysis of lncRNA Profiles. <i>BioMed Research International</i> , 2021, 2021, 1-9.	0.9	2
16968	Gut and Vagina Microbiota Associated With Estrus Return of Weaning Sows and Its Correlation With the Changes in Serum Metabolites. <i>Frontiers in Microbiology</i> , 2021, 12, 690091.	1.5	8
16969	Longitudinal survey reveals delayed effects of low gene expression on stingless bee colony health. <i>Journal of Apicultural Research</i> , 2022, 61, 654-663.	0.7	2
16970	SARS-CoV-2 infection initiates interleukin-17-enriched transcriptional response in different cells from multiple organs. <i>Scientific Reports</i> , 2021, 11, 16814.	1.6	43
16971	Transcriptional, Epigenetic, and Functional Reprogramming of Monocytes From Non-Human Primates Following Chronic Alcohol Drinking. <i>Frontiers in Immunology</i> , 2021, 12, 724015.	2.2	11
16972	A Network Pharmacology Approach for Exploring the Mechanisms of <i>Panax notoginseng</i> Saponins in Ischaemic Stroke. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-14.	0.5	1
16973	Elucidating the Molecular Mechanism of Ischemic Stroke Using Integrated Analysis of miRNA, mRNA, and lncRNA Expression Profiles. <i>Frontiers in Integrative Neuroscience</i> , 2021, 15, 638114.	1.0	8
16974	Assembling stable syntrophic <i>Escherichia coli</i> communities by comprehensively identifying beneficiaries of secreted goods. <i>Cell Systems</i> , 2021, 12, 1064-1078.e7.	2.9	24
16976	A Widespread Bacterial Secretion System with Diverse Substrates. <i>MBio</i> , 2021, 12, e0195621.	1.8	30
16977	Elucidating the Effects of Curcumin against Influenza Using In Silico and In Vitro Approaches. <i>Pharmaceuticals</i> , 2021, 14, 880.	1.7	6



#	ARTICLE	IF	CITATIONS
16978	A Comprehensive Genomic Analysis Constructs miRNA-mRNA Interaction Network in Hepatoblastoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 655703.	1.8	2
16979	Efficacy of signal peptide predictors in identifying signal peptides in the experimental secretome of <i>Picrophilous torridus</i> , a thermoacidophilic archaeon. <i>PLoS ONE</i> , 2021, 16, e0255826.	1.1	2
16980	The transcriptomic blueprint of molt in rooster using various tissues from Ginkkoridak (Korean) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 66	1.2	1
16981	Key aromatic amino acid players in soybean ( <i>Glycine max</i> ) genome under drought and salt stresses. <i>Biocatalysis and Agricultural Biotechnology</i> , 2021, 35, 102094.	1.5	10
16982	Expression profiles and functional prediction of long non-coding RNAs LINC01133, ZEB1-AS1 and ABHD11-AS1 in the luminal subtype of breast cancer. <i>Journal of Translational Medicine</i> , 2021, 19, 364.	1.8	8
16983	Screening for Higher Grain Yield and Biomass among Sixty Bread Wheat Genotypes Grown under Elevated CO <sub>2</sub> and High-Temperature Conditions. <i>Plants</i> , 2021, 10, 1596.	1.6	13
16984	Genome-wide analysis of HECT E3 ubiquitin ligase gene family in <i>Solanum lycopersicum</i> . <i>Scientific Reports</i> , 2021, 11, 15891.	1.6	10
16985	Fast and accurate exhaustive higher-order epistasis search with BitEpi. <i>Scientific Reports</i> , 2021, 11, 15923.	1.6	11
16986	Role of Potential COVID-19 Immune System Associated Genes and the Potential Pathways Linkage with Type-2 Diabetes. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 2452-2462.	0.6	11
16987	Centre-specific bacterial pathogen typing affects infection-control decision making. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
16988	p16INK4a Regulates Cellular Senescence in PD-1-Expressing Human T Cells. <i>Frontiers in Immunology</i> , 2021, 12, 698565.	2.2	16
16989	Proton exit pathways surrounding the oxygen evolving complex of photosystem II. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2021, 1862, 148446.	0.5	30
16990	Cross-Linking/Mass Spectrometry Combined with Ion Mobility on a timsTOF Pro Instrument for Structural Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 11442-11450.	3.2	26
16991	Investigating the Mechanism of <i>Scutellariae barbata</i> Herba in the Treatment of Colorectal Cancer by Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-18.	0.5	8
16993	A Two-Gene-Based Diagnostic Signature for Ruptured Intracranial Aneurysms. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 671655.	1.1	6
16994	Prednisone Reprograms the Transcriptional Immune Cell Landscape in CNS Autoimmune Disease. <i>Frontiers in Immunology</i> , 2021, 12, 739605.	2.2	6
16995	The molecular basis, genetic control and pleiotropic effects of local gene co-expression. <i>Nature Communications</i> , 2021, 12, 4842.	5.8	18
16997	Identification and characterization of metal uptake ABC transporters in <i>Mycobacterium tuberculosis</i> unveil their ligand specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 324-337.	3.6	4

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16999	Blood DNA Methylation and Incident Coronary Heart Disease. <i>JAMA Cardiology</i> , 2021, 6, 1237.	3.0	24
17000	PIP2-induced membrane binding of the Vinculin tail competes with its other binding partners. <i>Biophysical Journal</i> , 2021, 120, 4608-4622.	0.2	3
17001	Role of FAM134 paralogues in endoplasmic reticulum remodeling, ERâ€phagy, and Collagen quality control. <i>EMBO Reports</i> , 2021, 22, e52289.	2.0	55
17002	Genome-wide regulation of CpG methylation by ecCEBPÎ± in acute myeloid leukemia. <i>F1000Research</i> , 2021, 10, 204.	0.8	2
17003	Starch turnover is stimulated by nitric oxide in embryogenic cultures of <i>Araucaria angustifolia</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2021, 147, 583-597.	1.2	3
17005	Microbial Reconstitution Improves Aging-Driven Lacrimal Gland Circadian Dysfunction. <i>American Journal of Pathology</i> , 2021, 191, 2091-2116.	1.9	11
17006	An integrated systematic approach for investigating microcurrent electrical nerve stimulation (MENS) efficacy in STZ-induced diabetes mellitus. <i>Life Sciences</i> , 2021, 279, 119650.	2.0	4
17007	Synergistic efficacy of curcumin and anti-programmed cell death-1 in hepatocellular carcinoma. <i>Life Sciences</i> , 2021, 279, 119359.	2.0	30
17008	Molecular Effects of Pteryxin and Scopoletin in the 5xFAD Alzheimerâ€™s Disease Mouse Model. <i>Current Medicinal Chemistry</i> , 2022, 29, 2937-2950.	1.2	7
17009	Construction of a ceRNA network of hub genes affecting immune infiltration in ovarian cancer identified by WGCNA. <i>BMC Cancer</i> , 2021, 21, 970.	1.1	14
17012	Assessing the extent of community spread caused by mink-derived SARS-CoV-2 variants. <i>Innovation(China)</i> , 2021, 2, 100128.	5.2	16
17013	Catalytic mechanism of butane anaerobic oxidation for alkylâ€coenzyme M reductase. <i>Chemical Biology and Drug Design</i> , 2021, 98, 701-712.	1.5	1
17014	The Tyrosine Kinase-Driven Networks of Novel Long Non-coding RNAs and Their Molecular Targets in Myeloproliferative Neoplasms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 643043.	1.8	3
17015	Role of competitive endogenous RNA networks in the pathogenesis of coronary artery disease. <i>Annals of Translational Medicine</i> , 2021, 9, 1234-1234.	0.7	3
17016	Identification of EP300 as a Key Gene Involved in Antipsychotic-Induced Metabolic Dysregulation Based on Integrative Bioinformatics Analysis of Multi-Tissue Gene Expression Data. <i>Frontiers in Pharmacology</i> , 2021, 12, 729474.	1.6	3
17017	In Utero Fetal Weight in Pigs Is Regulated by microRNAs and Their Target Genes. <i>Genes</i> , 2021, 12, 1264.	1.0	8
17018	Exploring the effect of Polyphyllin I on hepatitis B virus-related liver cancer through network pharmacology and in vitro experiments. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, .	0.6	4
17019	Nitrate triggered phosphoproteome changes and a PIN2 phosphosite modulating root system architecture. <i>EMBO Reports</i> , 2021, 22, e51813.	2.0	22

#	ARTICLE	IF	CITATIONS
17020	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
17021	Exploring prevalence of potential pathogens and fecal indicators in geographically distinct river systems through comparative metagenomics. <i>Environmental Pollution</i> , 2021, 282, 117003.	3.7	7
17022	The effect of exercise on the protein profile of rat knee joint intra- and extra-articular ligaments. <i>Scandinavian Journal of Medicine and Science in Sports</i> , 2021, 31, 2033-2043.	1.3	2
17023	Cross-Species and Human Inter-Tissue Network Analysis of Genes Implicated in Longevity and Aging Reveal Strong Support for Nutrient Sensing. <i>Frontiers in Genetics</i> , 2021, 12, 719713.	1.1	13
17024	Deciphering the Dynamics of Signaling Cascades and Virulence Factors of <i>B. cinerea</i> during Tomato Cell Wall Degradation. <i>Microorganisms</i> , 2021, 9, 1837.	1.6	5
17025	Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in <i>Arabidopsis thaliana</i> . <i>IScience</i> , 2021, 24, 102848.	1.9	11
17026	Microbial Interactions and Roles in Soil Fertility in Seasonal Freeze-Thaw Periods under Different Straw Returning Strategies. <i>Agriculture (Switzerland)</i> , 2021, 11, 779.	1.4	8
17027	Influence of Amino Acid Feeding on Production of Calcimycin and Analogs in <i>Streptomyces chartreusis</i> . <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 8740.	1.2	2
17028	Bioinformatics analysis of the transcriptional expression of minichromosome maintenance proteins as potential indicators of survival in patients with cervical cancer. <i>BMC Cancer</i> , 2021, 21, 928.	1.1	14
17029	Investigation of Chemical Profiles of Different Parts of <i>Morus alba</i> Using a Combination of Molecular Networking Methods with Mass Spectral Data from Two Ionization Modes of LC/MS. <i>Plants</i> , 2021, 10, 1711.	1.6	6
17031	Less is more: simple algorithms for the minimum sum of squares clustering problem. <i>IMA Journal of Management Mathematics</i> , 0, , .	1.1	4
17035	A novel anti-infective molecule nesfactin identified from sponge associated bacteria <i>Nesterenkonia</i> sp. MSA31 against multidrug resistant <i>Pseudomonas aeruginosa</i> . <i>Microbial Pathogenesis</i> , 2021, 157, 104923.	1.3	11
17036	Genome-wide association study identifies the virulence-associated marker in <i>Streptococcus suis</i> serotype 2. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104894.	1.0	6
17037	Evolutionary and Characteristic Analysis of RING-DUF1117 E3 Ubiquitin Ligase Genes in <i>Gossypium</i> Discerning the Role of GhRDUF4D in <i>Verticillium dahliae</i> Resistance. <i>Biomolecules</i> , 2021, 11, 1145.	1.8	13
17038	Two Similar Signatures for Predicting the Prognosis and Immunotherapy Efficacy of Stomach Adenocarcinoma Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 704242.	1.8	5
17039	Identification of Key Histone Modifications and Hub Genes for Colorectal Cancer Metastasis. <i>Current Bioinformatics</i> , 2022, 17, 206-216.	0.7	2
17040	Untargeted metabolomics of purple and orange-fleshed sweet potatoes reveals a large structural diversity of anthocyanins and flavonoids. <i>Scientific Reports</i> , 2021, 11, 16408.	1.6	16
17041	Dissecting the critical pathway crosstalk mechanisms of thyroid cancer based on drug-target genes and disease genes. <i>Biologia (Poland)</i> , 2021, 76, 3489-3499.	0.8	1

#	ARTICLE	IF	CITATIONS
17043	Liver proteome response to torpor in a basoendothermic mammal, <i>Tenrec ecaudatus</i> , provides insights into the evolution of homeothermy. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2021, 321, R614-R624.	0.9	1
17044	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. <i>Biomolecules</i> , 2021, 11, 1245.	1.8	17
17045	An immune cell infiltration-related gene signature predicts prognosis for bladder cancer. <i>Scientific Reports</i> , 2021, 11, 16679.	1.6	15
17046	The Role of Adenosine Receptor A2A in the Regulation of Macrophage Exosomes and Vascular Endothelial Cells During Bone Healing. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4001-4017.	1.6	12
17047	Dysregulated lncRNAs are Involved in the Progress of Sepsis by Constructing Regulatory Networks in Whole Blood Cells. <i>Frontiers in Pharmacology</i> , 2021, 12, 678256.	1.6	5
17048	Comparative Analyses of Gene Co-expression Networks: Implementations and Applications in the Study of Evolution. <i>Frontiers in Genetics</i> , 2021, 12, 695399.	1.1	21
17049	Transcriptional profiling of macaque microglia reveals an evolutionary preserved gene expression program. <i>Brain, Behavior, &amp; Immunity - Health</i> , 2021, 15, 100265.	1.3	5
17050	AQPX-cluster aquaporins and aquaglyceroporins are asymmetrically distributed in trypanosomes. <i>Communications Biology</i> , 2021, 4, 953.	2.0	4
17051	Comparative transcriptome analyses reveal genes associated with SARS-CoV-2 infection of human lung epithelial cells. <i>Scientific Reports</i> , 2021, 11, 16212.	1.6	15
17052	Evaluation of drought resistance and transcriptome analysis for the identification of drought-responsive genes in <i>Iris germanica</i> . <i>Scientific Reports</i> , 2021, 11, 16308.	1.6	10
17054	Transcriptional Profiles of Diploid Mutant <i>Apis mellifera</i> Embryos after Knockout of <i>csd</i> by CRISPR/Cas9. <i>Insects</i> , 2021, 12, 704.	1.0	6
17055	Large-scale computational discovery and analysis of virus-derived microbial nanocompartments. <i>Nature Communications</i> , 2021, 12, 4748.	5.8	28
17057	Transcriptomic and Epigenetic Profiling of Fibroblasts in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 66, 53-63.	1.4	12
17058	KLF10 integrates circadian timing and sugar signaling to coordinate hepatic metabolism. <i>ELife</i> , 2021, 10, .	2.8	18
17059	Identification of miRNAs and related hub genes associated with the triple negative breast cancer using integrated bioinformatics analysis and <i>in vitro</i> approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 11676-11690.	2.0	13
17060	Transcriptomic links to muscle mass loss and declines in cumulative muscle protein synthesis during short-term disuse in healthy younger humans. <i>FASEB Journal</i> , 2021, 35, e21830.	0.2	8
17062	Transcriptome Signature of $\text{V}\alpha\text{9V}\beta\text{2}$ T Cells Treated With Phosphoantigens and Notch Inhibitor Reveals Interplay Between TCR and Notch Signaling Pathways. <i>Frontiers in Immunology</i> , 2021, 12, 660361.	2.2	6
17063	Hepatic toxicity of fluorene-9-bisphenol (BHPF) on CD-1 mice. <i>Ecotoxicology and Environmental Safety</i> , 2021, 219, 112298.	2.9	12

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17064	Using weighted gene co-expression network analysis (WGCNA) to identify the hub genes related to hypoxic adaptation in yak ( <i>Bos grunniens</i> ). <i>Genes and Genomics</i> , 2021, 43, 1231-1246.	0.5	12
17065	Effects of long-term exercise and a high-fat diet on synovial fluid metabolomics and joint structural phenotypes in mice: an integrated network analysis. <i>Osteoarthritis and Cartilage</i> , 2021, 29, 1549-1563.	0.6	10
17066	Prognostic targets recognition of rectal adenocarcinoma based on transcriptomics. <i>Medicine (United Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.4	2
17067	Microbial community and abiotic effects on aquatic bacterial communities in north temperate lakes. <i>Science of the Total Environment</i> , 2021, 781, 146771.	3.9	20
17068	Predictive Value of the TP53/PIK3CA/ATM Mutation Classifier for Patients With Bladder Cancer Responding to Immune Checkpoint Inhibitor Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 643282.	2.2	17
17069	Spatial transcriptomics analysis of uterine gene expression in enhancer of zeste homolog 2 conditional knockout mice. <i>Biology of Reproduction</i> , 2021, 105, 1126-1139.	1.2	10
17070	Identification of key proteins in the signaling crossroads between wound healing and cancer hallmark phenotypes. <i>Scientific Reports</i> , 2021, 11, 17245.	1.6	7
17071	Phosphorus availability increases pathobiome abundance and invasion of rhizosphere microbial networks by <i>Ralstonia</i> . <i>Environmental Microbiology</i> , 2021, 23, 5992-6003.	1.8	28
17072	The differences in SARS-CoV and SARS-CoV-2 specific co-expression network mediated biological process in human gut enterocytes. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104892.	1.0	4
17073	Mapping of de novo mutations in primary biliary cholangitis to a disease-specific co-expression network underlying homeostasis and metabolism. <i>Journal of Genetics and Genomics</i> , 2021, , .	1.7	1
17074	Exploring the Potential Key lncRNAs with Endometriosis by Construction of a ceRNA Network. <i>International Journal of General Medicine</i> , 2021, Volume 14, 4161-4170.	0.8	9
17075	Soy and Frequent Dairy Consumption with Subsequent Equol Production Reveals Decreased Gut Health in a Cohort of Healthy Puerto Rican Women. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 8254.	1.2	7
17076	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
17077	TMBIM1 is an inhibitor of adipogenesis and its depletion promotes adipocyte hyperplasia and improves obesity-related metabolic disease. <i>Cell Metabolism</i> , 2021, 33, 1640-1654.e8.	7.2	22
17078	The integrative bioinformatic analysis deciphers the predicted molecular target gene and pathway from curcumin derivative CCA-1.1 against triple-negative breast cancer (TNBC). <i>Journal of the Egyptian National Cancer Institute</i> , 2021, 33, 19.	0.6	6
17079	Bioinformatics Analysis Identifies Molecular Markers Regulating Development and Progression of Endometriosis and Potential Therapeutic Drugs. <i>Frontiers in Genetics</i> , 2021, 12, 622683.	1.1	8
17080	Immune and stromal scoring system associated with tumor microenvironment and prognosis: a gene-based multi-cancer analysis. <i>Journal of Translational Medicine</i> , 2021, 19, 330.	1.8	12
17081	Sex-Dependent Changes of miRNA Levels in the Hippocampus of Adrenalectomized Rats Following Acute Corticosterone Administration. <i>ACS Chemical Neuroscience</i> , 2021, 12, 2981-3001.	1.7	7

#	ARTICLE	IF	CITATIONS
17082	Genomics-guided identification of potential modulators of SARS-CoV-2 entry proteases, TMPRSS2 and Cathepsins B/L. <i>PLoS ONE</i> , 2021, 16, e0256141.	1.1	12
17083	Vascepa protects against high-fat diet-induced glucose intolerance, insulin resistance, and impaired $\beta$ -cell function. <i>IScience</i> , 2021, 24, 102909.	1.9	12
17084	Weighted Gene Co-Expression Network Analysis Combined with Machine Learning Validation to Identify Key Modules and Hub Genes Associated with SARS-CoV-2 Infection. <i>Journal of Clinical Medicine</i> , 2021, 10, 3567.	1.0	30
17085	Off-the-shelf proximity biotinylation for interaction proteomics. <i>Nature Communications</i> , 2021, 12, 5015.	5.8	31
17086	In silico interaction of HOX cluster-embedded microRNAs and long non-coding RNAs in oral cancer. <i>Journal of Oral Pathology and Medicine</i> , 2021, , .	1.4	2
17087	Global Identification and Systematic Analysis of Lysine Malonylation in Maize ( <i>Zea mays</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 728338.	1.7	4
17088	Comprehensive Analysis of Key Genes, Signaling Pathways and miRNAs in Human Knee Osteoarthritis: Based on Bioinformatics. <i>Frontiers in Pharmacology</i> , 2021, 12, 730587.	1.6	15
17090	Endophytic and rhizospheric bacterial communities are affected differently by the host plant species and environmental contamination. <i>Symbiosis</i> , 2021, 85, 191-206.	1.2	2
17091	Newly identified proviruses in <i>Thermotogota</i> suggest that viruses are the vehicles on the highways of interphylum gene sharing. <i>Environmental Microbiology</i> , 2021, 23, 7105-7120.	1.8	4
17092	Epithelial Cell Line Derived from Endometriotic Lesion Mimics Macrophage Nervous Mechanism of Pain Generation on Proteome and Metabolome Levels. <i>Biomolecules</i> , 2021, 11, 1230.	1.8	6
17093	Isotopically Dimethyl Labeling-Based Quantitative Proteomic Analysis of Phosphoproteomes of Soybean Cultivars. <i>Biomolecules</i> , 2021, 11, 1218.	1.8	5
17094	Integrated analysis of the expression, involved functions, and regulatory network of RUNX3 in melanoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, .	0.6	0
17096	Integrated high-throughput small RNA and transcriptome sequencing unveil the shape-dependent toxicity of nano-alumina in rat astrocytes. <i>Environmental Sciences Europe</i> , 2021, 33, .	2.6	2
17097	Differentially Expressed Functional LncRNAs in Human Subjects With Metabolic Syndrome Reflect a Competing Endogenous RNA Network in Circulating Extracellular Vesicles. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 667056.	1.6	4
17099	Replacement of Nitrite in Meat Products by Natural Bioactive Compounds Results in Reduced Exposure to Na-Nitroso Compounds: The PHYTOME Project. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001214.	1.5	13
17100	Comprehensive analysis of differentially expressed genes reveals the promotive effects of UBE2T on colorectal cancer cell proliferation. <i>Oncology Letters</i> , 2021, 22, 714.	0.8	3
17101	Network analysis identifies DAPK3 as a potential biomarker for lymphatic invasion and colon adenocarcinoma prognosis. <i>IScience</i> , 2021, 24, 102831.	1.9	5
17103	Computational and network pharmacology studies of <i>Phyllanthus emblica</i> to tackle SARS-CoV-2. <i>Phytomedicine Plus</i> , 2021, 1, 100095.	0.9	12



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17104	Purinergic P2Y2 and P2X4 Receptors Are Involved in the Epithelial-Mesenchymal Transition and Metastatic Potential of Gastric Cancer Derived Cell Lines. <i>Pharmaceutics</i> , 2021, 13, 1234.	2.0	12
17105	Identification of prognostic immune-related gene signature associated with tumor microenvironment of colorectal cancer. <i>BMC Cancer</i> , 2021, 21, 905.	1.1	10
17106	Investigation of Potential Molecular Biomarkers for Diagnosis and Prognosis of AFP-Negative HCC. <i>International Journal of General Medicine</i> , 2021, Volume 14, 4369-4380.	0.8	18
17107	Chromatin and transcriptomic profiling uncover dysregulation of the Tip60 HAT/HDAC2 epigenomic landscape in the neurodegenerative brain. <i>Epigenetics</i> , 2022, 17, 786-807.	1.3	5
17109	PI3K-AKT, JAK2-STAT3 pathways and cell-cell contact regulate maspin subcellular localization. <i>Cell Communication and Signaling</i> , 2021, 19, 86.	2.7	5
17110	Plant developmental stage drives the differentiation in ecological role of the maize microbiome. <i>Microbiome</i> , 2021, 9, 171.	4.9	164
17111	Network-Based Systems Analysis Explains Sequence-Dependent Synergism of Bortezomib and Vorinostat in Multiple Myeloma. <i>AAPS Journal</i> , 2021, 23, 101.	2.2	2
17112	High Matrix Metalloproteinase 28 Expression is Associated with Poor Prognosis in Pancreatic Adenocarcinoma. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 4391-4406.	1.0	4
17113	CARD11 is a prognostic biomarker and correlated with immune infiltrates in uveal melanoma. <i>PLoS ONE</i> , 2021, 16, e0255293.	1.1	4
17115	Establishment of an Immune-Related Gene Signature for Risk Stratification for Patients with Glioma. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-20.	0.7	2
17116	Network pharmacology study on the mechanism of QiangzhiFang in the treatment of panic disorder. <i>Annals of Translational Medicine</i> , 2021, 9, 1350-1350.	0.7	5
17117	Gene Expression Analysis Reveals Key Genes and Signalings Associated with the Prognosis of Prostate Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-13.	0.7	3
17118	A validated generally applicable approach using the systematic assessment of disease modules by GWAS reveals a multi-omic module strongly associated with risk factors in multiple sclerosis. <i>BMC Genomics</i> , 2021, 22, 631.	1.2	5
17119	Identification of key genes affecting porcine fat deposition based on co-expression network analysis of weighted genes. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 100.	2.1	22
17120	Identification and verification of HCAR3 and INSL5 as new potential therapeutic targets of colorectal cancer. <i>World Journal of Surgical Oncology</i> , 2021, 19, 248.	0.8	19
17121	Recurrent Vulvovaginal Candidiasis: a Dynamic Interkingdom Biofilm Disease of <i>Candida</i> and <i>Lactobacillus</i> . <i>MSystems</i> , 2021, 6, e0062221.	1.7	35
17122	Soil microbial community and network changes after long-term use of plastic mulch and nitrogen fertilization on semiarid farmland. <i>Geoderma</i> , 2021, 396, 115086.	2.3	65
17123	Lichenoid dysplasia is not a distinct pathological entity. <i>Oral Oncology</i> , 2021, 119, 105362.	0.8	14

#	ARTICLE	IF	CITATIONS
17124	Alterations of gut microbiota in gestational diabetes patients during the second trimester of pregnancy in the Shanghai Han population. <i>Journal of Translational Medicine</i> , 2021, 19, 366.	1.8	14
17125	Presence of Human Pathogens of the <i>Borrelia burgdorferi</i> sensu lato Complex Shifts the Sequence Read Abundances of Tick Microbiomes in Two German Locations. <i>Microorganisms</i> , 2021, 9, 1814.	1.6	7
17126	Comparative transcriptomic analysis uncovers conserved pathways involved in adventitious root formation in poplar. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1903-1918.	1.4	10
17127	Transcriptional landscape of cellular networks reveal interactions driving the dormancy mechanisms in cancer. <i>Scientific Reports</i> , 2021, 11, 15806.	1.6	6
17128	Potential <i>Arabidopsis thaliana</i> glucosinolate genes identified from the co-expression modules using graph clustering approach. <i>PeerJ</i> , 2021, 9, e11876.	0.9	7
17129	Profiling Analysis of Circular RNA and mRNA in Human Temporal Lobe Epilepsy with Hippocampal Sclerosis ILAE Type 1. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 2745-2755.	1.7	6
17130	Longitudinal stability of urinary extracellular vesicle protein patterns within and between individuals. <i>Scientific Reports</i> , 2021, 11, 15629.	1.6	6
17131	Identification of a circRNA-miRNA-mRNA regulatory network for exploring novel therapeutic options for glioma. <i>PeerJ</i> , 2021, 9, e11894.	0.9	5
17132	An Integrated Metabolomic Study of Osteoporosis: Discovery and Quantification of Hyocholic Acids as Candidate Markers. <i>Frontiers in Pharmacology</i> , 2021, 12, 725341.	1.6	18
17133	Mining Natural Products with Anticancer Biological Activity through a Systems Biology Approach. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-17.	1.9	8
17134	Identification of Potential Biomarkers for Psoriasis by DNA Methylation and Gene Expression Datasets. <i>Frontiers in Genetics</i> , 2021, 12, 722803.	1.1	14
17135	SARS-CoV-2 Impairs Dendritic Cells and Regulates DC-SIGN Gene Expression in Tissues. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9228.	1.8	15
17137	Single-cell transcriptome analysis reveals the dynamics of human immune cells during early fetal skin development. <i>Cell Reports</i> , 2021, 36, 109524.	2.9	16
17138	Genome-Wide Identification, Phylogenetic and Expression Pattern Analysis of GATA Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Plants</i> , 2021, 10, 1626.	1.6	11
17139	Alpha-Synuclein-induced DNA Methylation and Gene Expression in Microglia. <i>Neuroscience</i> , 2021, 468, 186-198.	1.1	8
17140	The parasite-derived peptide FhHDM-1 activates the PI3K/Akt pathway to prevent cytokine-induced apoptosis of $\beta$ -cells. <i>Journal of Molecular Medicine</i> , 2021, 99, 1605-1621.	1.7	7
17142	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , 2021, 22, 774-790.	7.7	46
17143	Identification of GNA12-driven gene signatures and key signaling networks in ovarian cancer. <i>Oncology Letters</i> , 2021, 22, 719.	0.8	3

#	ARTICLE	IF	CITATIONS
17144	Landscape of toll-like receptors expression in tumor microenvironment of triple negative breast cancer (TNBC): Distinct roles of TLR4 and TLR8. <i>Gene</i> , 2021, 792, 145728.	1.0	11
17145	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in <i>Mallotus japonicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 8835.	1.8	3
17146	Identification and Validation of an Immune-related Prognostic Signature for Hepatocellular Carcinoma. <i>Journal of Clinical and Translational Hepatology</i> , 2021, 000, 000-000.	0.7	4
17147	Effects of NaCl Concentrations on Growth Patterns, Phenotypes Associated With Virulence, and Energy Metabolism in <i>Escherichia coli</i> BW25113. <i>Frontiers in Microbiology</i> , 2021, 12, 705326.	1.5	24
17150	Identification of Circular RNA Expression Profiles in White Adipocytes and Their Roles in Adipogenesis. <i>Frontiers in Physiology</i> , 2021, 12, 728208.	1.3	9
17151	Keystone microbes affect the evolution and ecological coexistence of the community via species/strain specificity. <i>Journal of Applied Microbiology</i> , 2022, 132, 1227-1238.	1.4	6
17152	CD38 Deficiency Ameliorates Chronic Graft-Versus-Host Disease Murine Lupus via a B-Cell-Dependent Mechanism. <i>Frontiers in Immunology</i> , 2021, 12, 713697.	2.2	1
17153	Drug Discovery of Spinal Muscular Atrophy (SMA) from the Computational Perspective: A Comprehensive Review. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8962.	1.8	6
17154	MethylSPWNet and MethylCapsNet: Biologically Motivated Organization of DNAm Neural Networks, Inspired by Capsule Networks. <i>Npj Systems Biology and Applications</i> , 2021, 7, 33.	1.4	12
17155	Molecular Subtypes of Oral Squamous Cell Carcinoma Based on Immunosuppression Genes Using a Deep Learning Approach. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 687245.	1.8	7
17156	Genome-wide identification, phylogeny, and expression analysis of the bHLH gene family in tobacco ( <i>Nicotiana tabacum</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1747-1764.	1.4	15
17158	Metabolite Profiling Based on UPLC-QE-TOF-MS/MS and the Biological Evaluation of Medicinal Plants of Chinese <i>Dichocarpum</i> (Ranunculaceae). <i>Chemistry and Biodiversity</i> , 2021, 18, e2100432.	1.0	2
17159	Structure-Guided Creation of an Anti-HA Stalk Antibody F11 Derivative That Neutralizes Both F11-Sensitive and -Resistant Influenza A(H1N1)pdm09 Viruses. <i>Viruses</i> , 2021, 13, 1733.	1.5	3
17160	Chemical Gradients of Plant Substrates in an <i>Atta texana</i> Fungus Garden. <i>MSystems</i> , 2021, 6, e0060121.	1.7	2
17161	Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. <i>Cell Host and Microbe</i> , 2021, 29, 1249-1265.e9.	5.1	32
17162	An Integrative Systems Biology Approach Identifies Molecular Signatures Associated with Gallbladder Cancer Pathogenesis. <i>Journal of Clinical Medicine</i> , 2021, 10, 3520.	1.0	3
17163	Identification of lncRNA NR_028138.1 as a biomarker and construction of a ceRNA network for bipolar disorder. <i>Scientific Reports</i> , 2021, 11, 15653.	1.6	3
17164	Gut Bacterial Characteristics of Patients With Type 2 Diabetes Mellitus and the Application Potential. <i>Frontiers in Immunology</i> , 2021, 12, 722206.	2.2	38

#	ARTICLE	IF	CITATIONS
17165	Identification of <sc>PSMD14</sc> as a potential novel prognosis biomarker and therapeutic target for osteosarcoma. <i>Cancer Reports</i> , 2022, 5, e1522.	0.6	8
17166	Proteomics study on the effect of combined treatment of electrical pulses and tomato lipophilic extract in the downregulation of proliferating cell nuclear antigen in triple-negative breast cancer cell. <i>Phytomedicine Plus</i> , 2021, 1, 100064.	0.9	1
17167	HLA-E“restricted HIV-1“specific CD8+ T cell responses in natural infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	12
17168	Proteome plasticity in response to persistent environmental change. <i>Molecular Cell</i> , 2021, 81, 3294-3309.e12.	4.5	12
17169	Genetic variability and molecular evolution of arabis mosaic virus based on the coat protein gene sequence. <i>Plant Pathology</i> , 2021, 70, 2197-2206.	1.2	4
17170	Maturation State-Specific Alternative Splicing in FLT3-ITD and NPM1 Mutated AML. <i>Cancers</i> , 2021, 13, 3929.	1.7	5
17171	Mapping Transcriptome Data to Protein“Protein Interaction Networks of Inflammatory Bowel Diseases Reveals Disease-Specific Subnetworks. <i>Frontiers in Genetics</i> , 2021, 12, 688447.	1.1	2
17172	Effect of aerobic/anoxic duration on the performance, microbial activity and microbial community of sequencing batch biofilm reactor treating synthetic mariculture wastewater. <i>Bioresource Technology</i> , 2021, 333, 125198.	4.8	18
17173	Multi-omics analysis of respiratory specimen characterizes baseline molecular determinants associated with SARS-CoV-2 outcome. <i>IScience</i> , 2021, 24, 102823.	1.9	28
17174	Lithium preserves peritoneal membrane integrity by suppressing mesothelial cell Î±B-crystallin. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	20
17175	Exploring the Biological Mechanism of Huang Yam in Treating Tumors and Preventing Antitumor Drug-Induced Cardiotoxicity Using Network Pharmacology and Molecular Docking Technology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	2
17176	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. <i>MBio</i> , 2021, 12, e0144221.	1.8	12
17177	Identification of Key Transcription Factors Related to Bacterial Spot Resistance in Pepper through Regulatory Network Analyses. <i>Genes</i> , 2021, 12, 1351.	1.0	6
17178	Analyses of open-access multi-omics data sets reveal genetic and expression characteristics of maize <i>ZmCCT</i> family genes. <i>AoB PLANTS</i> , 2021, 13, plab048.	1.2	1
17179	Exploration of the molecular targets and mechanisms of suxiao xintong dropping pills for myocardial infarction by network pharmacology method. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
17180	Key Gene and Functional Pathways Identified in Unexplained Recurrent Spontaneous Abortion Using Targeted RNA Sequencing and Clinical Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 717832.	2.2	10
17181	Differential Protein Interactome in Esophageal Squamous Cell Carcinoma Offers Novel Systems Biomarker Candidates with High Diagnostic and Prognostic Performance. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 495-512.	1.0	2
17182	Pyk2 regulates cell-edge protrusion dynamics by interacting with Crk. <i>Molecular Biology of the Cell</i> , 2021, 32, mbc.E20-10-0640.	0.9	2

#	ARTICLE	IF	CITATIONS
17183	Phenylpropanoid Biosynthesis Gene Expression Precedes Lignin Accumulation During Shoot Development in Lowland and Upland Switchgrass Genotypes. <i>Frontiers in Plant Science</i> , 2021, 12, 640930.	1.7	4
17184	Identification of Photoperiod-Induced LncRNAs and mRNAs in Pituitary Pars Tuberalis of Sheep. <i>Frontiers in Veterinary Science</i> , 2021, 8, 644474.	0.9	10
17185	Application of miRNA-seq in neuropsychiatry: A methodological perspective. <i>Computers in Biology and Medicine</i> , 2021, 135, 104603.	3.9	7
17186	Dynamic bi-directional phosphorylation events associated with the reciprocal regulation of synapses during homeostatic up- and down-scaling. <i>Cell Reports</i> , 2021, 36, 109583.	2.9	21
17187	Genome-Scale Metabolic Models and Machine Learning Reveal Genetic Determinants of Antibiotic Resistance in <i>Escherichia coli</i> and Unravel the Underlying Metabolic Adaptation Mechanisms. <i>MSystems</i> , 2021, 6, e0091320.	1.7	26
17188	Comparative Genomics Reveals a Remarkable Biosynthetic Potential of the <i>Streptomyces</i> Phylogenetic Lineage Associated with Rugose-Ornamented Spores. <i>MSystems</i> , 2021, 6, e0048921.	1.7	6
17190	Effect of Tension on Human Periodontal Ligament Cells: Systematic Review and Network Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 695053.	2.0	16
17192	Alterations in bile acid metabolizing gut microbiota and specific bile acid genes as a precision medicine to subclassify NAFLD. <i>Physiological Genomics</i> , 2021, 53, 336-348.	1.0	17
17193	Morphological, Physiological, and Molecular Responses of Sweetly Fragrant <i>Luculia gratissima</i> During the Floral Transition Stage Induced by Short-Day Photoperiod. <i>Frontiers in Plant Science</i> , 2021, 12, 715683.	1.7	0
17194	Comprehensive Characterization of RNA Processing Factors in Gastric Cancer Identifies a Prognostic Signature for Predicting Clinical Outcomes and Therapeutic Responses. <i>Frontiers in Immunology</i> , 2021, 12, 719628.	2.2	19
17195	Target identification of hepatic fibrosis using Pien Tze Huang based on mRNA and lncRNA. <i>Scientific Reports</i> , 2021, 11, 16980.	1.6	6
17197	Metastasis-Entrained Eosinophils Enhance Lymphocyte-Mediated Antitumor Immunity. <i>Cancer Research</i> , 2021, 81, 5555-5571.	0.4	35
17198	Proteomic analysis of machine perfusion solution from brain dead donor kidneys reveals that elevated complement, cytoskeleton and lipid metabolism proteins are associated with 1-year outcome. <i>Transplant International</i> , 2021, 34, 1618-1629.	0.8	10
17200	Comparative genomic analysis of azasugar biosynthesis. <i>AMB Express</i> , 2021, 11, 120.	1.4	5
17201	The Role of Hemoglobin Subunit Delta in the Immunopathy of Multiple Sclerosis: Mitochondria Matters. <i>Frontiers in Immunology</i> , 2021, 12, 709173.	2.2	8
17202	A Novel STK4 Mutation Impairs T Cell Immunity Through Dysregulation of Cytokine-Induced Adhesion and Chemotaxis Genes. <i>Journal of Clinical Immunology</i> , 2021, 41, 1839-1852.	2.0	3
17203	Molecular Changes Induced in Melanoma by Cell Culturing in 3D Alginate Hydrogels. <i>Cancers</i> , 2021, 13, 4111.	1.7	4
17205	Time-series transcriptomics reveals a BBX32-directed control of acclimation to high light in mature <i>Arabidopsis</i> leaves. <i>Plant Journal</i> , 2021, 107, 1363-1386.	2.8	11

#	ARTICLE	IF	CITATIONS
17206	TRAIP modulates the IGFBP3/AKT pathway to enhance the invasion and proliferation of osteosarcoma by promoting KANK1 degradation. <i>Cell Death and Disease</i> , 2021, 12, 767.	2.7	15
17207	NK cells in hypoxic skin mediate a trade-off between wound healing and antibacterial defence. <i>Nature Communications</i> , 2021, 12, 4700.	5.8	29
17208	Shared Molecular Mechanisms of Hypertrophic Cardiomyopathy and Its Clinical Presentations: Automated Molecular Mechanisms Extraction Approach. <i>Life</i> , 2021, 11, 785.	1.1	5
17209	<scp>miRNA</scp>â€³4 and <scp>miRNA</scp>â€²10 target hexamerin genes enhancing their differential expression during early brain development of honeybee (<scp><i>Apis mellifera</i></scp>) castes. <i>Insect Molecular Biology</i> , 2021, 30, 594-604.	1.0	13
17210	Oncogene APOL1 promotes proliferation and inhibits apoptosis via activating NOTCH1 signaling pathway in pancreatic cancer. <i>Cell Death and Disease</i> , 2021, 12, 760.	2.7	19
17211	Towards engineering ectomycorrhization into switchgrass bioenergy crops via a lectin receptorâ€like kinase. <i>Plant Biotechnology Journal</i> , 2021, 19, 2454-2468.	4.1	14
17212	k-core genes underpin structural features of breast cancer. <i>Scientific Reports</i> , 2021, 11, 16284.	1.6	13
17214	Cell-type and subcellular compartment-specific APEX2 proximity labeling reveals activity-dependent nuclear proteome dynamics in the striatum. <i>Nature Communications</i> , 2021, 12, 4855.	5.8	33
17215	Identification of conserved transcriptome features between humans and <i>Drosophila</i> in the aging brain utilizing machine learning on combined data from the NIH Sequence Read Archive. <i>PLoS ONE</i> , 2021, 16, e0255085.	1.1	0
17216	Beta-adrenergic pathway activation enhances aggressiveness and inhibits stemness in head and neck cancer. <i>Translational Oncology</i> , 2021, 14, 101117.	1.7	9
17217	Deciphering the structural and functional impact of missense mutations in Egr1-DNA interacting interface: an integrative computational approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-13.	2.0	0
17218	GNAi2/gip2-Regulated Transcriptome and Its Therapeutic Significance in Ovarian Cancer. <i>Biomolecules</i> , 2021, 11, 1211.	1.8	8
17219	Genome-Wide Analysis for Early Growth-Related Traits of the Locally Adapted Egyptian Barki Sheep. <i>Genes</i> , 2021, 12, 1243.	1.0	8
17220	Transcriptomic Analyses Reveal B-Cell Translocation Gene 2 as a Potential Therapeutic Target in Ovarian Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 681250.	1.3	3
17221	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12122.	5.5	37
17222	Comprehensive Integrative Analysis Reveals the Association of KLF4 with Macrophage Infiltration and Polarization in Lung Cancer Microenvironment. <i>Cells</i> , 2021, 10, 2091.	1.8	18
17223	Differential Mucosal Microbiome Profiles across Stages of Human Colorectal Cancer. <i>Life</i> , 2021, 11, 831.	1.1	19
17224	Impact of Artificial Sputum Medium Formulation on <i>Pseudomonas aeruginosa</i> Secondary Metabolite Production. <i>Journal of Bacteriology</i> , 2021, 203, e0025021.	1.0	18



#	ARTICLE	IF	CITATIONS
17225	A convergent molecular network underlying autism and congenital heart disease. <i>Cell Systems</i> , 2021, 12, 1094-1107.e6.	2.9	19
17226	NCAPG promotes the progression of lung adenocarcinoma via the TGF- $\beta$ 2 signaling pathway. <i>Cancer Cell International</i> , 2021, 21, 443.	1.8	22
17227	Systematically integrative analysis identifies diagnostic and prognostic candidates and small-molecule drugs for lung adenocarcinoma. <i>Translational Cancer Research</i> , 2021, 10, 3619-3646.	0.4	2
17228	Mitochondrial Fragmentation Triggers Ineffective Hematopoiesis in Myelodysplastic Syndromes. <i>Cancer Discovery</i> , 2022, 12, 250-269.	7.7	14
17230	GSK2126458 has the potential to inhibit the proliferation of pancreatic cancer uncovered by bioinformatics analysis and pharmacological experiments. <i>Journal of Translational Medicine</i> , 2021, 19, 373.	1.8	11
17231	Seasonal succession of microbes in different size-fractions and their modular structures determined by both macro- and micro-environmental filtering in dynamic coastal waters. <i>Science of the Total Environment</i> , 2021, 784, 147046.	3.9	18
17232	The CCAAT/Enhancer Binding Protein Beta (cebpb) is essential for the development of enveloping layer (EVL) in zebrafish. <i>Aquaculture and Fisheries</i> , 2021, , .	1.2	0
17233	Gastroprotection against Rat Ulcers by Nephthea Sterol Derivative. <i>Biomolecules</i> , 2021, 11, 1247.	1.8	6
17234	The synergistic effect of potassium ferrate and peroxymonosulfate application on biogas production and shaping microbial community during anaerobic co-digestion of a cow manure-cotton straw mixture. <i>Bioresource Technology</i> , 2021, 333, 125166.	4.8	10
17236	Tumor microbiome contributes to an aggressive phenotype in the basal-like subtype of pancreatic cancer. <i>Communications Biology</i> , 2021, 4, 1019.	2.0	57
17237	Identification and Expression Analyses of Invertase Genes in Moso Bamboo Reveal Their Potential Drought Stress Functions. <i>Frontiers in Genetics</i> , 2021, 12, 696300.	1.1	5
17238	Nanopore-based full-length transcriptome sequencing of Muscovy duck ( <i>Cairina moschata</i> ) ovary. <i>Poultry Science</i> , 2021, 100, 101246.	1.5	16
17239	Investigation of RNA metabolism through large-scale genetic interaction profiling in yeast. <i>Nucleic Acids Research</i> , 2021, 49, 8535-8555.	6.5	4
17240	<i>Tripterygium wilfordii</i> derivative LLDT-8 targets CD2 in the treatment of rheumatoid arthritis. <i>Biomedical Reports</i> , 2021, 15, 81.	0.9	4
17241	Significant transcriptomic changes are associated with the inhibitory effects of 5-aza-2-deoxycytidine during adipogenic differentiation of MG-63 cells. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 7336-7348.	1.8	1
17242	Going further post-RNA-seq: In silico functional analyses revealing candidate genes and regulatory elements related to mastitis in dairy cattle. <i>Journal of Dairy Research</i> , 2021, 88, 286-292.	0.7	4
17243	Pan-transcriptome identifying master genes and regulation network in response to drought and salt stresses in Alfalfa ( <i>Medicago sativa</i> L.). <i>Scientific Reports</i> , 2021, 11, 17203.	1.6	16
17244	Ferroptosis-Related Genes in Lung Adenocarcinoma: Prognostic Signature and Immune, Drug Resistance, Mutation Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 672904.	1.1	34

#	ARTICLE	IF	CITATIONS
17245	Revealing protein-protein interactions at the transcriptome scale by sequencing. <i>Molecular Cell</i> , 2021, 81, 4091-4103.e9.	4.5	28
17246	A five-dimensional data collection strategy for multicomponent discovery and characterization in Traditional Chinese Medicine: <i>Gastrodia Rhizoma</i> as a case study. <i>Journal of Chromatography A</i> , 2021, 1653, 462405.	1.8	16
17247	Spatially Resolved Identification of Transglutaminase Substrates by Proteomics in Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 65, 319-330.	1.4	7
17248	Predicting Target Genes of San-Huang-Chai-Zhu Formula in Treating ANIT-Induced Acute Intrahepatic Cholestasis Rat Model via Bioinformatics Analysis Combined with Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	7
17249	<i>In-Silico</i> Analysis of Differentially Expressed Genes and Their Regulating microRNA Involved in Lymph Node Metastasis in Invasive Breast Carcinoma. <i>Cancer Investigation</i> , 2022, 40, 55-72.	0.6	4
17250	Biomarker Identification in Membranous Nephropathy Using a Long Non-coding RNA-Mediated Competitive Endogenous RNA Network. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 615-623.	2.2	7
17251	A modified density gradient proteomic-based method to analyze endolysosomal proteins in cardiac tissue. <i>IScience</i> , 2021, 24, 102949.	1.9	1
17252	Identification of Unique Peptides for SARS-CoV-2 Diagnostics and Vaccine Development by an <i>In Silico</i> Proteomics Approach. <i>Frontiers in Immunology</i> , 2021, 12, 725240.	2.2	12
17256	Towards Engineering an Ecosystem: A Review of Computational Approaches to Explore and Exploit the Human Microbiome for Healthcare. , 0, , 1.		0
17257	Comparative transcriptome analysis between abundant and deficient spore strains provides novel insight into gene regulatory networks and mechanisms of monospore production in bladed <i>Bangiales</i> . <i>Aquaculture and Fisheries</i> , 2021, , .	1.2	0
17258	Integrative analysis of GWAS and transcriptome to reveal novel loci regulation flowering time in semi-winter rapeseed. <i>Plant Science</i> , 2021, 310, 110980.	1.7	14
17259	The role of SPP1 as a prognostic biomarker and therapeutic target in head and neck squamous cell carcinoma. <i>International Journal of Oral and Maxillofacial Surgery</i> , 2022, 51, 732-741.	0.7	8
17260	Single-cell transcriptome and cell-specific network analysis reveal the reparative effect of neurotrophin-4 in preantral follicles grown <i>in vitro</i> . <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 133.	1.4	5
17261	Identification and validation of RNA-binding protein-related gene signature revealed potential associations with immunosuppression and drug sensitivity in glioma. <i>Cancer Medicine</i> , 2021, 10, 7418-7439.	1.3	15
17262	Gonadotropin-releasing hormone receptor pathway affects the function of human EBV-transformed B lymphocytes in an age-independent way. <i>Experimental Gerontology</i> , 2021, 152, 111471.	1.2	1
17264	Integrating Genetic and Transcriptomic Data to Reveal Pathogenesis and Prognostic Markers of Pancreatic Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 747270.	1.1	2
17265	Global analysis of lysine acetylation in soybean leaves. <i>Scientific Reports</i> , 2021, 11, 17858.	1.6	11
17266	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. <i>Blood Cancer Discovery</i> , 2021, 2, 586-599.	2.6	21

#	ARTICLE	IF	CITATIONS
17267	A network of core and subtype-specific gene expression programs in myositis. <i>Acta Neuropathologica</i> , 2021, 142, 887-898.	3.9	13
17269	Gibberellin Induced Transcriptome Profiles Reveal Gene Regulation of Loquat Flowering. <i>Frontiers in Genetics</i> , 2021, 12, 703688.	1.1	4
17270	Dissipation of antibiotic resistance genes in manure-amended agricultural soil. <i>Science of the Total Environment</i> , 2021, 787, 147582.	3.9	27
17271	Network-based approach to identify prognosis-related genes in tamoxifen-treated patients with estrogen receptor-positive breast cancer. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
17272	NOX2-Deficient Neutrophils Facilitate Joint Inflammation Through Higher Pro-Inflammatory and Weakened Immune Checkpoint Activities. <i>Frontiers in Immunology</i> , 2021, 12, 743030.	2.2	9
17273	Identification of Novel Molecular Therapeutic Targets and Their Potential Prognostic Biomarkers Among Kinesin Superfamily of Proteins in Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 708900.	1.3	7
17274	Integrative Analysis of the Roles of lncRNAs and mRNAs in Itaconate-Mediated Protection Against Liver Ischemia-Reperfusion Injury in Mice. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4519-4536.	1.6	5
17275	Dynamic network biomarker analysis discovers IbNAC083 in the initiation and regulation of sweet potato root tuberization. <i>Plant Journal</i> , 2021, 108, 793-813.	2.8	27
17276	Identification of a Four-Gene Signature With Prognostic Significance in Endometrial Cancer Using Weighted-Gene Correlation Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 678780.	1.1	9
17277	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. <i>Nature Communications</i> , 2021, 12, 5531.	5.8	31
17278	Prognostic and Predicted Significance of FENDRR in Colon and Rectum Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 668595.	1.3	3
17280	Integrated Analysis of Prognostic Genes Associated With Ischemia-â€œReperfusion Injury in Renal Transplantation. <i>Frontiers in Immunology</i> , 2021, 12, 747020.	2.2	6
17281	The Transcriptional Landscape and Hub Genes Associated with Physiological Responses to Drought Stress in <i>Pinus tabuliformis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 9604.	1.8	9
17282	Probiotic <i>Bifidobacterium longum</i> supplied with methimazole improved the thyroid function of Gravesâ€™ disease patients through the gut-thyroid axis. <i>Communications Biology</i> , 2021, 4, 1046.	2.0	17
17283	LPCAT1 reprogramming cholesterol metabolism promotes the progression of esophageal squamous cell carcinoma. <i>Cell Death and Disease</i> , 2021, 12, 845.	2.7	31
17284	Integrative analysis of ferroptosis-related genes in ulcerative colitis. <i>Journal of International Medical Research</i> , 2021, 49, 030006052110429.	0.4	18
17285	Strategy of Virtual Screening Based Discovery of HSP90 C-terminal Inhibitors and Network Pharmacological Analysis. <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, .	0.9	0
17286	Brain profiling in murine colitis and human epilepsy reveals neutrophils and TNFÎ± as mediators of neuronal hyperexcitability. <i>Journal of Neuroinflammation</i> , 2021, 18, 199.	3.1	15

#	ARTICLE	IF	CITATIONS
17287	Exploring the Molecular Mechanism of Liuwei Dihuang Pills for Treating Diabetic Nephropathy by Combined Network Pharmacology and Molecular Docking. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-14.	0.5	4
17288	Gut Microbiome: A Potential Indicator for Differential Diagnosis of Major Depressive Disorder and General Anxiety Disorder. Frontiers in Psychiatry, 2021, 12, 651536.	1.3	31
17289	Neurodevelopmental Disorders in Patients With Complex Phenotypes and Potential Complex Genetic Basis Involving Non-Coding Genes, and Double CNVs. Frontiers in Genetics, 2021, 12, 732002.	1.1	12
17290	Chromatin accessibility and regulatory vocabulary across indicine cattle tissues. Genome Biology, 2021, 22, 273.	3.8	21
17291	Combinatorial transcription factor profiles predict mature and functional human islet $\hat{1}\pm$ and $\hat{1}^2$ cells. JCI Insight, 2021, 6, .	2.3	22
17293	Idebenone-Activating Autophagic Degradation of $\hat{1}\pm$ -Synuclein via Inhibition of AKT-mTOR Pathway in a SH-SY5Y-A53T Model of Parkinson's Disease: A Network Pharmacological Approach. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-14.	0.5	7
17295	Liquid Organic Fertilizer Amendment Alters Rhizosphere Microbial Community Structure and Co-occurrence Patterns and Improves Sunflower Yield Under Salinity-Alkalinity Stress. Microbial Ecology, 2022, 84, 423-438.	1.4	19
17297	NRXN1 $\hat{1}\pm$ is associated with increased excitability in ASD iPSC-derived neurons. BMC Neuroscience, 2021, 22, 56.	0.8	14
17298	Intestinal Transcriptomic and Histologic Profiling Reveals Tissue Repair Mechanisms Underlying Resistance to the Parasite Ceratonychia shasta. Pathogens, 2021, 10, 1179.	1.2	8
17300	Morphological, physiological, and transcriptional responses to low nitrogen stress in Populus deltoides Marsh. clones with contrasting nitrogen use efficiency. BMC Genomics, 2021, 22, 697.	1.2	3
17301	CTCF knockout in zebrafish induces alterations in regulatory landscapes and developmental gene expression. Nature Communications, 2021, 12, 5415.	5.8	27
17302	Metabolomics of Healthy and Stony Coral Tissue Loss Disease Affected Montastraea cavernosa Corals. Frontiers in Marine Science, 2021, 8, .	1.2	12
17303	Integration and gene co-expression network analysis of scRNA-seq transcriptomes reveal heterogeneity and key functional genes in human spermatogenesis. Scientific Reports, 2021, 11, 19089.	1.6	12
17304	Molecular Insights into SARS-CoV2-Induced Alterations of the Gut/Brain Axis. International Journal of Molecular Sciences, 2021, 22, 10440.	1.8	19
17306	Performance of Multiple Metagenomics Pipelines in Understanding Microbial Diversity of a Low-Biomass Spacecraft Assembly Facility. Frontiers in Microbiology, 2021, 12, 685254.	1.5	9
17307	Regime transition Shapes the Composition, Assembly Processes, and Co-occurrence Pattern of Bacterioplankton Community in a Large Eutrophic Freshwater Lake. Microbial Ecology, 2022, 84, 336-350.	1.4	4
17308	Response of soil microbiome structure and its network profiles to four soil amendments in monocropping strawberry greenhouse. PLoS ONE, 2021, 16, e0245180.	1.1	7
17310	Systematic analysis of the mechanism of Xiaochaihu decoction in hepatitis B treatment via network pharmacology and molecular docking. Computers in Biology and Medicine, 2021, 138, 104894.	3.9	10

#	ARTICLE	IF	CITATIONS
17311	Dynamic Transcriptomic and Metabolomic Analyses of <i>Madhuca pasquieri</i> (Dubard) H. J. Lam During the Post-germination Stages. <i>Frontiers in Plant Science</i> , 2021, 12, 731203.	1.7	2
17312	Proteomic identification of ruminal epithelial protein expression profiles in response to starter feed supplementation in pre-weaned lambs. <i>Animal Nutrition</i> , 2021, 7, 1271-1282.	2.1	5
17315	Novel interferon-sensitive genes unveiled by correlation-driven gene selection and systems biology. <i>Scientific Reports</i> , 2021, 11, 18043.	1.6	3
17316	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	2.9	52
17317	Kinase-Catalyzed Biotinylation to Map Cell Signaling Pathways: Application to Epidermal Growth Factor Signaling. <i>Journal of Proteome Research</i> , 2021, 20, 4852-4861.	1.8	3
17318	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104921.	1.0	21
17319	Hypothalamic and ovarian transcriptome profiling reveals potential candidate genes in low and high egg production of white Muscovy ducks ( <i>Cairina moschata</i> ). <i>Poultry Science</i> , 2021, 100, 101310.	1.5	31
17320	Effects of estrogen inhibition formula herbal mixture for danazol-induced precocious puberty in female rats: An experimental study with network pharmacology. <i>Integrative Medicine Research</i> , 2021, 10, 100708.	0.7	8
17321	Genome-wide identification of DCL, AGO and RDR gene families and their associated functional regulatory elements analyses in banana ( <i>Musa acuminata</i> ). <i>PLoS ONE</i> , 2021, 16, e0256873.	1.1	14
17322	Exploring the topology and dynamic growth properties of co-invention networks and technology fields. <i>PLoS ONE</i> , 2021, 16, e0256956.	1.1	2
17324	Mechanisms of Paeoniflorin against myocardial ischemia reperfusion injury based on network pharmacology. <i>Materials Express</i> , 2021, 11, 1505-1515.	0.2	3
17325	Aberrant expression of lncRNAs SNHG6, TRPM2 and MIR4435 and hypomethylation of TRPM2 and AS1 promoter in colorectal cancer. <i>Cell Biology International</i> , 2021, 45, 2464-2478.	1.4	12
17326	QSPcc reduces bottlenecks in computational model simulations. <i>Communications Biology</i> , 2021, 4, 1022.	2.0	2
17327	Combined glyoxalase 1 dysfunction and vitamin B6 deficiency in a schizophrenia model system causes mitochondrial dysfunction in the prefrontal cortex. <i>Redox Biology</i> , 2021, 45, 102057.	3.9	12
17328	The feature of cervical microbiota associated with the progression of cervical cancer among reproductive females. <i>Gynecologic Oncology</i> , 2021, 163, 348-357.	0.6	28
17330	Identification of VCAN as Hub Gene for Diabetic Kidney Disease Immune Injury Using Integrated Bioinformatics Analysis. <i>Frontiers in Physiology</i> , 2021, 12, 651690.	1.3	7
17331	Electrogenic sodium bicarbonate cotransporter NBCe1 regulates pancreatic $\beta^2$ cell function in type 2 diabetes. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	11
17332	Identification of N-glycoproteins of hip cartilage in patients with osteonecrosis of femoral head using quantitative glycoproteomics. <i>International Journal of Biological Macromolecules</i> , 2021, 187, 892-902.	3.6	4

#	ARTICLE	IF	CITATIONS
17333	Understanding Competitive Endogenous RNA Network Mechanism in Type 1 Diabetes Mellitus Using Computational and Bioinformatics Approaches. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2021, Volume 14, 3865-3945.	1.1	6
17334	Detection of spreader nodes in human-SARS-CoV protein-protein interaction network. <i>PeerJ</i> , 2021, 9, e12117.	0.9	8
17335	Network Pharmacology and Molecular Docking-Based Prediction of the Mechanism of Qianghuo Shengshi Decoction against Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	14
17338	A Five-Gene-Based Prognostic Signature for Hepatocellular Carcinoma. <i>Frontiers in Medicine</i> , 2021, 8, 681388.	1.2	11
17339	Maturation of <i>Rhodobacter capsulatus</i> Multicopper Oxidase CutO Depends on the CopA Copper Efflux Pathway and Requires the cutF Product. <i>Frontiers in Microbiology</i> , 2021, 12, 720644.	1.5	8
17340	Circular RNA hsa_circ_0000073 Enhances Osteosarcoma Cells Malignant Behavior by Sponging miR-1252-5p and Modulating CCNE2 and MDM2. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 714601.	1.8	5
17342	Transcriptome and Methylome Analysis Reveal Complex Cross-Talks between Thyroid Hormone and Glucocorticoid Signaling at <i>Xenopus</i> Metamorphosis. <i>Cells</i> , 2021, 10, 2375.	1.8	11
17343	A role for arthropods as vectors of multidrug-resistant Enterobacterales in surgical site infections from South Asia. <i>Nature Microbiology</i> , 2021, 6, 1259-1270.	5.9	16
17344	Peptide Location Fingerprinting Reveals Tissue Region-Specific Differences in Protein Structures in an Ageing Human Organ. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10408.	1.8	9
17345	Analysing the role of Saraswatarishta in the treatment of neurological disorders based on network pharmacology. <i>Neuroscience Research Notes</i> , 2021, 3, 23-35.	0.5	2
17346	Systems biology analysis of lung fibrosis-related genes in the bleomycin mouse model. <i>Scientific Reports</i> , 2021, 11, 19269.	1.6	7
17347	Alterations in Skeletal Muscle Repair in Young Adults with Type 1 Diabetes Mellitus. <i>American Journal of Physiology - Cell Physiology</i> , 2021, 321, C876-C883.	2.1	7
17348	miR-24 and its target gene Prdx6 regulate viability and senescence of myogenic progenitors during aging. <i>Aging Cell</i> , 2021, 20, e13475.	3.0	9
17350	Intracellular and exosomal microRNAome profiling of human vascular smooth muscle cells during replicative senescence. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2021, 321, H770-H783.	1.5	11
17351	Containing epidemics in a local cluster via antidote distribution and partial quarantine. <i>Physical Review E</i> , 2021, 104, 034307.	0.8	0
17353	Four-Step Pathway from Phenylpyruvate to Benzylamine, an Intermediate to the High-Energy Propellant CL-20. <i>ACS Synthetic Biology</i> , 2021, 10, 2187-2196.	1.9	2
17354	Construction of transcriptional regulatory networks using total RNA-seq data. <i>STAR Protocols</i> , 2021, 2, 100769.	0.5	0
17355	Journal of Zhejiang University: Science		



#	ARTICLE	IF	CITATIONS
17356	Network-based analysis revealed significant interactions between risk genes of severe COVID-19 and host genes interacted with SARS-CoV-2 proteins. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
17357	WNT10A induces apoptosis of senescent synovial resident stem cells through Wnt/calcium pathway-mediated HDAC5 phosphorylation in OA joints. <i>Bone</i> , 2021, 150, 116006.	1.4	8
17358	Pan-proteome profiling of emerging and re-emerging zoonotic pathogen <i>Orientia tsutsugamushi</i> for getting insight into microbial pathogenesis. <i>Microbial Pathogenesis</i> , 2021, 158, 105103.	1.3	7
17360	Interferon regulatory factor family influences tumor immunity and prognosis of patients with colorectal cancer. <i>Journal of Translational Medicine</i> , 2021, 19, 379.	1.8	17
17361	Transcriptome Analysis of Immune Receptor Activation and Energy Metabolism Reduction as the Underlying Mechanisms in Interleukin-6-Induced Skeletal Muscle Atrophy. <i>Frontiers in Immunology</i> , 2021, 12, 730070.	2.2	11
17362	Life in the Wheat Litter: Effects of Future Climate on Microbiome and Function During the Early Phase of Decomposition. <i>Microbial Ecology</i> , 2022, 84, 90-105.	1.4	5
17363	Pyroptosis inhibition improves the symptom of acute myocardial infarction. <i>Cell Death and Disease</i> , 2021, 12, 852.	2.7	34
17364	Mechanism of <i>Paeoniae Radix Alba</i> in the Treatment of Non-alcoholic Fatty Liver Disease Based on Sequential Metabolites Identification Approach, Network Pharmacology, and Binding Affinity Measurement. <i>Frontiers in Nutrition</i> , 2021, 8, 677659.	1.6	10
17365	Identification and Characterization of <i>Verticillium nonalfalae</i> -Responsive MicroRNAs in the Roots of Resistant and Susceptible Hop Cultivars. <i>Plants</i> , 2021, 10, 1883.	1.6	1
17366	Uncovering Quercetin's Effects against Influenza A Virus Using Network Pharmacology and Molecular Docking. <i>Processes</i> , 2021, 9, 1627.	1.3	4
17367	A microenvironment-inspired synthetic three-dimensional model for pancreatic ductal adenocarcinoma organoids. <i>Nature Materials</i> , 2022, 21, 110-119.	13.3	79
17368	Gene co-expression network analysis in zebrafish reveals chemical class specific modules. <i>BMC Genomics</i> , 2021, 22, 658.	1.2	6
17371	Single-cell RNA sequencing analysis to characterize cells and gene expression landscapes in atrial septal defect. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 9660-9673.	1.6	2
17372	Physiological Characteristics and Transcriptomic Dissection in Two Root Segments with Contrasting Net Fluxes of Ammonium and Nitrate of Poplar Under Low Nitrogen Availability. <i>Plant and Cell Physiology</i> , 2022, 63, 30-44.	1.5	9
17373	Classifiers for Predicting Coronary Artery Disease Based on Gene Expression Profiles in Peripheral Blood Mononuclear Cells. <i>International Journal of General Medicine</i> , 2021, Volume 14, 5651-5663.	0.8	6
17374	WRKY Transcription Factors in Cassava Contribute to Regulation of Tolerance and Susceptibility to Cassava Mosaic Disease through Stress Responses. <i>Viruses</i> , 2021, 13, 1820.	1.5	11
17375	Quantitative proteomics identifies PTP1B as modulator of B cell antigen receptor signaling. <i>Life Science Alliance</i> , 2021, 4, e202101084.	1.3	2
17376	Computational workflow for functional characterization of COVID-19 through secondary data analysis. <i>STAR Protocols</i> , 2021, 2, 100873.	0.5	2

#	ARTICLE	IF	CITATIONS
17377	Scouting for common genes in the heterogenous hypoxic tumor microenvironment and their validation in glioblastoma. <i>3 Biotech</i> , 2021, 11, 451.	1.1	6
17378	Phosphorylated protein modification analysis on normal liver and Exoâ€œeliac liver of <i>Glyptosternum maculatum</i>. <i>Journal of Fish Biology</i> , 2021, 99, 1696-1707.	0.7	2
17379	Deficiency of PolÎ· in <i>Saccharomyces cerevisiae</i> reveals the impact of transcription on damage-induced cohesion. <i>PLoS Genetics</i> , 2021, 17, e1009763.	1.5	0
17380	Immuneâ€œrelated eightâ€œncRNA signature for improving prognosis prediction of lung adenocarcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24018.	0.9	13
17381	Chemical Inhibition of Apurinic-Apyrimidinic Endonuclease 1 Redox and DNA Repair Functions Affects the Inflammatory Response via Different but Overlapping Mechanisms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 731588.	1.8	7
17382	Chemical composition and vasodilator activity of different <i>Alpinia zerumbet</i> leaf extracts, a potential source of bioactive flavonoids. <i>Medicinal Chemistry Research</i> , 2021, 30, 2103.	1.1	1
17384	Understanding Responses of Soil Microbiome to the Nitrogen and Phosphorus Addition in <i>Metasequoia glyptostroboides</i> Plantations of Different Ages. <i>Microbial Ecology</i> , 2022, 84, 565-579.	1.4	5
17385	Prenatal Î³-Tetrahydrocannabinol Exposure in Males Leads to Motivational Disturbances Related to Striatal Epigenetic Dysregulation. <i>Biological Psychiatry</i> , 2022, 92, 127-138.	0.7	22
17386	GWAS Meta-Analysis Reveals Shared Genes and Biological Pathways between Major Depressive Disorder and Insomnia. <i>Genes</i> , 2021, 12, 1506.	1.0	7
17387	PRDM12 Is Transcriptionally Active and Required for Nociceptor Function Throughout Life. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 720973.	1.4	7
17388	Skyllamycins D and E, Non-Ribosomal Cyclic Depsipeptides from Lichen-Sourced <i>Streptomyces anulatus</i>. <i>Journal of Natural Products</i> , 2021, 84, 2536-2543.	1.5	15
17389	miR-223-3p and miR-24-3p as novel serum-based biomarkers for myotonic dystrophy type 1. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 23, 169-183.	1.8	6
17390	Comprehensive Transcriptomic Analysis of Critical RNA Regulation Associated With Metabolism and Prognosis in Clear Cell Renal Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 709490.	1.8	1
17391	Aberrant nuclear lamina contributes to the malignancy of human gliomas. <i>Journal of Genetics and Genomics</i> , 2022, 49, 132-144.	1.7	6
17392	Spatial variation in gene expression of Tasmanian devil facial tumors despite minimal host transcriptomic response to infection. <i>BMC Genomics</i> , 2021, 22, 698.	1.2	6
17393	Integrative proteome analysis implicates aberrant RNA splicing in impaired developmental potential of aged mouse oocytes. <i>Aging Cell</i> , 2021, 20, e13482.	3.0	12
17394	Identifying cancer specific signaling pathways based on the dysregulation between genes. <i>Computational Biology and Chemistry</i> , 2021, 95, 107586.	1.1	1
17395	Identification of Pulpitis-Related Potential Biomarkers Using Bioinformatics Approach. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-12.	0.7	6

#	ARTICLE	IF	CITATIONS
17396	Identification and functional characterization of Gh_D01G0514 (GhNAC072) transcription factor in response to drought stress tolerance in cotton. <i>Plant Physiology and Biochemistry</i> , 2021, 166, 361-375.	2.8	15
17397	A 3-D human model of complex cardiac arrhythmias. <i>Acta Biomaterialia</i> , 2021, 132, 149-161.	4.1	15
17398	MicroRNAâ€545â€5p regulates apoptosis, migration and invasion of osteosarcoma by targeting dimethyladenosine transferase 1. <i>Oncology Letters</i> , 2021, 22, 763.	0.8	1
17399	Differential Expression Pattern of Goat Uterine Fluids Extracellular Vesicles miRNAs during Peri-Implantation. <i>Cells</i> , 2021, 10, 2308.	1.8	8
17400	Genome Mining and Molecular Networking-Based Metabolomics of the Marine Facultative <i>Aspergillus</i> sp. MEXU 27854. <i>Molecules</i> , 2021, 26, 5362.	1.7	4
17401	Identification of novel key molecular signatures in the pathogenesis of experimental diabetic retinopathy. <i>IUBMB Life</i> , 2021, 73, 1307-1324.	1.5	5
17402	Molecular underpinnings of the early brain developmental response to differential feeding in the honey bee <i>Apis mellifera</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194732.	0.9	5
17403	Glutathione is an aging-related metabolic signature in the mouse kidney. <i>Aging</i> , 2021, 13, 21009-21028.	1.4	8
17405	Comparative proteomics of <i>Pinus</i> â€ <i>Fusarium</i> interactions reveal metabolic clues to biotic stress resistance. <i>Physiologia Plantarum</i> , 2021, 173, 2142-2154.	2.6	10
17406	Microarray analysis of hub genes and pathways in damaged cartilage tissues of knee. <i>Medicine (United Tj ETQq1 1.0,784314 rgBT /Ove</i>	0.4	1
17407	FACT-seq: profiling histone modifications in formalin-fixed paraffin-embedded samples with low cell numbers. <i>Nucleic Acids Research</i> , 2021, 49, e125-e125.	6.5	10
17408	circRNA Regulates Dopaminergic Synapse, MAPK, and Long-term Depression Pathways in Huntington Disease. <i>Molecular Neurobiology</i> , 2021, 58, 6222-6231.	1.9	7
17409	Metabolomic and Transcriptomic Changes Induced by Potassium Deficiency During <i>Sarocladium oryzae</i> Infection Reveal Insights into Rice Sheath Rot Disease Resistance. <i>Rice</i> , 2021, 14, 81.	1.7	10
17410	Integrative Analyses of Genes Associated With Right Ventricular Cardiomyopathy Induced by Tricuspid Regurgitation. <i>Frontiers in Genetics</i> , 2021, 12, 708275.	1.1	6
17411	Characterization and engineering of <i>Streptomyces griseofuscus</i> DSM 40191 as a potential host for heterologous expression of biosynthetic gene clusters. <i>Scientific Reports</i> , 2021, 11, 18301.	1.6	11
17412	Strong agricultural management effects on soil microbial community in a non-experimental agroecosystem. <i>Applied Soil Ecology</i> , 2021, 165, 103970.	2.1	15
17413	Development of a Multi-Target Strategy for the Treatment of Vitiligo via Machine Learning and Network Analysis Methods. <i>Frontiers in Pharmacology</i> , 2021, 12, 754175.	1.6	5
17414	Computational Analysis Illustrates the Mechanism of Qingfei Paidu Decoction in Blocking the Transition of COVID-19 Patients from Mild to Severe Stage. <i>Current Gene Therapy</i> , 2022, 22, 277-289.	0.9	13

#	ARTICLE	IF	CITATIONS
17415	N6-methyladenosine-related lncRNAs play an important role in the prognosis and immune microenvironment of pancreatic ductal adenocarcinoma. <i>Scientific Reports</i> , 2021, 11, 17844.	1.6	6
17416	Scoparone inhibits pancreatic cancer through PI3K/Akt signaling pathway. <i>World Journal of Gastrointestinal Oncology</i> , 2021, 13, 1164-1183.	0.8	17
17417	Apolipoprotein Signature of HDL and LDL from Atherosclerotic Patients in Relation with Carotid Plaque Typology: A Preliminary Report. <i>Biomedicines</i> , 2021, 9, 1156.	1.4	3
17418	Identification of Potential Prognostic Biomarker for Predicting Survival in Multiple Myeloma Using Bioinformatics Analysis and Experiments. <i>Frontiers in Genetics</i> , 2021, 12, 722132.	1.1	1
17419	In-Silico Analysis of rSNPs in miRNA:mRNA Duplex Involved in Insulin Signaling Genes Shows a Possible Pathogenesis of Insulin Resistance. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2021, 10, .	0.6	0
17420	Xiaoyu Xiezhao Drink Protects against Ischemia-Reperfusion Acute Kidney Injury in Aged Mice through Inhibiting the TGF- $\beta$ 1/Smad3 and HIF1 Signaling Pathways. <i>BioMed Research International</i> , 2021, 2021, 1-19.	0.9	3
17423	General Caspase Inhibition in Primary Chondrogenic Cultures Impacts Their Transcription Profile Including Osteoarthritis-Related Factors. <i>Cartilage</i> , 2021, , 194760352110448.	1.4	4
17424	Prognostic Impact and Functional Annotations of KIF11 and KIF14 Expression in Patients with Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9732.	1.8	9
17425	Genome-resolved metagenome and metatranscriptome analyses of thermophilic composting reveal key bacterial players and their metabolic interactions. <i>BMC Genomics</i> , 2021, 22, 652.	1.2	16
17426	Full-Scale Clinical Data and Reshaped Intestinal Microbiome on a Short-Term Low-Phosphorus Diet among Healthy Adults. , 2021, 31, 448-458.		2
17427	The regulatory pattern of target gene expression by aberrant enhancer methylation in glioblastoma. <i>BMC Bioinformatics</i> , 2021, 22, 420.	1.2	5
17428	Preservation Analysis on Spatiotemporal Specific Co-expression Networks Suggests the Immunopathogenesis of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 727928.	1.7	1
17429	Systematic Analysis of the Impact of R-Methylation on RBPs-RNA Interactions: A Proteomic Approach. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 688973.	1.6	8
17430	The effect of aging on facial attractiveness: An empirical and computational investigation. <i>Acta Psychologica</i> , 2021, 219, 103385.	0.7	17
17432	Myrtenal and $\beta$ -caryophyllene oxide screened from <i>Liquidambaris Fructus</i> suppress NLRP3 inflammasome components in rheumatoid arthritis. <i>BMC Complementary Medicine and Therapies</i> , 2021, 21, 242.	1.2	15
17433	Molecular and Cellular Characterization of Pyoderma Gangrenosum: Implications for the Use of Gene Expression. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1217-1220.e14.	0.3	18
17434	Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy. <i>Nature Microbiology</i> , 2021, 6, 1319-1333.	5.9	23
17435	Interactome Networks of FOSL1 and FOSL2 in Human Th17 Cells. <i>ACS Omega</i> , 2021, 6, 24834-24847.	1.6	6

#	ARTICLE	IF	CITATIONS
17436	AMPK/SIRT1 signaling through p38MAPK mediates Interleukin-6 induced neuroendocrine differentiation of LNCaP prostate cancer cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021, 1868, 119085.	1.9	8
17437	Erythrocyte miRNA regulators and malarial pathophysiology. <i>Infection, Genetics and Evolution</i> , 2021, 93, 105000.	1.0	5
17438	Comparative Transcriptomic Analyses of Antibiotic-Treated and Normally Reared <i>Bactrocera dorsalis</i> Reveals a Possible Gut Self-Immunity Mechanism. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647604.	1.8	2
17439	R-group replacement database for medicinal chemistry. <i>Future Science OA</i> , 2021, 7, FSO742.	0.9	5
17443	Growth factor signaling predicts therapy resistance mechanisms and defines neuroblastoma subtypes. <i>Oncogene</i> , 2021, 40, 6258-6272.	2.6	19
17444	Deep proteome profiling of human mammary epithelia at lineage and age resolution. <i>IScience</i> , 2021, 24, 103026.	1.9	3
17446	Transcriptional expression of ZICs as an independent indicator of survival in gliomas. <i>Scientific Reports</i> , 2021, 11, 17532.	1.6	5
17448	A New Concept of ICT on Eduinformatics in Higher Education. <i>Lecture Notes in Networks and Systems</i> , 2022, , 693-700.	0.5	7
17449	Identification of 5 Hub Genes Related to the Early Diagnosis, Tumour Stage, and Poor Outcomes of Hepatitis B Virus-Related Hepatocellular Carcinoma by Bioinformatics Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-20.	0.7	15
17450	Identification of key miRNAs and mRNAs related to coronary artery disease by meta-analysis. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 443.	0.7	3
17451	Investigating drug-target interactions in frontotemporal dementia using a network pharmacology approach. <i>Beni-Suef University Journal of Basic and Applied Sciences</i> , 2021, 10, .	0.8	1
17452	Multomics Analysis Reveals the Prognostic Non-tumor Cell Landscape in Glioblastoma Niches. <i>Frontiers in Genetics</i> , 2021, 12, 741325.	1.1	0
17455	Diversification of the Type VI Secretion System in <i>Agrobacteria</i> . <i>MBio</i> , 2021, 12, e0192721.	1.8	15
17457	A bioinformatics approach for identifying potential molecular mechanisms and key genes involved in COVID-19 associated cardiac remodeling. <i>Gene Reports</i> , 2021, 24, 101246.	0.4	8
17458	Comparative Analysis of <i>Botrytis cinerea</i> in Response to the Microbial Secondary Metabolite Benzothiazole Using iTRAQ-Based Quantitative Proteomics. <i>Phytopathology</i> , 2021, 111, 1313-1326.	1.1	6
17459	Development of an immune-related <i>lncRNA</i> - <i>miRNA</i> - <i>mRNA</i> network based on competing endogenous <i>RNA</i> in periodontitis. <i>Journal of Clinical Periodontology</i> , 2021, 48, 1470-1479.	2.3	22
17460	Single-cell intracellular epitope and transcript detection reveals signal transduction dynamics. <i>Cell Reports Methods</i> , 2021, 1, 100070.	1.4	21
17461	Quantitative Temporal Viromics. <i>Annual Review of Virology</i> , 2021, 8, 159-181.	3.0	5

#	ARTICLE	IF	CITATIONS
17462	Effects of Bacille Calmette Guerin (BCG) vaccination during COVID-19 infection. <i>Computers in Biology and Medicine</i> , 2021, 138, 104891.	3.9	3
17463	Hypothalamus-pituitary axis transcriptomic modification dependent on growth rate in geese ( <i>Anser</i> ) Tj ETQq1 1,0,784314,0rgBT /Ome	0.6	0
17464	Global identification of long non-coding RNAs involved in the induction of spinach flowering. <i>BMC Genomics</i> , 2021, 22, 704.	1.2	13
17465	Exploring the Extracellular Vesicle MicroRNA Expression Repertoire in Patients with Rheumatoid Arthritis and Ankylosing Spondylitis Treated with TNF Inhibitors. <i>Disease Markers</i> , 2021, 2021, 1-15.	0.6	4
17466	Adaptive defence and sensing responses of host plant roots to fungal pathogen attack revealed by transcriptome and metabolome analyses. <i>Plant, Cell and Environment</i> , 2021, 44, 3756-3774.	2.8	10
17467	IGFBP-2 as a biomarker in NAFLD improves hepatic steatosis: an integrated bioinformatics and experimental study. <i>Endocrine Connections</i> , 2021, 10, 1315-1325.	0.8	9
17468	Gelatin methacrylate hydrogels culture model for glioblastoma cells enriches for mesenchymal-like state and models interactions with immune cells. <i>Scientific Reports</i> , 2021, 11, 17727.	1.6	8
17469	Detecting Rewiring Events in Protein-Protein Interaction Networks Based on Transcriptomic Data. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	4
17470	CG7379 and ING1 suppress cancer cell invasion by maintaining cell-cell junction integrity. <i>Open Biology</i> , 2021, 11, 210077.	1.5	1
17471	Decrypting the role of predicted SARS-CoV-2 miRNAs in COVID-19 pathogenesis: A bioinformatics approach. <i>Computers in Biology and Medicine</i> , 2021, 136, 104669.	3.9	16
17472	Transcriptome profiling reveal key hub genes in co-expression networks involved in Iridoid glycosides biosynthetic machinery in <i>Picrorhiza kurroa</i> . <i>Genomics</i> , 2021, 113, 3381-3394.	1.3	5
17473	Capturing <i>Salmonella</i> SspH2 Host Targets in Virus-Like Particles. <i>Frontiers in Medicine</i> , 2021, 8, 725072.	1.2	4
17474	Identification of Autophagy Related circRNA-miRNA-mRNA-Subtypes Network With Radiotherapy Responses and Tumor Immune Microenvironment in Non-small Cell Lung Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 730003.	1.1	17
17475	Uncovering the pharmacological mechanisms of Xijiao Dihuang decoction combined with Yinqiao powder in treating influenza viral pneumonia by an integrative pharmacology strategy. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111676.	2.5	11
17476	Potential of testis-derived circular RNAs in seminal plasma to predict the outcome of microdissection testicular sperm extraction in patients with idiopathic non-obstructive azoospermia. <i>Human Reproduction</i> , 2021, 36, 2649-2660.	0.4	11
17477	Quantitative Proteomic Analysis for High- and Low-Aflatoxin-Yield <i>Aspergillus flavus</i> Strains Isolated From Natural Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 741875.	1.5	4
17478	<i>Escherichia coli</i> Nissle 1917 secondary metabolism: aryl polyene biosynthesis and phosphopantetheinyl transferase crosstalk. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7785-7799.	1.7	3
17479	Screening of key genes during early embryonic development of Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>Gene Reports</i> , 2021, 24, 101262.	0.4	0



#	ARTICLE	IF	CITATIONS
17480	Integrated mRNA and miRNA transcriptome analysis provides novel insights into the molecular mechanisms underlying goose pituitary development during the embryo-to-hatchling transition. <i>Poultry Science</i> , 2021, 100, 101380.	1.5	0
17481	Network Pharmacology Integrated with Molecular Docking Explores the Mechanisms of Naringin against Osteoporotic Fracture by Regulating Oxidative Stress. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	4
17482	Low CCL19 expression is associated with adverse clinical outcomes for follicular lymphoma patients treated with chemoimmunotherapy. <i>Journal of Translational Medicine</i> , 2021, 19, 399.	1.8	2
17483	Comparative physiology and transcriptome response patterns in cold-tolerant and cold-sensitive varieties of <i>Zanthoxylum bungeanum</i> Maxim. <i>Industrial Crops and Products</i> , 2021, 167, 113562.	2.5	25
17484	Circular RNAs Repertoire and Expression Profile during <i>Brassica rapa</i> Pollen Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10297.	1.8	13
17485	Organelle Genome Variation in the Red Algal Genus <i>Ahnfeltia</i> (Florideophyceae). <i>Frontiers in Genetics</i> , 2021, 12, 724734.	1.1	0
17486	Murine Norovirus Infection Results in Anti-inflammatory Response Downstream of Amino Acid Depletion in Macrophages. <i>Journal of Virology</i> , 2021, 95, e0113421.	1.5	4
17487	Human blood serum proteome changes after 6 hours of sleep deprivation at night. <i>Sleep Science and Practice</i> , 2021, 5, .	0.6	3
17488	Coexpression network analysis identified lncRNAs-mRNAs with potential relevance in African ancestry prostate cancer. <i>Future Science OA</i> , 2021, 7, FSO749.	0.9	0
17489	Comprehensive analysis of lncRNAs as biomarkers for diagnosis, prognosis, and treatment response in clear cell renal cell carcinoma. <i>Molecular Therapy - Oncolytics</i> , 2021, 22, 209-218.	2.0	6
17491	The aroma profile and microbiota structure in oil furu, a Chinese fermented soybean curd. <i>Food Research International</i> , 2021, 147, 110473.	2.9	12
17492	Cell-specific gene association network construction from single-cell RNA sequence. <i>Cell Cycle</i> , 2021, 20, 1-16.	1.3	3
17493	Identifying key genes and small molecule compounds for nasopharyngeal carcinoma by various bioinformatic analysis. <i>Medicine (United States)</i> , 2021, 100, e27257.	0.4	5
17496	Discovery of potential biomarkers for human atherosclerotic abdominal aortic aneurysm through untargeted metabolomics and transcriptomics. <i>Journal of Zhejiang University: Science B</i> , 2021, 22, 733-745.	1.3	5
17497	Abiotic and biotic regulation on carbon mineralization and stabilization in paddy soils along iron oxide gradients. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108312.	4.2	36
17498	Aberrant gut-microbiota-immune-brain axis development in premature neonates with brain damage. <i>Cell Host and Microbe</i> , 2021, 29, 1558-1572.e6.	5.1	80
17500	Gene Expression Profiling of Contralateral Dorsal Root Ganglia Associated with Mirror-Image Pain in a Rat Model of Complex Regional Pain Syndrome Type-I. <i>Journal of Pain Research</i> , 2021, Volume 14, 2739-2756.	0.8	10
17501	Bioinformatics-based study to identify immune infiltration and inflammatory-related hub genes as biomarkers for the treatment of rheumatoid arthritis. <i>Immunogenetics</i> , 2021, 73, 435-448.	1.2	2

#	ARTICLE	IF	CITATIONS
17504	Analysis of potential genetic biomarkers and molecular mechanism of smoking-related postmenopausal osteoporosis using weighted gene co-expression network analysis and machine learning. PLoS ONE, 2021, 16, e0257343.	1.1	8
17505	Proteomic Characterization of Spontaneous Stress-Induced In Vitro Apoptosis of Human Acute Myeloid Leukemia Cells; Focus on Patient Heterogeneity and Endoplasmic Reticulum Stress. Hemato, 2021, 2, 607-627.	0.2	3
17506	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. Briefings in Bioinformatics, 2022, 23, .	3.2	7
17507	Midkine promotes glioblastoma progression via PI3K-Akt signaling. Cancer Cell International, 2021, 21, 509.	1.8	16
17508	A virus-free cellular model recapitulates several features of severe COVID-19. Scientific Reports, 2021, 11, 17473.	1.6	4
17509	Transcriptome responses in polar cod ( <i>Boreogadus saida</i> ) liver slice culture exposed to benzo[a]pyrene and ethynylestradiol: insights into anti-estrogenic effects. Toxicology in Vitro, 2021, 75, 105193.	1.1	7
17510	Identification of a miRNA-mRNA Regulatory Networks in Placental Tissue Associated With Tibetan High Altitude Adaptation. Frontiers in Genetics, 2021, 12, 671119.	1.1	3
17511	Transcriptome Analysis of Effects of Folic Acid Supplement on Gene Expression in Liver of Broiler Chickens. Frontiers in Veterinary Science, 2021, 8, 686609.	0.9	3
17512	Biofilm microbiome in extracorporeal membrane oxygenator catheters. PLoS ONE, 2021, 16, e0257449.	1.1	8
17513	Navigating through chemical space and evolutionary time across the Australian continent in plant genus <i>Eremophila</i> . Plant Journal, 2021, 108, 555-578.	2.8	13
17514	Modelling Nonalcoholic Steatohepatitis In Vivo-A Close Transcriptomic Similarity Supports the Guinea Pig Disease Model. Biomedicines, 2021, 9, 1198.	1.4	4
17516	Visualization of individual cell division history in complex tissues using iCOUNT. Cell Stem Cell, 2021, 28, 2020-2034.e12.	5.2	14
17517	Sulfur ion irradiation experiments simulating space weathering of Solar System body surfaces. Astronomy and Astrophysics, 2021, 655, A74.	2.1	10
17518	Loss of the mitochondrial phosphate carrier SLC25A3 induces remodeling of the cardiac mitochondrial protein acylome. American Journal of Physiology - Cell Physiology, 2021, 321, C519-C534.	2.1	8
17519	Identification of hub genes in common cancers of women in India and targeting for the search of anticancer agent from <i>Punica granatum</i> phytoconstituent using interaction network analysis and virtual screening. Journal of Biomolecular Structure and Dynamics, 2021, , 1-7.	2.0	1
17520	Complement-containing small extracellular vesicles from adventitial fibroblasts induce proinflammatory and metabolic reprogramming in macrophages. JCI Insight, 2021, 6, .	2.3	13
17521	Beyond the Biosynthetic Gene Cluster Paradigm: Genome-Wide Coexpression Networks Connect Clustered and Unclustered Transcription Factors to Secondary Metabolic Pathways. Microbiology Spectrum, 2021, 9, e0089821.	1.2	17
17522	A small-molecule SUMOylation inhibitor activates antitumor immune responses and potentiates immune therapies in preclinical models. Science Translational Medicine, 2021, 13, eaba7791.	5.8	49

#	ARTICLE	IF	CITATIONS
17523	Artificial Intelligence-Assisted Identification of Genetic Factors Predisposing High-Risk Individuals to Asymptomatic Heart Failure. <i>Cells</i> , 2021, 10, 2430.	1.8	7
17524	Interactome and evolutionary conservation of Dictyostelid small GTPases and their direct regulators. <i>Small GTPases</i> , 2022, 13, 239-254.	0.7	3
17525	Clinical and functional characterization of a novel STUB1 frameshift mutation in autosomal dominant spinocerebellar ataxia type 48 (SCA48). <i>Journal of Biomedical Science</i> , 2021, 28, 65.	2.6	6
17526	Conserved and species-specific chromatin remodeling and regulatory dynamics during mouse and chicken limb bud development. <i>Nature Communications</i> , 2021, 12, 5685.	5.8	6
17527	Integrated Chemical Molecular Docking with Network Pharmacology to Study the Molecular Mechanism of JianPi YiQi BuSui Method for Treating Myasthenia Gravis. <i>Chinese Journal of Analytical Chemistry</i> , 2021, 50, 1-1.	0.9	4
17528	The lanthipeptide biosynthetic clusters of the domain Archaea. <i>Microbiological Research</i> , 2021, 253, 126884.	2.5	9
17529	Network Pharmacology-Based Dissection of the Comprehensive Molecular Mechanisms of the Herbal Prescription FDY003 Against Estrogen Receptor-Positive Breast Cancer. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110443.	0.2	1
17530	The aerobiome uncovered: Multi-marker metabarcoding reveals potential drivers of turn-over in the full microbial community in the air. <i>Environment International</i> , 2021, 154, 106551.	4.8	27
17531	Polydatin Ameliorates Osteoporosis via Suppression of the Mitogen-Activated Protein Kinase Signaling Pathway. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 730362.	1.8	4
17532	Transcriptome-Wide Identification of WRKY Transcription Factor and Functional Characterization of RgWRKY37 Involved in Acteoside Biosynthesis in <i>Rehmannia glutinosa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 739853.	1.7	8
17533	Ecological Dichotomies Arise in Microbial Communities Due to Mixing of Deep Hydrothermal Waters and Atmospheric Gas in a Circumneutral Hot Spring. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0159821.	1.4	6
17534	Differential DNA methylation and transcriptional signatures characterize impairment of muscle stem cells in pediatric human muscle contractures after brain injury. <i>FASEB Journal</i> , 2021, 35, e21928.	0.2	8
17535	Defining the Dynamic Regulation of O-GlcNAc Proteome in the Mouse Cortex--the O-GlcNAcylation of Synaptic and Trafficking Proteins Related to Neurodegenerative Diseases. <i>Frontiers in Aging</i> , 2021, 2, .	1.2	10
17536	Whole genome characterization of <i>Streptococcus pneumoniae</i> from respiratory and blood cultures collected from Canadian hospitals before and after PCV-13 implementation in Canada: Focus on serotypes 22F and 33F from CANWARD 2007-2018. <i>Vaccine</i> , 2021, 39, 5474-5483.	1.7	6
17537	Hsp90-associated DNA replication checkpoint protein and proteasome-subunit components are involved in the age-related macular degeneration. <i>Chinese Medical Journal</i> , 2021, 134, 2322-2332.	0.9	2
17538	Phytochemical Characterization, Antioxidant, Anti-inflammatory, Anti-diabetic properties, Molecular Docking, Pharmacokinetic Profiling, and Network Pharmacology Analysis of the Major Phytoconstituents of Raw and Differently Dried <i>Mangifera indica</i> (Himsagar cultivar): an In Vitro and In Silico Investigations. <i>Applied Biochemistry and Biotechnology</i> . 2022. 194, 950-987.	1.4	32
17539	Cell death mechanisms involved in cell injury caused by SARS-CoV-2. <i>Reviews in Medical Virology</i> , 2022, 32, e2292.	3.9	19
17541	Immune Mechanism, Gene Module, and Molecular Subtype Identification of <i>Astragalus Membranaceus</i> in the Treatment of Dilated Cardiomyopathy: An Integrated Bioinformatics Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-29.	0.5	1

#	ARTICLE	IF	CITATIONS
17542	Genetic differentiation of mainland-island sheep of Greece: Implications for identifying candidate genes for long-term local adaptation. <i>PLoS ONE</i> , 2021, 16, e0257461.	1.1	6
17543	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. <i>Nature Communications</i> , 2021, 12, 5466.	5.8	24
17544	Human placental gene sets improve analysis of placental pathologies and link trophoblast and cancer invasion genes. <i>Placenta</i> , 2021, 112, 9-15.	0.7	5
17545	Immune response gene coexpression network analysis of <i>Arachis hypogaea</i> infected with <i>Aspergillus flavus</i> . <i>Genomics</i> , 2021, 113, 2977-2988.	1.3	5
17546	Application of Genetic Algorithm-Based Support Vector Machine in Identification of Gene Expression Signatures for Psoriasis Classification: A Hybrid Model. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	14
17547	Genome-Wide Analysis of the HSP20 Gene Family and Expression Patterns of HSP20 Genes in Response to Abiotic Stresses in <i>Cynodon transvaalensis</i> . <i>Frontiers in Genetics</i> , 2021, 12, 732812.	1.1	11
17548	Characterising the shared genetic determinants of bipolar disorder, schizophrenia and risk-taking. <i>Translational Psychiatry</i> , 2021, 11, 466.	2.4	15
17549	Identification of distinct tumor cell populations and key genetic mechanisms through single cell sequencing in hepatoblastoma. <i>Communications Biology</i> , 2021, 4, 1049.	2.0	17
17550	Integrating Network Pharmacology and RT-qPCR Analysis to Investigate the Mechanisms Underlying ZeXie Decoction-Mediated Treatment of Non-alcoholic Fatty Liver Disease. <i>Frontiers in Pharmacology</i> , 2021, 12, 722016.	1.6	8
17553	Genome-Wide Association Studies in Indian Buffalo Revealed Genomic Regions for Lactation and Fertility. <i>Frontiers in Genetics</i> , 2021, 12, 696109.	1.1	17
17555	Newly-Discovered Neural Features Expand the Pathobiological Knowledge of Blastic Plasmacytoid Dendritic Cell Neoplasm. <i>Cancers</i> , 2021, 13, 4680.	1.7	6
17557	Fuxin Granules ameliorate diabetic nephropathy in db/db mice through TGF- $\beta$ 21/Smad and VEGF/VEGFR2 signaling pathways. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111806.	2.5	17
17558	Influence of Maternal Lifestyle and Diet on Perinatal DNA Methylation Signatures Associated With Childhood Arterial Stiffness at 8 to 9 Years. <i>Hypertension</i> , 2021, 78, 787-800.	1.3	10
17559	LncRNA TCONS_00021861 is functionally associated with drought tolerance in rice ( <i>Oryza sativa</i> L.) via competing endogenous RNA regulation. <i>BMC Plant Biology</i> , 2021, 21, 410.	1.6	39
17560	Nonredundant, isoform-specific roles of HDAC1 in glioma stem cells. <i>JCI Insight</i> , 2021, 6, .	2.3	12
17562	Association of Pericardiac Adipose Tissue With Coronary Artery Disease. <i>Frontiers in Endocrinology</i> , 2021, 12, 724859.	1.5	9
17563	A pathway map of signaling events triggered upon SARS-CoV infection. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 595-600.	1.8	4
17564	Novel diagnostic and prognostic biomarkers of colorectal cancer: Capable to overcome the heterogeneity-specific barrier and valid for global applications. <i>PLoS ONE</i> , 2021, 16, e0256020.	1.1	7

#	ARTICLE	IF	CITATIONS
17565	Damage-Net: A program for DNA repair meta-analysis identifies a network of novel repair genes that facilitate cancer evolution. <i>DNA Repair</i> , 2021, 105, 103158.	1.3	3
17567	Development and Validation of an Mesenchymal-Related Long Non-Coding RNA Prognostic Model in Glioma. <i>Frontiers in Oncology</i> , 2021, 11, 726745.	1.3	5
17568	Role of a high centrality residue in protein dynamics and thermal stability. <i>Journal of Structural Biology</i> , 2021, 213, 107773.	1.3	3
17569	A Shotgun Proteomic Platform for a Global Mapping of Lymphoblastoid Cells to Gain Insight into Nasu-Hakola Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9959.	1.8	2
17570	Cyclic Hypoxia Conditioning Alters the Content of Myoblast-Derived Extracellular Vesicles and Enhances Their Cell-Protective Functions. <i>Biomedicines</i> , 2021, 9, 1211.	1.4	4
17571	The Effects of Adoptively Transferred IL-23/IL-18-Polarized Neutrophils on Tumor and Collagen-Induced Arthritis in Mice. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4669-4686.	1.6	9
17572	Genetic variation in genes regulating skeletal muscle regeneration and tissue remodelling associated with weight loss in chronic obstructive pulmonary disease. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 1803-1817.	2.9	11
17573	Multiplexed drug-based selection and counterselection genetic manipulations in <i>Drosophila</i> . <i>Cell Reports</i> , 2021, 36, 109700.	2.9	10
17574	Identification of Oleanolic Acid as Allosteric Agonist of Integrin $\beta$ 1 by Combination of In Silico Modeling and In Vitro Analysis. <i>Frontiers in Pharmacology</i> , 2021, 12, 702529.	1.6	5
17575	miRNome profiling in Duchenne muscular dystrophy; identification of asymptomatic and manifesting female carriers. <i>Bioscience Reports</i> , 2021, 41, .	1.1	0
17577	Identification of Vital Hub Genes and Potential Molecular Pathways of Dermatomyositis by Bioinformatics Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	4
17578	Genomic-Wide Identification and Characterization of the Uridine Diphosphate Glycosyltransferase Family in <i>Eucommia ulmoides</i> Oliver. <i>Plants</i> , 2021, 10, 1934.	1.6	7
17579	PATHOME-Drug: a subpathway-based polypharmacology drug-repositioning method. <i>Bioinformatics</i> , 2022, 38, 444-452.	1.8	5
17580	Genome-Wide Identification and Analysis of the NF-Y Gene Family in Potato ( <i>Solanum tuberosum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 739989.	1.1	9
17581	Prediction and Boolean logical modelling of synergistic microRNA regulatory networks during reprogramming of male germline pluripotent stem cells. <i>BioSystems</i> , 2021, 207, 104453.	0.9	1
17582	Effect of MAP3K8 on Prognosis and Tumor-Related Inflammation in Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 674613.	1.1	6
17583	Novel variants in <i>KAT6B</i> spectrum of disorders expand our knowledge of clinical manifestations and molecular mechanisms. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2021, 9, e1809.	0.6	4
17584	Differential Interactome Based Drug Repositioning Unraveled Abacavir, Exemestane, Nortriptyline Hydrochloride, and Tolcapone as Potential Therapeutics for Colorectal Cancers. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	2

#	ARTICLE	IF	CITATIONS
17585	Construction of miRNA-mRNA network for the identification of key biological markers and their associated pathways in IgA nephropathy by employing the integrated bioinformatics analysis. Saudi Journal of Biological Sciences, 2021, 28, 4938-4945.	1.8	18
17586	Transcriptomic analysis of ovarian signaling at the emergence of the embryo from obligate diapause in the American mink ( <i>Neovison vison</i> ). Animal Reproduction Science, 2021, 232, 106823.	0.5	3
17587	Integrin $\beta$ 1 orchestrates the abnormal cell-matrix attachment and invasive behaviour of E-cadherin dysfunctional cells. Gastric Cancer, 2022, 25, 124-137.	2.7	13
17588	Comprehensive analysis of abnormal expression, prognostic value and oncogenic role of the hub gene FN1 in pancreatic ductal adenocarcinoma via bioinformatic analysis and in vitro experiments. PeerJ, 2021, 9, e12141.	0.9	4
17589	Gene and prognostic value of N6-methyladenosine (m6A) modification regulatory factors in lung adenocarcinoma. European Journal of Cancer Prevention, 2022, 31, 354-362.	0.6	5
17590	Comprehensive Analysis of mRNA Expression Profiling and Identification of Potential Diagnostic Biomarkers in Coronary Artery Disease. ACS Omega, 2021, 6, 24016-24026.	1.6	7
17591	SWATH-MS for prospective identification of protein blood biomarkers of rtPA-associated intracranial hemorrhage in acute ischemic stroke: a pilot study. Scientific Reports, 2021, 11, 18765.	1.6	0
17592	Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. Cell Reports, 2021, 36, 109742.	2.9	15
17593	Revelation of candidate genes and molecular mechanism of reproductive seasonality in female rohu ( <i>Labeo rohita</i> Ham.) by RNA sequencing. BMC Genomics, 2021, 22, 685.	1.2	3
17594	Mechanism of Fuzheng Kangai Formula Regulating Tumor Microenvironment in Non-Small Cell Lung Cancer. Chinese Journal of Integrative Medicine, 2022, 28, 425-433.	0.7	2
17595	Gene Expression Profiling of Tricarboxylic Acid Cycle and One Carbon Metabolism Related Genes for Prognostic Risk Signature of Colon Carcinoma. Frontiers in Genetics, 2021, 12, 647152.	1.1	9
17596	The ubiquitin ligase RNF5 determines acute myeloid leukemia growth and susceptibility to histone deacetylase inhibitors. Nature Communications, 2021, 12, 5397.	5.8	20
17597	Investigation of Diagnostic Biomarkers for Osteoporosis Based on Differentially Expressed Gene Profile with QCT and mDixon Quant Techniques. Orthopaedic Surgery, 2021, 13, 2137-2144.	0.7	2
17598	The Interactions of Small Proline-Rich Proteins with Late Cornified Envelope Proteins are Involved in the Pathogenesis of Psoriasis. Clinical, Cosmetic and Investigational Dermatology, 2021, Volume 14, 1355-1365.	0.8	6
17599	Novel Approach Combining Transcriptional and Evolutionary Signatures to Identify New Multiciliation Genes. Genes, 2021, 12, 1452.	1.0	3
17600	The Protective Effects of Live and Pasteurized <i>Akkermansia muciniphila</i> and Its Extracellular Vesicles against HFD/CCl4-Induced Liver Injury. Microbiology Spectrum, 2021, 9, e0048421.	1.2	61
17601	Computational analysis of human host binding partners of chikungunya and dengue viruses during coinfection. Pathogens and Disease, 2021, 79, .	0.8	2
17602	Bioinformatic analysis identifies potential key genes of epilepsy. PLoS ONE, 2021, 16, e0254326.	1.1	5



#	ARTICLE	IF	CITATIONS
17603	Landscape of functional interactions of human processive ribonucleases revealed by high-throughput siRNA screenings. <i>IScience</i> , 2021, 24, 103036.	1.9	6
17604	A Network Pharmacology Study on the Molecular Mechanism of Protocatechualdehyde in the Treatment of Diabetic Cataract. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 4011-4023.	2.0	4
17605	Characterisation of the rumen resistome in Spanish dairy cattle. <i>Animal Microbiome</i> , 2021, 3, 63.	1.5	8
17606	Machine learning model for predicting Major Depressive Disorder using RNA-Seq data: optimization of classification approach. <i>Cognitive Neurodynamics</i> , 2022, 16, 443-453.	2.3	9
17607	Results of the Seventh Scientific Workshop of ECCO: Precision Medicine in IBD—What, Why, and How. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 1410-1430.	0.6	28
17608	MitoLink: A Generic Integrated Web-based Workflow System to Evaluate Genotype-Phenotype Correlations in Human Mitochondrial Diseases: Observations from The GenomeAsia Pilot Project. <i>Mitochondrion</i> , 2021, 61, 54-61.	1.6	0
17609	Voatriafricanines A and B, Trimeric Vobasine-Aspidosperma-Aspidosperma Alkaloids from <i>Voacanga africana</i> . <i>Journal of Natural Products</i> , 2021, 84, 2755-2761.	1.5	7
17610	Histone H3 lysine 27 acetylation profile undergoes two global shifts in undernourished children and suggests altered one-carbon metabolism. <i>Clinical Epigenetics</i> , 2021, 13, 182.	1.8	7
17611	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. <i>Gastroenterology</i> , 2021, 161, 1953-1968.e15.	0.6	14
17612	NDEx: Accessing Network Models and Streamlining Network Biology Workflows. <i>Current Protocols</i> , 2021, 1, e258.	1.3	13
17613	The Dynamic Network of RNP RNase P Subunits. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10307.	1.8	6
17614	Effects of Fluoride on Submandibular Glands of Mice: Changes in Oxidative Biochemistry, Proteomic Profile, and Genotoxicity. <i>Frontiers in Pharmacology</i> , 2021, 12, 715394.	1.6	7
17615	Bioinformatics Analysis of the MicroRNA-Metabolic Gene Regulatory Network in Neuropathic Pain and Prediction of Corresponding Potential Therapeutics. <i>Journal of Molecular Neuroscience</i> , 2021, , 1.	1.1	0
17616	New Genes Interacted With Recent Whole-Genome Duplicates in the Fast Stem Growth of Bamboos. <i>Molecular Biology and Evolution</i> , 2021, 38, 5752-5768.	3.5	28
17617	Antimelanoma Effects of Concomitant Inhibition of SIRT1 and SIRT3 in Braf/Pten Mice. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1145-1157.e7.	0.3	5
17618	The transcriptomic revolution and radiation biology. <i>International Journal of Radiation Biology</i> , 2022, 98, 428-438.	1.0	7
17621	ULK1 phosphorylation of striatin activates protein phosphatase 2A and autophagy. <i>Cell Reports</i> , 2021, 36, 109762.	2.9	23
17622	In Silico Methods for the Identification of Diagnostic and Favorable Prognostic Markers in Acute Myeloid Leukemia. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9601.	1.8	8

#	ARTICLE	IF	CITATIONS
17623	Tomato Domestication Affects Potential Functional Molecular Pathways of Root-Associated Soil Bacteria. <i>Plants</i> , 2021, 10, 1942.	1.6	10
17624	MR-PheWAS for the causal effects of serum magnesium on multiple disease outcomes in Caucasian descent. <i>IScience</i> , 2021, 24, 103191.	1.9	4
17625	COVIDrugNet: a network-based web tool to investigate the drugs currently in clinical trial to contrast COVID-19. <i>Scientific Reports</i> , 2021, 11, 19426.	1.6	4
17626	C9ORF72 Repeat Expansion Affects the Proteome of Primary Skin Fibroblasts in ALS. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10385.	1.8	6
17627	Phenotypic and Transcriptomic Responses to Stress Differ According to Population Geography in an Invasive Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	0
17628	Chemical contamination alters the interactions between bacteria and phytoplankton. <i>Chemosphere</i> , 2021, 278, 130457.	4.2	9
17629	Molecular processes mediating hyperhomocysteinemia-induced metabolic reprogramming, redox regulation and growth inhibition in endothelial cells. <i>Redox Biology</i> , 2021, 45, 102018.	3.9	16
17630	OTUB1 expression and interaction network analyses in MCF-7 breast cancer cells. <i>Gene Reports</i> , 2021, 24, 101273.	0.4	1
17631	Rambutan genome revealed gene networks for spine formation and aril development. <i>Plant Journal</i> , 2021, 108, 1037-1052.	2.8	7
17632	A 3-Gene-Based Diagnostic Signature in Alzheimer's Disease. <i>European Neurology</i> , 2022, 85, 6-13.	0.6	7
17633	Biodata Mining of Differentially Expressed Genes between Acute Myocardial Infarction and Unstable Angina Based on Integrated Bioinformatics. <i>BioMed Research International</i> , 2021, 2021, 1-19.	0.9	5
17634	Unraveling Gene Content Variation Across Eukaryotic Giant Viruses Based on Network Analyses and Host Associations. <i>Virus Evolution</i> , 2021, 7, veab081.	2.2	5
17635	DNA methylation and gene expression profiles to identify childhood atopic asthma associated genes. <i>BMC Pulmonary Medicine</i> , 2021, 21, 292.	0.8	6
17636	Transcriptome landscape of the late-stage alcohol-induced osteonecrosis of the human femoral head. <i>Bone</i> , 2021, 150, 116012.	1.4	4
17637	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phage-bacteria interplay in deep-sea snail holobionts. <i>Microbiome</i> , 2021, 9, 182.	4.9	7
17638	Self-sustaining IL-8 loops drive a prothrombotic neutrophil phenotype in severe COVID-19. <i>JCI Insight</i> , 2021, 6, .	2.3	71
17640	<i>Streptococcus pneumoniae</i> serotypes that frequently colonise the human nasopharynx are common recipients of penicillin-binding protein gene fragments from <i>Streptococcus mitis</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
17641	Bioinformatics analyses of gene expression profile identify key genes and functional pathways involved in cutaneous lupus erythematosus. <i>Clinical Rheumatology</i> , 2022, 41, 437-452.	1.0	4

#	ARTICLE	IF	CITATIONS
17642	Genome-wide analysis provides a deeper understanding of the population structure of the Salmonella enterica serotype Paratyphi B complex in Bangladesh. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
17643	Concordance of HIV transmission risk factors elucidated using viral diversification rate and phylogenetic clustering. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 338-348.	1.1	5
17644	STING nuclear partners contribute to innate immune signaling responses. <i>IScience</i> , 2021, 24, 103055.	1.9	22
17645	Multiscale Biology of Cardiovascular Risk in Psoriasis: Protocol for a Case-Control Study. <i>JMIR Research Protocols</i> , 2021, 10, e28669.	0.5	7
17646	Screening of anti-chronic nonbacterial prostatitis activity of different extractions of the aerial part of <i>Glycyrrhiza Auralensis</i> , and network pharmacology research. <i>Biomedical Reports</i> , 2021, 15, 99.	0.9	5
17647	Analysis of differentially expressed proteins between HER2 positive and triple negative breast cancer and their prognostic significance. <i>Annals of Diagnostic Pathology</i> , 2021, 55, 151834.	0.6	2
17648	CCL2 is a critical mechano-responsive mediator in crosstalk between osteoblasts and bone mesenchymal stromal cells. <i>FASEB Journal</i> , 2021, 35, e21851.	0.2	9
17649	Large-scale prospection of genes on caffeine-free <i>Coffea arabica</i> plants – Discovery of novel markers associated with development and secondary metabolism. <i>Plant Gene</i> , 2021, 27, 100314.	1.4	3
17650	HuD Regulates mRNA-circRNA-miRNA Networks in the Mouse Striatum Linked to Neuronal Development and Drug Addiction. <i>Biology</i> , 2021, 10, 939.	1.3	5
17651	Metabolite elucidation of 2-fluoro-deschloroketamine (2F- $\Delta$ DK) using molecular networking across three complementary <i>in vitro</i> and <i>in vivo</i> models. <i>Drug Testing and Analysis</i> , 2022, 14, 144-153.	1.6	15
17652	Proteomic landscape of Japanese encephalitis virus-infected fibroblasts. <i>Journal of General Virology</i> , 2021, 102, .	1.3	15
17653	Systematic Evaluation of Liquid Chromatography (LC) Column Combinations for Application in Two-Dimensional LC Metabolomic Studies. <i>Analytical Chemistry</i> , 2021, 93, 12565-12573.	3.2	8
17654	Integrative analysis of hub genes and key pathway in two subtypes of diffuse large B-cell lymphoma by bioinformatics and basic experiments. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23978.	0.9	5
17655	LysM domain-containing proteins modulate stress response and signalling in <i>Triticum aestivum</i> L.. <i>Environmental and Experimental Botany</i> , 2021, 189, 104558.	2.0	27
17656	Integrative Map of HIF1A Regulatory Elements and Variations. <i>Genes</i> , 2021, 12, 1526.	1.0	11
17657	Pan-Genome of the Genus <i>Streptomyces</i> and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. <i>Frontiers in Microbiology</i> , 2021, 12, 677558.	1.5	21
17658	Genome-Wide Identification and Transcriptional Expression Profiles of Transcription Factor WRKY in Common Walnut ( <i>Juglans regia</i> L.). <i>Genes</i> , 2021, 12, 1444.	1.0	17
17659	Identifying molecular insight of synergistic complexities for SARS-CoV-2 infection with pre-existing type 2 diabetes. <i>Computers in Biology and Medicine</i> , 2021, 136, 104668.	3.9	12

#	ARTICLE	IF	CITATIONS
17660	SnoRNAs and miRNAs Networks Underlying COVID-19 Disease Severity. <i>Vaccines</i> , 2021, 9, 1056.	2.1	22
17661	Establishment of a Ciliogenesis-Associated Signaling Model for Polycystic Kidney Disease. <i>Kidney and Blood Pressure Research</i> , 2021, , 1-9.	0.9	2
17662	HOX cluster and their cofactors showed an altered expression pattern in eutopic and ectopic endometriosis tissues. <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 132.	1.4	6
17663	Prospects and challenges of cancer systems medicine: from genes to disease networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
17664	Identification of Mutation Landscape and Immune Cell Component for Liver Hepatocellular Carcinoma Highlights Potential Therapeutic Targets and Prognostic Markers. <i>Frontiers in Genetics</i> , 2021, 12, 737965.	1.1	4
17665	Disease-induced changes in plant microbiome assembly and functional adaptation. <i>Microbiome</i> , 2021, 9, 187.	4.9	157
17666	Integrated analysis of lncRNA and mRNA in liver of <i>Megalobrama amblycephala</i> post <i>Aeromonas hydrophila</i> infection. <i>BMC Genomics</i> , 2021, 22, 653.	1.2	11
17667	The Dynamic Changes of Transcription Factors During the Development Processes of Human Biparental and Uniparental Embryos. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 709498.	1.8	4
17668	Transcriptome-wide analysis of intracranial artery in patients with moyamoya disease showing upregulation of immune response, and downregulation of oxidative phosphorylation and DNA repair. <i>Neurosurgical Focus</i> , 2021, 51, E3.	1.0	15
17670	Metabolic Profiling of Transgenic Tobacco Plants Synthesizing Bovine Interferon-Gamma. , 0, , .		1
17671	Microbial Composition and Co-occurrence Patterns in the Gut Microbial Community of Normal and Obese Mice in Response to Astaxanthin. <i>Frontiers in Microbiology</i> , 2021, 12, 671271.	1.5	5
17672	Proneural genes define ground-state rules to regulate neurogenic patterning and cortical folding. <i>Neuron</i> , 2021, 109, 2847-2863.e11.	3.8	26
17673	Effects of Naodesheng tablets on amyloid beta-induced dysfunction: A traditional Chinese herbal formula with novel therapeutic potential in Alzheimer's disease revealed by systems pharmacology. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111916.	2.5	5
17674	Proteome and Nutritional Shifts Observed in Hordein Double-Mutant Barley Lines. <i>Frontiers in Plant Science</i> , 2021, 12, 718504.	1.7	4
17675	Exploring the Potential Mechanism of Tang-Shen-Ning Decoction against Diabetic Nephropathy Based on the Combination of Network Pharmacology and Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-16.	0.5	2
17676	TNK1 is a ubiquitin-binding and 14-3-3-regulated kinase that can be targeted to block tumor growth. <i>Nature Communications</i> , 2021, 12, 5337.	5.8	14
17677	Tumor Mutation Burden-Associated LINC00638/miR-4732-3p/ULBP1 Axis Promotes Immune Escape via PD-L1 in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 729340.	1.3	17
17678	Global gene expression analysis of pigeonpea with male sterility conditioned by A 2 cytoplasm. <i>Plant Genome</i> , 2021, 14, e20132.	1.6	7

#	ARTICLE	IF	CITATIONS
17679	Time Course Transcriptomic Study Reveals the Gene Regulation During Liver Development and the Correlation With Abdominal Fat Weight in Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 723519.	1.1	9
17680	Systems Biology Applied to the Study of Papaya Fruit Ripening: The Influence of Ethylene on Pulp Softening. <i>Cells</i> , 2021, 10, 2339.	1.8	9
17681	Transcriptomic Analysis of Short/Branched-Chain Acyl-Coenzyme a Dehydrogenase Knocked Out bMECs Revealed Its Regulatory Effect on Lipid Metabolism. <i>Frontiers in Veterinary Science</i> , 2021, 8, 744287.	0.9	7
17682	Transcriptional network involving ERG and AR orchestrates Distal-less homeobox-1 mediated prostate cancer progression. <i>Nature Communications</i> , 2021, 12, 5325.	5.8	23
17684	Slow Off-Rate Modified Aptamer (SOMAmer) Proteomic Analysis of Patient-Derived Malignant Glioma Identifies Distinct Cellular Proteomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9566.	1.8	6
17685	The Construction and Analysis of ceRNA Network and Immune Infiltration in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 667610.	1.1	14
17686	Identification, evolution and expression analysis of WRKY gene family in <i>Eucommia ulmoides</i> . <i>Genomics</i> , 2021, 113, 3294-3309.	1.3	20
17687	Hybrid Deep Learning Based on a Heterogeneous Network Profile for Functional Annotations of <i>Plasmodium falciparum</i> Genes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10019.	1.8	5
17688	Defining Functions of Mannoproteins in <i>Saccharomyces cerevisiae</i> by High-Dimensional Morphological Phenotyping. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 769.	1.5	6
17689	Targeting DNA Homologous Repair Proficiency With Concomitant Topoisomerase II and c-Abl Inhibition. <i>Frontiers in Oncology</i> , 2021, 11, 733700.	1.3	4
17690	Specific Engineered G Protein Coupling to Histamine Receptors Revealed from Cellular Assay Experiments and Accelerated Molecular Dynamics Simulations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10047.	1.8	4
17691	Metagenomics Reveals That Proper Placement After Long-Distance Transportation Significantly Affects Calf Nasopharyngeal Microbiota and Is Critical for the Prevention of Respiratory Diseases. <i>Frontiers in Microbiology</i> , 2021, 12, 700704.	1.5	3
17692	Microbial communities in floodplain ecosystems in relation to altered flow regimes and experimental flooding. <i>Science of the Total Environment</i> , 2021, 788, 147497.	3.9	16
17693	mGWAS identification of six novel single nucleotide polymorphism loci with strong correlation to gastric cancer. <i>Cancer &amp; Metabolism</i> , 2021, 9, 34.	2.4	5
17694	Selenium nanoparticles ameliorate <i>Brassica napus</i> L. cadmium toxicity by inhibiting the respiratory burst and scavenging reactive oxygen species. <i>Journal of Hazardous Materials</i> , 2021, 417, 125900.	6.5	70
17696	CXCL10 and its related key genes as potential biomarkers for psoriasis. <i>Medicine (United States)</i> , 2021, 100, e27365.	0.4	7
17697	Comprehensive analyses of glycolysis-related lncRNAs for ovarian cancer patients. <i>Journal of Ovarian Research</i> , 2021, 14, 124.	1.3	22
17699	Glucocorticoid-induced Fingerprints on Visceral Adipose Tissue Transcriptome and Epigenome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 150-166.	1.8	5

#	ARTICLE	IF	CITATIONS
17701	Prediction of Biochemical Recurrence-Free Survival of Prostate Cancer Patients Leveraging Multiple Gene Expression Profiles in Tumor Microenvironment. <i>Frontiers in Oncology</i> , 2021, 11, 632571.	1.3	11
17702	Interaction Between Functionally Activate Endometrial Microbiota and Host Gene Regulation in Endometrial Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 727286.	1.8	6
17703	The landscape of accessible chromatin in quiescent cardiac fibroblasts and cardiac fibroblasts activated after myocardial infarction. <i>Epigenetics</i> , 2022, 17, 1020-1039.	1.3	12
17704	The HTLV-1 viral oncoproteins Tax and HBZ reprogram the cellular mRNA splicing landscape. <i>PLoS Pathogens</i> , 2021, 17, e1009919.	2.1	19
17705	Quantitative proteomics analysis reveals novel insights into mechanisms of action of disulfiram (DSF). <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100031.	0.8	0
17706	Limited TCR repertoire and ENTPD1 dysregulation mark late-stage COVID-19. <i>IScience</i> , 2021, 24, 103205.	1.9	12
17707	Integrative Network Pharmacology of <i>Moringa oleifera</i> Combined with Gemcitabine against Pancreatic Cancer. <i>Processes</i> , 2021, 9, 1742.	1.3	0
17708	Quantitative proteomics identifies the universally conserved ATPase Ola1p as a positive regulator of heat shock response in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101050.	1.6	6
17710	Weighted genes associated with the progression of retinoblastoma: Evidence from bioinformatic analysis. <i>Experimental Eye Research</i> , 2021, 211, 108730.	1.2	9
17711	Integrative analysis of metabolome and transcriptome reveals molecular regulatory mechanism of flavonoid biosynthesis in <i>Cyclocarya paliurus</i> under salt stress. <i>Industrial Crops and Products</i> , 2021, 170, 113823.	2.5	36
17712	Multi-omic data integration: A review of concepts, considerations, and approaches. <i>Seminars in Perinatology</i> , 2021, 45, 151456.	1.1	37
17713	Can orchid mycorrhizal fungi be persistently harbored by the plant host?. <i>Fungal Ecology</i> , 2021, 53, 101071.	0.7	10
17714	The diversity of soil mesofauna declines after bamboo invasion in subtropical China. <i>Science of the Total Environment</i> , 2021, 789, 147982.	3.9	14
17715	Comprehensive computational analysis reveals human respiratory syncytial virus encoded microRNA and host specific target genes associated with antiviral immune responses and protein binding. <i>Journal of King Saud University - Science</i> , 2021, 33, 101562.	1.6	9
17716	Dataset and analysis of molecular dynamics simulation of EpCAM ectodomain dimer. <i>Data in Brief</i> , 2021, 38, 107403.	0.5	1
17717	Integrating systematic pharmacology-based strategy and experimental validation to explore the synergistic pharmacological mechanisms of Guanxin V in treating ventricular remodeling. <i>Bioorganic Chemistry</i> , 2021, 115, 105187.	2.0	19
17718	Multitarget mechanism of Yiqi Jiedu Huayu decoction on diabetic cardiomyopathy based on network pharmacology. <i>European Journal of Integrative Medicine</i> , 2021, 47, 101388.	0.8	1
17719	Chitosan as additive affects the bacterial community, accelerates the removals of antibiotics and related resistance genes during chicken manure composting. <i>Science of the Total Environment</i> , 2021, 792, 148381.	3.9	22



#	ARTICLE	IF	CITATIONS
17720	Quantitative phosphoproteomics reveals GSK3A substrate network is involved in the cryodamage of sperm motility. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
17721	Tropical cyclone effects on water and sediment chemistry and the microbial community in estuarine ecosystems. <i>Environmental Pollution</i> , 2021, 286, 117228.	3.7	13
17722	Alkaloids from <i>Lepidium meyenii</i> (Maca), structural revision of macaridine and UPLC-MS/MS feature-based molecular networking. <i>Phytochemistry</i> , 2021, 190, 112863.	1.4	7
17723	Complex evolutionary history of felid anelloviruses. <i>Virology</i> , 2021, 562, 176-189.	1.1	13
17724	Elicitation of <i>Streptomyces lunalinharesii</i> secondary metabolism through co-cultivation with <i>Rhizoctonia solani</i> . <i>Microbiological Research</i> , 2021, 251, 126836.	2.5	6
17725	The transcriptome of saline-alkaline resistant industrial hemp ( <i>Cannabis sativa</i> L.) exposed to NaHCO <sub>3</sub> stress. <i>Industrial Crops and Products</i> , 2021, 170, 113766.	2.5	8
17726	Soybeans agroindustrial residues as <i>Staphylococcus epidermidis</i> and <i>S. aureus</i> biofilm inhibitors. <i>Industrial Crops and Products</i> , 2021, 170, 113713.	2.5	5
17727	Differential gene expression and network-based analyses of the placental transcriptome reveal distinct potential biomarkers for gestational diabetes mellitus. <i>Diabetes Research and Clinical Practice</i> , 2021, 180, 109046.	1.1	2
17728	Revealing new therapeutic opportunities in hypertension through network-driven integrative genetic analysis and drug target prediction approach. <i>Gene</i> , 2021, 801, 145856.	1.0	5
17729	Integrated omics approaches for deciphering antifungal metabolites produced by a novel <i>Bacillus</i> species, <i>B. cabrialesii</i> TE3T, against the spot blotch disease of wheat ( <i>Triticum turgidum</i> L. subsp.) Tj ETQq1 1 0.78431 4 rgBT46overload		
17730	Transcriptomics reveal triphenyltin-induced molecular toxicity in the marine mussel <i>Perna viridis</i> . <i>Science of the Total Environment</i> , 2021, 790, 148040.	3.9	7
17731	Predictive protein markers for depression severity in mood disorders: A preliminary trans-diagnostic approach study. <i>Journal of Psychiatric Research</i> , 2021, 142, 63-72.	1.5	5
17732	Aircraft noise exposure drives the activation of white blood cells and induces microvascular dysfunction in mice. <i>Redox Biology</i> , 2021, 46, 102063.	3.9	18
17733	Oxylipin responses to fasting and insulin infusion in a large mammalian model of fasting-induced insulin resistance, the northern elephant seal. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2021, 321, R537-R546.	0.9	0
17734	MTDH associates with m6A RNA methylation and predicts cancer response for immune checkpoint treatment. <i>IScience</i> , 2021, 24, 103102.	1.9	4
17735	Erianin, the main active ingredient of <i>Dendrobium chrysotoxum</i> Lindl, inhibits precancerous lesions of gastric cancer (PLGC) through suppression of the HRAS-PI3K-AKT signaling pathway as revealed by network pharmacology and in vitro experimental verification. <i>Journal of Ethnopharmacology</i> , 2021, 279, 114399.	2.0	38
17736	Polypharmacy-associated risk of hospitalisation among people ageing with and without HIV: an observational study. <i>The Lancet Healthy Longevity</i> , 2021, 2, e639-e650.	2.0	18
17737	Transcriptomic analyses and experimental verification reveal potential biomarkers and biological pathways of urinary tract infection. <i>Bioengineered</i> , 2021, 12, 8529-8539.	1.4	2

#	ARTICLE	IF	CITATIONS
17738	Soil microbial community and association network shift induced by several tall fescue cultivars during the phytoremediation of a petroleum hydrocarbon-contaminated soil. <i>Science of the Total Environment</i> , 2021, 792, 148411.	3.9	24
17739	CD151 enrichment in exosomes of luminal androgen receptor breast cancer cell line contributes to cell invasion. <i>Biochimie</i> , 2021, 189, 65-75.	1.3	4
17740	Environmental level bisphenol A accelerates alterations of the reno-cardiac axis by the MAPK cascades in male diabetic rats: An analysis based on transcriptomic profiling and bioinformatics. <i>Environmental Pollution</i> , 2021, 287, 117671.	3.7	3
17741	Disentangling the distinct mechanisms shaping the subsurface oil reservoir bacterial and archaeal communities across northern China. <i>Science of the Total Environment</i> , 2021, 789, 148074.	3.9	8
17742	Concentration-dependent transcriptome of zebrafish larvae for environmental bisphenol S assessment. <i>Ecotoxicology and Environmental Safety</i> , 2021, 223, 112574.	2.9	3
17743	Transcriptomic response of the intertidal limpet <i>Patella vulgata</i> to temperature extremes. <i>Journal of Thermal Biology</i> , 2021, 101, 103096.	1.1	4
17744	Organic manure induced soil food web of microbes and nematodes drive soil organic matter under jackfruit planting. <i>Applied Soil Ecology</i> , 2021, 166, 103994.	2.1	19
17745	Placental Changes in the serotonin transporter ( <i>Slc6a4</i> ) knockout mouse suggest a role for serotonin in controlling nutrient acquisition. <i>Placenta</i> , 2021, 115, 158-168.	0.7	8
17746	A Key Silencing Histone Mark on Chromatin Is Lost When Colorectal Adenocarcinoma Cells Are Depleted of Methionine by Methionine <sup>13</sup> -Lyase. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 735303.	1.6	7
17747	Genome-Wide Identification and Low-Temperature Expression Analysis of bHLH Genes in <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 2021, 12, 762135.	1.1	15
17748	Identification, expression, and functional analysis of <i>Hsf</i> and <i>Hsp20</i> gene families in <i>Brachypodium distachyon</i> under heat stress. <i>PeerJ</i> , 2021, 9, e12267.	0.9	5
17749	Exploring the mechanisms of anti-ovarian cancer of <i>Hedyotis diffusa</i> Willd and <i>Scutellaria barbata</i> D. Don through focal adhesion pathway. <i>Journal of Ethnopharmacology</i> , 2021, 279, 114343.	2.0	17
17750	Dipteran endoparasitoid infestation actively suppressed host defense components in hemocytes of silkworm <i>Bombyx mori</i> for successful parasitism. <i>Animal Gene</i> , 2021, 22, 200118.	0.2	7
17751	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. <i>BMC Biology</i> , 2021, 19, 219.	1.7	21
17752	DNA Repair and Immune Response Pathways Are Deregulated in Melanocyte-Keratinocyte Co-cultures Derived From the Healthy Skin of Familial Melanoma Patients. <i>Frontiers in Medicine</i> , 2021, 8, 692341.	1.2	2
17754	The proximal proteome of 17 SARS-CoV-2 proteins links to disrupted antiviral signaling and host translation. <i>PLoS Pathogens</i> , 2021, 17, e1009412.	2.1	27
17755	The profile analysis of circular RNAs in cervical cancer. <i>Medicine (United States)</i> , 2021, 100, e27404.	0.4	5
17756	Study on the Mechanism of <i>Salvia miltiorrhiza</i> in the Treatment of Traumatic Bone Defects. <i>Journal of Chemistry</i> , 2021, 2021, 1-9.	0.9	2

#	ARTICLE	IF	CITATIONS
17757	A time-resolved transcriptome landscape of the developing mouse ovary. <i>Biochemical and Biophysical Research Communications</i> , 2021, 572, 57-64.	1.0	3
17758	Transcriptomic study of the mechanism by which the Kai Yu Zhong Yu recipe improves oocyte quality in a stressed mouse model. <i>Journal of Ethnopharmacology</i> , 2021, 278, 114298.	2.0	1
17759	Post mortem changes in M. iliobialis lateralis muscle protein profile of emu ( <i>Dromaius</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,662 Td (n	2.7	2
17760	Comparative transcriptome analysis of the molecular mechanism underlying the golden red colour in mutant Taiwanese loach. <i>Aquaculture</i> , 2021, 543, 736979.	1.7	12
17761	Applying cooperative module pair analysis to uncover compatibility mechanism of Fangjis: An example of Wenxin Keli decoction. <i>Journal of Ethnopharmacology</i> , 2021, 278, 114214.	2.0	7
17762	Liming alters microbial community composition and its co-occurrence patterns in Cd- and Pb-contaminated agricultural soil. <i>Applied Soil Ecology</i> , 2021, 166, 104064.	2.1	20
17763	Characterization and correlation of microbial communities and metabolite and volatile compounds in doenjang fermentation. <i>Food Research International</i> , 2021, 148, 110645.	2.9	33
17764	Soil properties have more significant effects on the community composition of protists than the rhizosphere effect of rice plants in alkaline paddy field soils. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108397.	4.2	21
17765	Specific network and phyllosymbiosis pattern in endophyte community of coastal halophytes. <i>Fungal Ecology</i> , 2021, 53, 101088.	0.7	3
17766	Colonization by dark septate endophytes improves the growth and rhizosphere soil microbiome of licorice plants under different water treatments. <i>Applied Soil Ecology</i> , 2021, 166, 103993.	2.1	16
17767	Drivers and ecological consequences of arsenite detoxification in aged semi-aerobic landfill. <i>Journal of Hazardous Materials</i> , 2021, 420, 126597.	6.5	10
17768	Transcriptome analysis of human neural cells derived from isogenic embryonic stem cells with 16p11.2 deletion. <i>Neuroscience Research</i> , 2021, 171, 114-123.	1.0	2
17769	Characterization of the Zebrafish Cell Landscape at Single-Cell Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 743421.	1.8	42
17770	A network understanding of FinTech (in)capabilities in the global South. <i>Applied Geography</i> , 2021, 135, 102538.	1.7	7
17771	Targeting cathepsins: A potential link between COVID-19 and associated neurological manifestations. <i>Heliyon</i> , 2021, 7, e08089.	1.4	11
17772	Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021, 374, eabf3067.	6.0	29
17773	Identification of key genes in osteosarcoma " before and after CDK7 treatment. <i>Medicine (United Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	6.4	0
17774	Bacterial diversity and community composition changes in paddy soils that have different parent materials and fertility levels. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2797-2806.	1.7	8

#	ARTICLE	IF	CITATIONS
17775	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. <i>Science Bulletin</i> , 2021, 66, 2014-2024.	4.3	6
17776	Groundwater contaminated with short-chain chlorinated paraffins and microbial responses. <i>Water Research</i> , 2021, 204, 117605.	5.3	12
17777	Comparative transcriptome analysis to identify fruit coloration-related genes of late-ripening litchi mutants and their wild type. <i>Scientia Horticulturae</i> , 2021, 288, 110369.	1.7	2
17778	Muscles proteome analysis; irisin administration mimics some molecular effects of exercise in quadriceps muscle. <i>Biochimie</i> , 2021, 189, 144-157.	1.3	8
17779	Protective effects of cannabidiol on the membrane proteins of skin keratinocytes exposed to hydrogen peroxide via participation in the proteostasis network. <i>Redox Biology</i> , 2021, 46, 102074.	3.9	10
17780	Extracellular Vesicle Proteomes Shed Light on the Evolutionary, Interactive, and Functional Divergence of Their Biogenesis Mechanisms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 734950.	1.8	7
17781	Impact of dimethylpyrazole-based nitrification inhibitors on soil-borne bacteria. <i>Science of the Total Environment</i> , 2021, 792, 148374.	3.9	18
17782	Transcriptome analysis of immune response in recombinant cell vaccine expressing OmpK vaccinated juvenile seabass ( <i>lates calcarifer</i> ) head kidney against <i>vibrio harveyi</i> infection. <i>Aquaculture Reports</i> , 2021, 21, 100799.	0.7	4
17783	Integrated small RNA, mRNA, and degradome sequencing reveals the important role of miRNAs in the interactions between parasitic plant <i>Cuscuta australis</i> and its host <i>Trifolium repens</i> . <i>Scientia Horticulturae</i> , 2021, 289, 110458.	1.7	5
17784	Detecting imperative genes and infiltrating immune cells in chronic Chagas cardiomyopathy by bioinformatics analysis. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105079.	1.0	4
17785	Cannabinoids vs. whole metabolome: Relevance of cannabinomics in analyzing Cannabis varieties. <i>Analytica Chimica Acta</i> , 2021, 1184, 339020.	2.6	16
17786	Impact of carbon/nitrogen ratio on the performance and microbial community of sequencing batch biofilm reactor treating synthetic mariculture wastewater. <i>Journal of Environmental Management</i> , 2021, 298, 113528.	3.8	35
17787	Arbuscular mycorrhizal fungi and goethite promote carbon sequestration via hyphal-aggregate mineral interactions. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108417.	4.2	31
17788	Analysis of the proximal promoter of the human colon-specific B4GALNT2 (Sda synthase) gene: B4GALNT2 is transcriptionally regulated by ETS1. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194747.	0.9	4
17789	A candidate biological network formed by genes from genomic and hypothesis-free scans of suicide. <i>Preventive Medicine</i> , 2021, 152, 106604.	1.6	4
17790	Transcriptional characterization of subcutaneous adipose tissue in obesity affected women highlights metabolic dysfunction and implications for lncRNAs. <i>Genomics</i> , 2021, 113, 3919-3934.	1.3	3
17791	Longitudinal change of genetic variations in cetuximab-treated metastatic colorectal cancer. <i>Cancer Genetics</i> , 2021, 258-259, 27-36.	0.2	2
17792	Characterization of eukaryotic microbiome and associated bacteria communities in a drinking water treatment plant. <i>Science of the Total Environment</i> , 2021, 797, 149070.	3.9	9

#	ARTICLE	IF	CITATIONS
17793	Ecological network analysis reveals distinctive microbial modules associated with heavy metal contamination of abandoned mine soils in Korea. <i>Environmental Pollution</i> , 2021, 289, 117851.	3.7	49
17794	Epiphytic <i>Acampe ochracea</i> orchid relieves paracetamol-induced hepatotoxicity by inhibiting oxidative stress and upregulating antioxidant genes in in vivo and virtual screening. <i>Biomedicine and Pharmacotherapy</i> , 2021, 143, 112215.	2.5	13
17795	Genome-wide analysis of the MYB-related transcription factor family and associated responses to abiotic stressors in <i>Populus</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 191, 359-376.	3.6	21
17796	Genomics-guided targeting of stress granule proteins G3BP1/2 to inhibit SARS-CoV-2 propagation. <i>International Journal of Biological Macromolecules</i> , 2021, 190, 636-648.	3.6	13
17797	Seasonal variations in soil physicochemical properties and microbial community structure influenced by <i>Spartina alterniflora</i> invasion and <i>Kandelia obovata</i> restoration. <i>Science of the Total Environment</i> , 2021, 797, 149213.	3.9	25
17798	PIK3CB is involved in metastasis through the regulation of cell adhesion to collagen I in pancreatic cancer. <i>Journal of Advanced Research</i> , 2021, 33, 127-140.	4.4	19
17799	Micro-encapsulated grape pomace extract (MGPE) as a feed additive improves growth performance, antioxidant capacity, and shifts the gut microbiome of rainbow trout. <i>Aquaculture</i> , 2021, 544, 737129.	1.7	8
17800	Single cell functional genomics reveals plasticity of subcutaneous white adipose tissue (WAT) during early postnatal development. <i>Molecular Metabolism</i> , 2021, 53, 101307.	3.0	14
17801	Computational investigation of FDA approved drugs as selective PARP-1 inhibitors by targeting BRCT domain for cancer therapy. <i>Journal of Molecular Graphics and Modelling</i> , 2021, 108, 107919.	1.3	2
17802	Genomic and transcriptomic inventory of membrane transporters in coffee: Exploring molecular mechanisms of metabolite accumulation. <i>Plant Science</i> , 2021, 312, 111018.	1.7	3
17803	Pharmacological validation of <i>Solanum mammosum</i> L. as an anti-infective agent: Role of solamargine. <i>Journal of Ethnopharmacology</i> , 2021, 280, 114473.	2.0	8
17804	Evolutionarily conserved transcriptional landscape of the heart defining the chamber specific physiology. <i>Genomics</i> , 2021, 113, 3782-3792.	1.3	1
17805	BZD9L1 sirtuin inhibitor: Identification of key molecular targets and their biological functions in HCT 116 colorectal cancer cells. <i>Life Sciences</i> , 2021, 284, 119747.	2.0	7
17806	Quantitative proteomic analysis uncovers inhibition of melanin synthesis by silk fibroin via MITF/tyrosinase axis in B16 melanoma cells. <i>Life Sciences</i> , 2021, 284, 119930.	2.0	8
17807	Introduction of <i>Trichoderma</i> spp. biocontrol strains against <i>Sclerotinia sclerotiorum</i> (Lib.) de Bary change soil microbial community composition in common bean ( <i>Phaseolus vulgaris</i> L.) cultivation. <i>Biological Control</i> , 2021, 163, 104755.	1.4	4
17808	Identification and expression analysis of miRNAs in germination and seedling growth of Tibetan hulless barley. <i>Genomics</i> , 2021, 113, 3735-3749.	1.3	9
17809	Integrating GC-MS and ssRNA-Seq analysis to identify long non-coding RNAs related to terpenoid biosynthesis in <i>Cinnamomum camphora</i> . <i>Industrial Crops and Products</i> , 2021, 171, 113875.	2.5	8
17810	Biochar-based fertilizer amendments improve the soil microbial community structure in a karst mountainous area. <i>Science of the Total Environment</i> , 2021, 794, 148757.	3.9	75

#	ARTICLE	IF	CITATIONS
17811	Identification and characterization of circRNAs in the liver of blunt snout bream ( <i>Megalobrama</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 2021, 124, 104185.	1.0	16
17812	Distinct transcriptomic profiles of naïve CD4+ T cells distinguish HIV-1 infected patients initiating antiretroviral therapy at acute or chronic phase of infection. <i>Genomics</i> , 2021, 113, 3487-3500.	1.3	6
17813	Effects of design parameters, microbial community and nitrogen removal on the field-scale multi-pond constructed wetlands. <i>Science of the Total Environment</i> , 2021, 797, 148989.	3.9	14
17814	Prognostic molecular markers for motor recovery in acute hemorrhagic stroke: A systematic review. <i>Clinica Chimica Acta</i> , 2021, 522, 45-60.	0.5	3
17815	Transcriptome analysis of hepatopancreas from different living states oriental river prawn ( <i>Macrobrachium nipponense</i> ) in response to hypoxia. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100902.	0.4	7
17816	Integrative analysis reveals clinically relevant molecular fingerprints in pancreatic cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 11-21.	2.3	3
17817	Systems level insights into the impact of airborne exposure on SARS-CoV-2 pathogenesis and COVID-19 outcome – A multi-omics big data study. <i>Gene Reports</i> , 2021, 25, 101312.	0.4	4
17818	Salivary miRNA-21 expression as a potential non-invasive diagnostic biomarker in breast cancer. <i>Gene Reports</i> , 2021, 25, 101317.	0.4	8
17819	Effects of chronic exposure to environmental levels of tributyltin on the lined seahorse ( <i>Hippocampus erectus</i> ) liver: Analysis of bioaccumulation, antioxidant defense, and immune gene expression. <i>Science of the Total Environment</i> , 2021, 801, 149646.	3.9	16
17820	Deciphering functional biomolecule potential of marine diatoms through complex network approach. <i>Bioresource Technology</i> , 2021, 342, 125927.	4.8	2
17821	Systematic mapping of R-group space enables the generation of an R-group replacement system for medicinal chemistry. <i>European Journal of Medicinal Chemistry</i> , 2021, 225, 113771.	2.6	6
17822	Localized reshaping of the fungal community in response to a forest fungal pathogen reveals resilience of Mediterranean mycobiota. <i>Science of the Total Environment</i> , 2021, 800, 149582.	3.9	7
17823	Elevation-related climate trends dominate fungal co-occurrence network structure and the abundance of keystone taxa on Mt. Norikura, Japan. <i>Science of the Total Environment</i> , 2021, 799, 149368.	3.9	17
17824	Transcriptome analysis reveals key genes and pathways associated with egg production in Nandan-Yao domestic chicken. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100889.	0.4	13
17825	Effects of low temperatures on the conformation of apo-lactoferrin and its interactions with $\beta$ -lactalbumin and $\beta$ -lactoglobulin: Application of in silico approaches. <i>Food Hydrocolloids</i> , 2021, 121, 107055.	5.6	6
17826	Almost famous: Human adenoviruses (and what they have taught us about cancer). <i>Tumour Virus Research</i> , 2021, 12, 200225.	1.5	11
17827	Systems biology under heat stress in Indian cattle. <i>Gene</i> , 2021, 805, 145908.	1.0	4
17828	Integrative analysis of potential biomarkers and immune cell infiltration in Parkinson's disease. <i>Brain Research Bulletin</i> , 2021, 177, 53-63.	1.4	5



#	ARTICLE	IF	CITATIONS
17829	Three-compartment septic tanks as sustainable on-site treatment facilities? Watch out for the potential dissemination of human-associated pathogens and antibiotic resistance. <i>Journal of Environmental Management</i> , 2021, 300, 113709.	3.8	12
17830	Differential protein expression due to Se deficiency and Se toxicity in rat liver. <i>Journal of Nutritional Biochemistry</i> , 2021, 98, 108831.	1.9	8
17831	Bacterial community demonstrates stronger network connectivity than fungal community in desert-grassland salt marsh. <i>Science of the Total Environment</i> , 2021, 798, 149118.	3.9	24
17832	Optimal start-up conditions for the efficient treatment of acid mine drainage using sulfate-reducing bioreactors based on physicochemical and microbiome analyses. <i>Journal of Hazardous Materials</i> , 2022, 423, 127089.	6.5	15
17833	Linking microbial community composition to farming pattern in selenium-enriched region: Potential role of microorganisms on Se geochemistry. <i>Journal of Environmental Sciences</i> , 2022, 112, 269-279.	3.2	9
17834	Gut interkingdom predator-prey interactions are key determinants of shrimp health. <i>Aquaculture</i> , 2022, 546, 737304.	1.7	15
17835	Effect of polysaccharide fractions from <i>Fortunella margarita</i> on the fecal microbiota of mice and SCFA production in vitro. <i>Food Science and Human Wellness</i> , 2022, 11, 97-108.	2.2	13
17836	Network pharmacology-based study on immunomodulatory mechanism of danggui-yimucao herb pair for the treatment of RU486-induced abortion. <i>Journal of Ethnopharmacology</i> , 2022, 282, 114609.	2.0	4
17837	Transcriptomic analysis of the immune response against <i>A. hydrophila</i> infection in striped catfish <i>Pangasianodon hypophthalmus</i> . <i>Aquaculture</i> , 2022, 547, 737446.	1.7	4
17838	Metagenomic insights into the profile of antibiotic resistomes in sediments of aquaculture wastewater treatment system. <i>Journal of Environmental Sciences</i> , 2022, 113, 345-355.	3.2	33
17839	Computational modeling predicts potential effects of the herbal infusion <i>Æthorchata</i> against COVID-19. <i>Food Chemistry</i> , 2022, 366, 130589.	4.2	18
17840	Phytoremediation of cadmium-contaminated sediment using <i>Hydrilla verticillata</i> and <i>Elodea canadensis</i> harbor two same keystone rhizobacteria <i>Pedospaeraceae</i> and <i>Parasegetibacter</i> . <i>Chemosphere</i> , 2022, 286, 131648.	4.2	22
17841	Fatty acid profile as an efficient bioindicator of PCB bioaccumulation in a freshwater lake food web: A stable isotope guided investigation. <i>Journal of Hazardous Materials</i> , 2022, 423, 127121.	6.5	10
17842	Demonstration of an aggregated biomarker response approach to assess the impact of point and diffuse contaminant sources in feral fish in a small river case study. <i>Science of the Total Environment</i> , 2022, 804, 150020.	3.9	4
17843	Improvements of immune genes and intestinal microbiota composition of turbot ( <i>Scophthalmus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	19
17844	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. <i>Science of the Total Environment</i> , 2022, 805, 150372.	3.9	15
17845	Effect of external acetate on lactate-based carboxylate platform: Shifted lactate overloading limit and hydrogen co-production. <i>Science of the Total Environment</i> , 2022, 802, 149885.	3.9	13
17846	Land-use affects soil microbial co-occurrence networks and their putative functions. <i>Applied Soil Ecology</i> , 2022, 169, 104184.	2.1	32

#	ARTICLE	IF	CITATIONS
17847	Microbiota associated with the rhizosphere of <i>Paeonia lactiflora</i> Pall. (ornamental cultivar). <i>Applied Soil Ecology</i> , 2022, 169, 104214.	2.1	9
17848	Insight of bacteria and archaea in Feammox community enriched from different soils. <i>Environmental Research</i> , 2022, 203, 111802.	3.7	22
17849	Fumigation practice combined with organic fertilizer increase antibiotic resistance in watermelon rhizosphere soil. <i>Science of the Total Environment</i> , 2022, 805, 150426.	3.9	7
17850	Scalable Scalable Vector Graphics: Automatic Translation of Interactive SVGs to a Multithread VDOM for Fast Rendering. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2022, 28, 3219-3234.	2.9	7
17851	Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis. <i>AIMS Neuroscience</i> , 2021, 8, 254-283.	1.0	7
17852	Network Analysis Reveals Proteins Associated with Aortic Dilatation in Mucopolysaccharidoses. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 34-43.	2.2	3
17854	Integrated Weighted Gene Co-expression Network Analysis Identified That TLR2 and CD40 Are Related to Coronary Artery Disease. <i>Frontiers in Genetics</i> , 2020, 11, 613744.	1.1	9
17856	Subcutaneous and intramuscular fat transcriptomes show large differences in network organization and associations with adipose traits in pigs. <i>Science China Life Sciences</i> , 2021, 64, 1732-1746.	2.3	19
17857	Assessing the genetic impact of <i>Enterococcus faecalis</i> infection on gastric cell line MKN74. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	0
17858	Region-Specific Network Analysis Reveals That Epigenetic Modifications Outside Transcriptional Start Sites Are Tightly Linked to mRNA. <i>IEEE Access</i> , 2021, 9, 17041-17048.	2.6	0
17859	Glutamine Uptake via SNAT6 and Caveolin Regulates Glutamineâ€“Glutamate Cycle. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1167.	1.8	16
17860	Seasonal Changes in <i>Pinus tabulaeformis</i> Root-Associated Fungal Microbiota Drive N and P Cycling in Terrestrial Ecosystem. <i>Frontiers in Microbiology</i> , 2020, 11, 526898.	1.5	13
17861	The mutational repertoire of uterine sarcomas and carcinosarcomas in a Brazilian cohort: A preliminary study. <i>Clinics</i> , 2021, 76, e2324.	0.6	6
17863	SOX4 maintains the stemness of cancer cells via transcriptionally enhancing HDAC1 revealed by comparative proteomics study. <i>Cell and Bioscience</i> , 2021, 11, 23.	2.1	20
17864	Effects of maternal immune activation in porcine transcript isoforms of neuropeptide and receptor genes. <i>Journal of Integrative Neuroscience</i> , 2021, 20, 21.	0.8	10
17865	Inoculation of <i>Mimosa pudica</i> with <i>Paraburkholderia phymatum</i> ; Results in Changes to the Rhizoplane Microbial Community Structure. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
17866	Qualitative and Quantitative Shotgun Proteomics Data Analysis from Data-Dependent Acquisition Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2259, 297-308.	0.4	19
17867	Massâ€“spectrometry analysis of the human pineal proteome during night and day and in autism. <i>Journal of Pineal Research</i> , 2021, 70, e12713.	3.4	4

#	ARTICLE	IF	CITATIONS
17868	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. <i>Scientific Data</i> , 2021, 8, 10.	2.4	12
17869	Intake of Natural Compounds and Circulating microRNA Expression Levels: Their Relationship Investigated in Healthy Subjects With Different Dietary Habits. <i>Frontiers in Pharmacology</i> , 2020, 11, 619200.	1.6	32
17870	Transcriptome analysis and postharvest behavior of the kiwifruit <i>Actinidia deliciosa</i> ™ reveal the role of ethylene-related phytohormones during fruit ripening. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	15
17871	Prediction of Human-Plasmodium vivax Protein Associations From Heterogeneous Network Structures Based on Machine-Learning Approach. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110133.	1.0	9
17872	Integrated analysis of mRNA and miRNA profiles revealed the role of miR-193 and miR-210 as potential regulatory biomarkers in different molecular subtypes of breast cancer. <i>BMC Cancer</i> , 2021, 21, 76.	1.1	12
17873	Bioinformatics analysis identified MMP14 and COL12A1 as immune-related biomarkers associated with pancreatic adenocarcinoma prognosis. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 5921-5942.	1.0	12
17874	Loss of FLCN-FNIP1/2 induces a non-canonical interferon response in human renal tubular epithelial cells. <i>ELife</i> , 2021, 10, .	2.8	15
17875	Spatiotemporal Gene Expression Profiling and Network Inference: A Roadmap for Analysis, Visualization, and Key Gene Identification. <i>Methods in Molecular Biology</i> , 2021, 2328, 47-65.	0.4	2
17877	Identification of Potential Risk Genes and the Immune Landscape of Idiopathic Pulmonary Arterial Hypertension via Microarray Gene Expression Dataset Reanalysis. <i>Genes</i> , 2021, 12, 125.	1.0	7
17878	Exploring the underlying mechanism of action of a traditional Chinese medicine formula, Youdujing ointment, for cervical cancer treatment. <i>Quantitative Biology</i> , 2021, 9, 292-303.	0.3	4
17879	rANOMALY: AmplicoN wOrkflow for Microbial community AnaLYsis. <i>F1000Research</i> , 2021, 10, 7.	0.8	23
17880	Identification of potential therapeutic target of naringenin in breast cancer stem cells inhibition by bioinformatics and in vitro studies. <i>Saudi Pharmaceutical Journal</i> , 2021, 29, 12-26.	1.2	26
17881	Systemic immune microenvironment and regulatory network analysis in patients with lung adenocarcinoma. <i>Translational Cancer Research</i> , 2021, 10, 2859-2872.	0.4	5
17882	Identification of Seven Cell Cycle-Related Genes with Unfavorable Prognosis and Construction of their TF-miRNA-mRNA regulatory network in Breast Cancer. <i>Journal of Cancer</i> , 2021, 12, 740-753.	1.2	15
17883	Comprehensive computational target fishing approach to identify Xanthorrhizol putative targets. <i>Scientific Reports</i> , 2021, 11, 1594.	1.6	17
17884	Exploring the Active Components of Simotang Oral Liquid and Their Potential Mechanism of Action on Gastrointestinal Disorders by Integrating Ultrahigh-Pressure Liquid Chromatography Coupled with Linear Ion Trap-Orbitrap Analysis and Network Pharmacology. <i>ACS Omega</i> , 2021, 6, 2354-2366.	1.6	6
17885	Control of SRC molecular dynamics encodes distinct cytoskeletal responses by specifying signaling pathway usage. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	7
17886	Differential gene expression in duodenum of colored broiler chicken divergently selected for residual feed intake. <i>Tropical Animal Health and Production</i> , 2021, 53, 59.	0.5	1

#	ARTICLE	IF	CITATIONS
17887	The anti-inflammatory mechanism of the medicinal fungus puffball analysis based on network pharmacology. <i>Informatics in Medicine Unlocked</i> , 2021, 23, 100549.	1.9	3
17888	Fly-over phylogeny across invertebrate to vertebrate: The giant panda and insects share a highly similar gut microbiota. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4676-4683.	1.9	7
17889	Usage of Metatranscriptomics to Understand Disease. <i>Methods in Molecular Biology</i> , 2021, 2327, 191-204.	0.4	0
17890	Identification of hub genes with prognostic values in multiple myeloma by bioinformatics analysis. <i>Hematology</i> , 2021, 26, 453-459.	0.7	5
17891	Predicting Genotype Information Related to COVID-19 for Molecular Mechanism Based on Computational Methods. <i>CMES - Computer Modeling in Engineering and Sciences</i> , 2021, 129, 31-45.	0.8	2
17892	Transcriptome landscapes of differentially expressed genes related to fat deposits in Nandan-Yao chicken. <i>Functional and Integrative Genomics</i> , 2021, 21, 113-124.	1.4	14
17893	Gene Expression Microarray: Technical Fundamentals and Data Analysis. , 2021, , 291-312.		3
17894	FAK regulates IL-33 expression by controlling chromatin accessibility at c-Jun motifs. <i>Scientific Reports</i> , 2021, 11, 229.	1.6	14
17895	Mapping the landscape of synthetic lethal interactions in liver cancer. <i>Theranostics</i> , 2021, 11, 9038-9053.	4.6	10
17896	Autosomal recessive variants in TUBGCP2 alter the $\beta$ -tubulin ring complex leading to neurodevelopmental disease. <i>iScience</i> , 2021, 24, 101948.	1.9	6
17897	Comprehensive analysis of alternative splicing profiling reveals novel events associated with prognosis and the infiltration of immune cells in prostate cancer. <i>Translational Andrology and Urology</i> , 2021, 10, 3056-3068.	0.6	2
17898	Identification of COVID-19 Related Fake News via Neural Stacking. <i>Communications in Computer and Information Science</i> , 2021, , 177-188.	0.4	6
17899	A disorder-related variant (E420K) of a PP2A-regulatory subunit (PPP2R5D) causes constitutively active AKT-mTOR signaling and uncoordinated cell growth. <i>Journal of Biological Chemistry</i> , 2021, 296, 100313.	1.6	18
17900	Modulation of SETDB1 activity by APQ ameliorates heterochromatin condensation, motor function, and neuropathology in a Huntington's disease mouse model. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2021, 36, 856-868.	2.5	7
17901	Mucociliary Respiratory Epithelium Integrity in Molecular Defense and Susceptibility to Pulmonary Viral Infections. <i>Biology</i> , 2021, 10, 95.	1.3	31
17902	Beyond adverse outcome pathways: making toxicity predictions from event networks, SAR models, data and knowledge. <i>Toxicology Research</i> , 2021, 10, 102-122.	0.9	9
17903	A Protocol for Isolation, Purification, Characterization, and Functional Dissection of Exosomes. <i>Methods in Molecular Biology</i> , 2021, 2261, 105-149.	0.4	33
17904	Identification of tumor mutation burden-related hub genes and the underlying mechanism in melanoma. <i>Journal of Cancer</i> , 2021, 12, 2440-2449.	1.2	10

#	ARTICLE	IF	CITATIONS
17905	Protective effect of <i>Ganoderma lucidum</i> spore extract in trimethylamine-N-oxide induced cardiac dysfunction in rats. <i>Journal of Food Science</i> , 2021, 86, 546-562.	1.5	20
17906	Construction of lncRNA-related ceRNA regulatory network in diabetic subdermal endothelial cells. <i>Bioengineered</i> , 2021, 12, 2592-2602.	1.4	17
17907	Label-Free Comparative Proteomics Analysis Revealed Heat Stress Responsive Mechanism in <i>Hypsizygus marmoreus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 541967.	1.5	16
17908	Extracellular vesicle-encapsulated microRNA-424 exerts inhibitory function in ovarian cancer by targeting MYB. <i>Journal of Translational Medicine</i> , 2021, 19, 4.	1.8	21
17909	Differential contribution of transcriptomic regulatory layers in the definition of neuronal identity. <i>Nature Communications</i> , 2021, 12, 335.	5.8	20
17910	Genome-Wide Phylogenetic Analysis, Expression Pattern, and Transcriptional Regulatory Network of the Pig C/EBP Gene Family. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110413.	0.6	0
17911	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021, 184, 334-351.e20.	13.5	78
17912	Alterations in microbiota and their metabolites are associated with beneficial effects of bile acid sequestrant on icteric primary biliary Cholangitis. <i>Gut Microbes</i> , 2021, 13, 1946366.	4.3	25
17913	Tripartite collaboration of blood-derived endothelial cells, next generation scRNA sequencing and bioengineered vessel chip may distinguish vasculopathy and thrombosis among sickle cell disease patients. <i>Bioengineering and Translational Medicine</i> , 2021, 6, e10211.	3.9	10
17914	Single-cell transcriptomic profiling provides insights into the toxic effects of Zearalenone exposure on primordial follicle assembly. <i>Theranostics</i> , 2021, 11, 5197-5213.	4.6	24
17915	Comprehensive genomic resources related to domestication and crop improvement traits in Lima bean. <i>Nature Communications</i> , 2021, 12, 702.	5.8	39
17916	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. <i>Journal of Physical Chemistry B</i> , 2021, 125, 850-873.	1.2	66
17917	Heterotrimeric G-protein $\beta$ subunit (RGA1) regulates tiller development, yield, cell wall, nitrogen response and biotic stress in rice. <i>Scientific Reports</i> , 2021, 11, 2323.	1.6	14
17919	Protein-protein interaction network analysis applied to DNA copy number profiling suggests new perspectives on the aetiology of Mayer-Rokitansky-Kuster-Hauser syndrome. <i>Scientific Reports</i> , 2021, 11, 448.	1.6	13
17920	Gene regulatory networks for compatible versus incompatible grafts identify a role for SIWOX4 during junction formation. <i>Plant Cell</i> , 2022, 34, 535-556.	3.1	24
17921	Determination of hypoxia signature to predict prognosis and the tumor immune microenvironment in melanoma. <i>Molecular Omics</i> , 2021, 17, 307-316.	1.4	20
17922	Comparative modelling unravels the structural features of eukaryotic TCTP implicated in its multifunctional properties: an in silico approach. <i>Journal of Molecular Modeling</i> , 2021, 27, 20.	0.8	5
17923	Protein-Protein Interaction Network for the Identification of New Targets Against Novel Coronavirus. <i>Methods in Pharmacology and Toxicology</i> , 2021, , 213-230.	0.1	5

#	ARTICLE	IF	CITATIONS
17924	A Systemic Storm in Critically Injured Humans Revealed by Longitudinal Multi-Omics. SSRN Electronic Journal, 0, , .	0.4	0
17925	Expression Profiles Reveal Involvement of VEGF, IGF1, BIRC5, and MMP1 in Vulvar Carcinogenesis. Technology in Cancer Research and Treatment, 2021, 20, 153303382110049.	0.8	1
17926	Profiles of alternative splicing events in the diagnosis and prognosis of Gastric Cancer. Journal of Cancer, 2021, 12, 2982-2992.	1.2	0
17927	Genome analysis and identification of key pathway in visceral adipose tissue from obesity-related diabetes. , 2021, , .		0
17928	Study on Differential Expression Genes in HCC Based on GEO Database. , 2021, , .		2
17929	Conservation Genetics in the Neotropical Carnivorous Mammals: A Systematic Review. , 2021, , 277-295.		0
17930	Inferring Phylogenomic Relationship of Microbes Using Scalable Alignment-Free Methods. Methods in Molecular Biology, 2021, 2242, 69-76.	0.4	4
17931	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	5
17932	Learning Biomedical Networks: Toward Data-Informed Clinical Decision and Therapy. Computational Biology, 2021, , 77-92.	0.1	0
17933	DUSP7 regulates the activity of ERK2 to promote proper chromosome alignment during cell division. Journal of Biological Chemistry, 2021, 296, 100676.	1.6	6
17935	Handling High-Throughput Data for Analysis. Methods in Molecular Biology, 2021, 2325, 183-190.	0.4	0
17937	Analysis of Serum miRNAs in Alzheimer's Disease. American Journal of Alzheimer's Disease and Other Dementias, 2021, 36, 153331752110217.	0.9	14
17938	Transcriptomic Profiling Revealed Genes Involved in Response to Drought Stress in Alfalfa. Journal of Plant Growth Regulation, 2022, 41, 92-112.	2.8	7
17939	Pattern Recognition Algorithms for Multi-Omics Data Analysis. , 2021, , 141-158.		3
17940	Bioinformatics Approaches for Interpreting Metabolomics Datasets. , 2021, , 370-384.		0
17941	Comparison and interpretation of characteristics of Rhizosphere microbiomes of three blueberry varieties. BMC Microbiology, 2021, 21, 30.	1.3	12
17943	Identification of core genes for early diagnosis and the EMT modulation of ovarian serous cancer by bioinformatics perspective. Aging, 2021, 13, 3112-3145.	1.4	7
17944	Construction and Analysis of a ceRNA Network in Cardiac Fibroblast During Fibrosis Based on in vivo and in vitro Data. Frontiers in Genetics, 2020, 11, 503256.	1.1	7



#	ARTICLE	IF	CITATIONS
17945	Identification of prognostic alternative splicing signatures in uveal melanoma. <i>International Ophthalmology</i> , 2021, 41, 1347-1362.	0.6	3
17947	Genome-Wide Mining of MYB Transcription Factors in the Anthocyanin Biosynthesis Pathway of <i>Gossypium Hirsutum</i> . <i>Biochemical Genetics</i> , 2021, 59, 678-696.	0.8	12
17948	Improved Prediction of Cancer Outcome Using Graph-Embedded Generative Adversarial Networks. <i>IEEE Access</i> , 2021, 9, 20076-20088.	2.6	9
17949	Qualitative Modeling, Analysis and Control of Synthetic Regulatory Circuits. <i>Methods in Molecular Biology</i> , 2021, 2229, 1-40.	0.4	3
17950	Investigation of MicroRNA and transcription factor mediated regulatory network for silicosis using systems biology approach. <i>Scientific Reports</i> , 2021, 11, 1265.	1.6	10
17952	Variation of rhizosphere microbial community in continuous mono-maize seed production. <i>Scientific Reports</i> , 2021, 11, 1544.	1.6	34
17953	NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. <i>Journal of Computational Biology</i> , 2021, 28, 469-484.	0.8	8
17955	Identification of Potential Diagnostic and Prognostic Biomarkers for Colorectal Cancer Based on GEO and TCGA Databases. <i>Frontiers in Genetics</i> , 2020, 11, 602922.	1.1	7
17956	Periostin Contributes to Immunoglobulin a Nephropathy by Promoting the Proliferation of Mesangial Cells: A Weighted Gene Correlation Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 595757.	1.1	5
17957	Is gene expression among women with rheumatoid arthritis dysregulated during a postpartum flare?. <i>Arthritis Research and Therapy</i> , 2021, 23, 30.	1.6	0
17960	Systems biology and bioinformatics approaches in leishmaniasis. , 2021, , 509-548.		6
17961	RNA-Seq in Nonmodel Organisms. <i>Methods in Molecular Biology</i> , 2021, 2243, 143-167.	0.4	4
17962	Genome-wide expression profiling of long non-coding RNAs and competing endogenous RNA networks in alopecia areata. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 696-711.	1.0	2
17963	Biomedical and Clinical Research Data Management. , 2021, , 532-543.		2
17964	Screening the key genes of prognostic value in the microenvironment for head and neck squamous cell carcinoma. <i>Medicine (United States)</i> , 2021, 100, e24184.	0.4	5
17965	Pearl Sac Gene Expression Profiles Associated With Pearl Attributes in the Silver-Lip Pearl Oyster, <i>Pinctada maxima</i> . <i>Frontiers in Genetics</i> , 2020, 11, 597459.	1.1	11
17966	Sedimentary microeukaryotes reveal more dispersal limitation and form networks with less connectivity than planktonic microeukaryotes in a highly regulated river. <i>Freshwater Biology</i> , 2021, 66, 826-841.	1.2	13
17967	Comprehensive Analysis of Cardiac Xeno-Graft Unveils Rejection Mechanisms. <i>International Journal of Molecular Sciences</i> , 2021, 22, 751.	1.8	7

#	ARTICLE	IF	CITATIONS
17968	A Reductionist Approach Using Primary and Metastatic Cellâ€‘Derived Extracellular Vesicles Reveals Hub Proteins Associated with Oral Cancer Prognosis. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100118.	2.5	12
17969	Immune gene prognostic signature for disease free survival of gastric cancer: Translational research of an artificial intelligence survival predictive system. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2329-2346.	1.9	5
17970	Reaction Tracking and High-Throughput Screening of Active Compounds in Combinatorial Chemistry by Tandem Mass Spectrometry Molecular Networking. <i>Analytical Chemistry</i> , 2021, 93, 2456-2463.	3.2	2
17971	Ubiquitylome analysis reveals a central role for the ubiquitin-proteasome system in plant innate immunity. <i>Plant Physiology</i> , 2021, 185, 1943-1965.	2.3	30
17972	Exploration of the immune cell infiltration-related gene signature in the prognosis of melanoma. <i>Aging</i> , 2021, 13, 3459-3482.	1.4	19
17973	Feasibility of Phosphoproteomics on Leftover Samples After RNA Extraction With Guanidinium Thiocyanate. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100078.	2.5	9
17974	Data-independent acquisition-based proteome and phosphoproteome profiling across six melanoma cell lines reveals determinants of proteotypes. <i>Molecular Omics</i> , 2021, 17, 413-425.	1.4	26
17975	The yellow perch ( <i>Perca flavescens</i> ) microbiome revealed resistance to colonisation mostly associated with neutralism driven by rare taxa under cadmium disturbance. <i>Animal Microbiome</i> , 2021, 3, 3.	1.5	9
17976	MALDI-IMS combined with shotgun proteomics identify and localize new factors in male infertility. <i>Life Science Alliance</i> , 2021, 4, e202000672.	1.3	7
17977	Identification of hub genes and biological pathways in hepatocellular carcinoma by integrated bioinformatics analysis. <i>PeerJ</i> , 2021, 9, e10594.	0.9	8
17978	Identification of Genes with Altered Methylation and Its Role in Early Diagnosis of Sepsis-Induced Acute Respiratory Distress Syndrome. <i>International Journal of General Medicine</i> , 2021, Volume 14, 243-253.	0.8	10
17979	Carriage Dynamics of Pneumococcal Serotypes in Naturally Colonized Infants in a Rural African Setting During the First Year of Life. <i>Frontiers in Pediatrics</i> , 2020, 8, 587730.	0.9	8
17980	Understanding thioamide biosynthesis using pathway engineering and untargeted metabolomics. <i>Chemical Science</i> , 2021, 12, 7138-7150.	3.7	18
17981	Type 2 diabetes mellitus-associated transcriptome alterations in cortical neurones and associated neurovascular unit cells in the ageing brain. <i>Acta Neuropathologica Communications</i> , 2021, 9, 5.	2.4	17
17982	Plant Health and Sound Vibration: Analyzing Implications of the Microbiome in Grape Wine Leaves. <i>Pathogens</i> , 2021, 10, 63.	1.2	13
17983	Transcriptome of nasopharyngeal samples from COVID-19 patients and a comparative analysis with other SARS-CoV-2 infection models reveal disparate host responses against SARS-CoV-2. <i>Journal of Translational Medicine</i> , 2021, 19, 32.	1.8	44
17984	Comparative transcriptomic analysis between â€‘Summer Blackâ€™™ and its bud sport â€‘Nantaihutezaoâ€™™ during developmental stages. <i>Planta</i> , 2021, 253, 23.	1.6	6
17985	Transcriptome Based System Biology Exploration Reveals Homogeneous Tumorigenicity of Alimentary Tract Malignancy. <i>Frontiers in Oncology</i> , 2020, 10, 580276.	1.3	2

#	ARTICLE	IF	CITATIONS
17986	DGraph Clusters Flaviviruses and $\hat{I}^2$ -Coronaviruses According to Their Hosts, Disease Type, and Human Cell Receptors. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110203.	1.0	8
17987	Natural variation in the promoter of <i>GsERD15B</i> affects salt tolerance in soybean. <i>Plant Biotechnology Journal</i> , 2021, 19, 1155-1169.	4.1	34
17988	Network pharmacology integrated molecular docking reveals the bioactive components and potential targets of <i>Morinda officinalis</i> and <i>Lycium barbarum</i> coupled-herbs against oligoasthenozoospermia. <i>Scientific Reports</i> , 2021, 11, 2220.	1.6	18
17989	Comparative analysis of the <i>TCP</i> gene family in celery, coriander and carrot (family) <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	0.2	9
17990	Downregulation of <i>m<sup>6</sup>A</i> Reader YTHDC2 Promotes the Proliferation and Migration of Malignant Lung Cells via CYLD/NF- $\kappa$ B Pathway. <i>International Journal of Biological Sciences</i> , 2021, 17, 2633-2651.	2.6	16
17991	Comparative transcriptomics highlights convergent evolution of energy metabolic pathways in group-living spiders. <i>Zoological Research</i> , 2021, 42, 195-206.	0.9	4
17992	A Signature of Five Long Non-Coding RNAs for Predicting the Prognosis of Alzheimer's Disease Based on Competing Endogenous RNA Networks. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 598606.	1.7	27
17993	Computational biology approaches for mapping transcriptional regulatory networks. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4884-4895.	1.9	14
17995	Identification of Regeneration and Hub Genes and Pathways at Different Time Points after Spinal Cord Injury. <i>Molecular Neurobiology</i> , 2021, 58, 2643-2662.	1.9	10
17996	A Pipeline for Non-model Organisms for de novo Transcriptome Assembly, Annotation, and Gene Ontology Analysis Using Open Tools: Case Study with Scots Pine. <i>Bio-protocol</i> , 2021, 11, e3912.	0.2	7
17997	Therapeutic effects of Sheng Xue Fang in a cyclophosphamide-induced anaemia mouse model. <i>Pharmaceutical Biology</i> , 2021, 59, 787-796.	1.3	2
17998	DPP4 gene silencing inhibits proliferation and epithelial-mesenchymal transition of papillary thyroid carcinoma cells through suppression of the MAPK pathway. <i>Journal of Endocrinological Investigation</i> , 2021, 44, 1609-1623.	1.8	15
17999	An enriched biosignature of gut microbiota-dependent metabolites characterizes maternal plasma in a mouse model of fetal alcohol spectrum disorder. <i>Scientific Reports</i> , 2021, 11, 248.	1.6	21
18000	A risk progression breast epithelial 3D culture model reveals <i>Cx43/hsa_circ_0077755/miR-182</i> as a biomarker axis for heightened risk of breast cancer initiation. <i>Scientific Reports</i> , 2021, 11, 2626.	1.6	4
18001	The hard clam genome reveals massive expansion and diversification of inhibitors of apoptosis in <i>Bivalvia</i> . <i>BMC Biology</i> , 2021, 19, 15.	1.7	52
18002	Identification and characterization of MeERF genes and their targets in pathogen response by cassava ( <i>Manihot esculenta</i> ). <i>Crop Journal</i> , 2021, , .	2.3	2
18003	Community structure of fungal pathogens causing spikelet rot disease of naked oat from different ecological regions of China. <i>Scientific Reports</i> , 2021, 11, 1243.	1.6	5
18004	Deep muscle-proteomic analysis of freeze-dried human muscle biopsies reveals fiber type-specific adaptations to exercise training. <i>Nature Communications</i> , 2021, 12, 304.	5.8	79

#	ARTICLE	IF	CITATIONS
18005	The prognostic and diagnostic value of tissue inhibitor of metalloproteinases gene family and potential function in gastric cancer. <i>Journal of Cancer</i> , 2021, 12, 4086-4098.	1.2	8
18006	Are bacterial symbionts associated with gall induction in insects?. <i>Arthropod-Plant Interactions</i> , 2021, 15, 1-12.	0.5	12
18007	Essentiality of c-di-AMP in <i>Bacillus subtilis</i> : Bypassing mutations converge in potassium and glutamate homeostasis. <i>PLoS Genetics</i> , 2021, 17, e1009092.	1.5	28
18008	Centromere protein E as a novel biomarker and potential therapeutic target for retinoblastoma. <i>Bioengineered</i> , 2021, 12, 5950-5970.	1.4	10
18009	Identification of potential targets of triptolide in regulating the tumor microenvironment of stomach adenocarcinoma patients using bioinformatics. <i>Bioengineered</i> , 2021, 12, 4304-4319.	1.4	7
18010	Identification of biomarkers, pathways and potential therapeutic target for docetaxel resistant prostate cancer. <i>Bioengineered</i> , 2021, 12, 2377-2388.	1.4	6
18011	Interplay among Structural Stability, Plasticity, and Energetics Determined by Conformational Attuning of Flexible Loops in PD-1. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 358-384.	2.5	34
18012	Aggresomes predict poor outcomes and implicate proteostasis in the pathogenesis of pediatric choroid plexus tumors. <i>Journal of Neuro-Oncology</i> , 2021, 152, 67-78.	1.4	6
18013	MicroRNAs expression dynamics reveal post-transcriptional mechanisms regulating seed development in <i>Phaseolus vulgaris</i> L.. <i>Horticulture Research</i> , 2021, 8, 18.	2.9	9
18014	Exploration of the typical features of tubulovillous adenoma using in-depth quantitative proteomics analysis. <i>Bioengineered</i> , 2021, 12, 6831-6843.	1.4	2
18015	Identification of Potential Prognostic Competing Triplets in High-Grade Serous Ovarian Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 607722.	1.1	14
18016	Systematic detection of brain protein-coding genes under positive selection during primate evolution and their roles in cognition. <i>Genome Research</i> , 2021, 31, 484-496.	2.4	25
18017	TDP-43 aggregation induced by oxidative stress causes global mitochondrial imbalance in ALS. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 132-142.	3.6	92
18018	Bacterial seed endophyte shapes disease resistance in rice. <i>Nature Plants</i> , 2021, 7, 60-72.	4.7	220
18019	Recent Advances in Rapid Antimicrobial Susceptibility Testing. <i>Clinical Chemistry</i> , 2021, 68, 91-98.	1.5	14
18020	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021, 38, 1994-2023.	5.2	76
18021	Mining plant endogenous target mimics from miRNA-lncRNA interactions based on dual-path parallel ensemble pruning method. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
18022	HiDeF: identifying persistent structures in multiscale omics data. <i>Genome Biology</i> , 2021, 22, 21.	3.8	29

#	ARTICLE	IF	CITATIONS
18023	Extensive tissue-specific expression variation and novel regulators underlying circadian behavior. <i>Science Advances</i> , 2021, 7, .	4.7	21
18024	Transcriptome Analysis Identifies Altered Biological Processes and Novel Markers in Human Immunodeficiency Virus-1 Long-Term Non-Progressors. <i>Infection and Chemotherapy</i> , 2021, 53, 489.	1.0	2
18025	Bioinformatics and machine learning methodologies to identify the effects of central nervous system disorders on glioblastoma progression. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
18027	<i>Systems Biology: Principles and Applications in Plant Research.</i> , 0, , 1-40.		6
18028	Changes in the transcriptional fingerprint of satellite glial cells following peripheral nerve injury. <i>Glia</i> , 2020, 68, 1375-1395.	2.5	65
18029	Secretome of Activated Fibroblasts Induced by Exosomes for the Discovery of Biomarkers in Nonâ€Small Cell Lung Cancer. <i>Small</i> , 2021, 17, e2004750.	5.2	18
18030	Prokaryotic Systems Biology. <i>Cell Engineering</i> , 2007, , 395-423.	0.4	1
18031	Knowledge-Based Integrative Framework for Hypothesis Formation in Biochemical Networks. <i>Lecture Notes in Computer Science</i> , 2005, , 121-136.	1.0	4
18032	Reaction Motifs in Metabolic Networks. <i>Lecture Notes in Computer Science</i> , 2005, , 178-191.	1.0	7
18033	<i>Systems Biology: A Renaissance of the Top-down Approach for Plant Analysis.</i> , 2006, , 185-198.		2
18034	<i>Systems Genetics and Complex Traits.</i> , 2009, , 9105-9124.		1
18036	Network Modeling of Complex Data Sets. <i>Methods in Molecular Biology</i> , 2020, 2096, 197-215.	0.4	5
18037	Feature-Based Molecular Networking for Metabolite Annotation. <i>Methods in Molecular Biology</i> , 2020, 2104, 227-243.	0.4	21
18038	Pathway Analysis for Targeted and Untargeted Metabolomics. <i>Methods in Molecular Biology</i> , 2020, 2104, 387-400.	0.4	35
18039	Network-Based Approaches for Multi-omics Integration. <i>Methods in Molecular Biology</i> , 2020, 2104, 469-487.	0.4	38
18040	A Systems Bioinformatics Approach to Interconnect Biological Pathways. <i>Methods in Molecular Biology</i> , 2021, 2189, 231-249.	0.4	3
18041	Predicting Host Phenotype Based on Gut Microbiome Using a Convolutional Neural Network Approach. <i>Methods in Molecular Biology</i> , 2021, 2190, 249-266.	0.4	6
18042	Applications of Network Analysis in Biomedicine. <i>Methods in Molecular Biology</i> , 2020, 2204, 39-50.	0.4	1

#	ARTICLE	IF	CITATIONS
18043	Network Analysis of Integrin Adhesion Complexes. <i>Methods in Molecular Biology</i> , 2021, 2217, 149-179.	0.4	7
18044	Functional Bioinformatics Analyses of the Matrisome and Integrin Adhesome. <i>Methods in Molecular Biology</i> , 2021, 2217, 285-300.	0.4	8
18045	From Protein-Protein Complexes to Interactomics. , 2007, 43, 135-183.		21
18046	The caBIG® Life Sciences Distribution. , 2010, , 253-266.		3
18047	GNCPro: Navigate Human Genes and Relationships Through Net-Walking. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 253-259.	0.8	9
18048	Integrated Weighted Correlation Network Analysis of Mouse Liver Gene Expression Data. , 2011, , 321-351.		4
18049	Link Prediction in Highly Fractional Data Sets. , 2013, , 283-300.		17
18050	Visual Methods and Tools for Social Network Analysis. , 2014, , 2314-2327.		2
18051	Plug-and-Play Macroscopes: Network Workbench (NWB), Science of Science Tool (Sci2), and Epidemiology Tool (EpiC). , 2014, , 1280-1290.		1
18052	Tulip III. , 2014, , 2216-2240.		9
18053	Tulip 5. , 2017, , 1-28.		23
18054	Biofilm-Growing Bacteria Involved in the Corrosion of Concrete Wastewater Pipes: Protocols for Comparative Metagenomic Analyses. <i>Methods in Molecular Biology</i> , 2014, 1147, 323-340.	0.4	6
18055	Identifying Stem Cell Gene Expression Patterns and Phenotypic Networks with AutoSOME. <i>Methods in Molecular Biology</i> , 2014, 1150, 115-130.	0.4	1
18056	Quantitative Transcriptome Analysis Using RNA-seq. <i>Methods in Molecular Biology</i> , 2014, 1158, 71-91.	0.4	20
18057	Biological Information Extraction and Co-occurrence Analysis. <i>Methods in Molecular Biology</i> , 2014, 1159, 77-92.	0.4	19
18058	Candidate Gene Discovery and Prioritization in Rare Diseases. <i>Methods in Molecular Biology</i> , 2014, 1168, 295-312.	0.4	2
18059	Bioinformatics Approach to Understanding Interacting Pathways in Neuropsychiatric Disorders. <i>Methods in Molecular Biology</i> , 2014, 1168, 157-172.	0.4	4
18060	Investigating Host-Pathogen Behavior and Their Interaction Using Genome-Scale Metabolic Network Models. <i>Methods in Molecular Biology</i> , 2014, 1184, 523-562.	0.4	10



#	ARTICLE	IF	CITATIONS
18061	Synthetic Genetic Array Analysis for Global Mapping of Genetic Networks in Yeast. <i>Methods in Molecular Biology</i> , 2014, 1205, 143-168.	0.4	30
18062	Prediction of miRNA Targets. <i>Methods in Molecular Biology</i> , 2015, 1269, 207-229.	0.4	29
18063	Constructing Simple Biological Networks for Understanding Complex High-Throughput Data in Plants. <i>Methods in Molecular Biology</i> , 2015, 1284, 503-526.	0.4	6
18064	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. <i>Methods in Molecular Biology</i> , 2015, 1306, 195-205.	0.4	1
18065	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
18066	Systemic Analysis of Regulated Functional Networks. <i>Methods in Molecular Biology</i> , 2016, 1394, 287-310.	0.4	1
18067	Bioinformatics Methods to Deduce Biological Interpretation from Proteomics Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 147-161.	0.4	2
18068	Proteotypic Peptides and Their Applications. <i>Methods in Molecular Biology</i> , 2017, 1549, 101-107.	0.4	11
18069	Analysis of Protein Phosphorylation and Its Functional Impact on Protein-Protein Interactions via Text Mining of the Scientific Literature. <i>Methods in Molecular Biology</i> , 2017, 1558, 213-232.	0.4	7
18070	Functional Interaction Network Construction and Analysis for Disease Discovery. <i>Methods in Molecular Biology</i> , 2017, 1558, 235-253.	0.4	96
18071	NDEx: A Community Resource for Sharing and Publishing of Biological Networks. <i>Methods in Molecular Biology</i> , 2017, 1558, 271-301.	0.4	71
18072	Antibody Validation by Immunoprecipitation Followed by Mass Spectrometry Analysis. <i>Methods in Molecular Biology</i> , 2017, 1575, 175-187.	0.4	10
18073	Rat Genome Databases, Repositories, and Tools. <i>Methods in Molecular Biology</i> , 2019, 2018, 71-96.	0.4	14
18074	Phosphoproteomics Profiling to Identify Altered Signaling Pathways and Kinase-Targeted Cancer Therapies. <i>Methods in Molecular Biology</i> , 2020, 2051, 241-264.	0.4	3
18075	Open-Source Software Tools, Databases, and Resources for Single-Cell and Single-Cell-Type Metabolomics. <i>Methods in Molecular Biology</i> , 2020, 2064, 191-217.	0.4	11
18076	Generation and Interpretation of Context-Specific Human Protein-Protein Interaction Networks with HIPPIE. <i>Methods in Molecular Biology</i> , 2020, 2074, 135-144.	0.4	4
18077	Perform Pathway Enrichment Analysis Using ReactomeFIViz. <i>Methods in Molecular Biology</i> , 2020, 2074, 165-179.	0.4	10
18078	Methods for the Inference of Biological Pathways and Networks. <i>Methods in Molecular Biology</i> , 2009, 541, 225-245.	0.4	18

#	ARTICLE	IF	CITATIONS
18079	Connecting Protein Interaction Data, Mutations, and Disease Using Bioinformatics. <i>Methods in Molecular Biology</i> , 2009, 541, 449-461.	0.4	11
18080	Learning Global Models of Transcriptional Regulatory Networks from Data. <i>Methods in Molecular Biology</i> , 2009, 541, 181-210.	0.4	12
18081	Integrated Network Modeling of Molecular and Genetic Interactions. , 2008, , 67-74.		2
18082	Data Standards and Controlled Vocabularies for Proteomics. <i>Methods in Molecular Biology</i> , 2008, 484, 279-286.	0.4	7
18083	Multiplexed Isobaric Tagging Protocols for Quantitative Mass Spectrometry Approaches to Auditory Research. <i>Methods in Molecular Biology</i> , 2009, 493, 345-366.	0.4	6
18084	System Biology of Gene Regulation. <i>Methods in Molecular Biology</i> , 2009, 569, 55-87.	0.4	7
18085	Bioinformatics: Databasing and Gene Annotation. <i>Methods in Molecular Biology</i> , 2008, 460, 145-157.	0.4	4
18086	Biomolecular Pathway Databases. <i>Methods in Molecular Biology</i> , 2010, 609, 129-144.	0.4	23
18087	Reconstructing Regulatory Kinase Pathways from Phosphopeptide Data: A Bioinformatics Approach. <i>Methods in Molecular Biology</i> , 2009, 527, 311-319.	0.4	3
18088	Mining Protein-Protein Interactions from Published Literature Using Linguamatics I2E. <i>Methods in Molecular Biology</i> , 2009, 563, 3-13.	0.4	26
18089	Off-Target Networks Derived from Ligand Set Similarity. <i>Methods in Molecular Biology</i> , 2009, 575, 195-205.	0.4	20
18090	The PeptideAtlas Project. <i>Methods in Molecular Biology</i> , 2010, 604, 285-296.	0.4	121
18091	Phosphoproteome Resource for Systems Biology Research. <i>Methods in Molecular Biology</i> , 2011, 694, 307-322.	0.4	11
18092	The Evolution of Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2011, 696, 273-289.	0.4	5
18093	Statistical Analysis of Dynamic Transcriptional Regulatory Network Structure. <i>Methods in Molecular Biology</i> , 2011, 781, 337-352.	0.4	2
18094	Construction of Protein Interaction Networks Based on the Label-Free Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2011, 781, 71-85.	0.4	4
18095	Data Mining in Psychiatric Research. <i>Methods in Molecular Biology</i> , 2012, 829, 593-603.	0.4	8
18096	The Use of Open Source Bioinformatics Tools to Dissect Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2012, 835, 311-331.	0.4	9

#	ARTICLE	IF	CITATIONS
18097	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2012, 850, 483-494.	0.4	14
18098	Gene Expression Networks. <i>Methods in Molecular Biology</i> , 2013, 930, 165-178.	0.4	2
18099	Construction of Cell Type-Specific Logic Models of Signaling Networks Using CellNOpt. <i>Methods in Molecular Biology</i> , 2013, 930, 179-214.	0.4	4
18100	A Comparative Analysis of Feature Selection Methods for Biomarker Discovery in Study of Toxicant-Treated Atlantic Cod ( <i>Gadus Morhua</i> ) Liver. <i>Communications in Computer and Information Science</i> , 2019, , 114-123.	0.4	3
18101	Data Journeys Beyond Databases in Systems Biology: Cytoscape and NDEx. , 2020, , 121-143.		3
18102	Can Genetic Programming Perform Explainable Machine Learning for Bioinformatics?. <i>Genetic and Evolutionary Computation</i> , 2020, , 63-77.	1.0	2
18103	The Extracellular Matrix Goes -Omics: Resources and Tools. <i>Biology of Extracellular Matrix</i> , 2020, , 1-16.	0.3	6
18104	Extracellular Matrix Networks: From Connections to Functions. <i>Biology of Extracellular Matrix</i> , 2020, , 101-129.	0.3	3
18105	NeoHiC: A Web Application for the Analysis of Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2020, , 98-107.	1.0	1
18106	Protein-protein interactions: analysis and prediction. , 2008, , 353-410.		1
18107	Computational Modeling of the Main Signaling Pathways Involved in Mast Cell Activation. <i>Current Topics in Microbiology and Immunology</i> , 2014, 382, 69-93.	0.7	22
18108	Graph Clustering Using Mutual K-Nearest Neighbors. <i>Lecture Notes in Computer Science</i> , 2014, , 35-48.	1.0	6
18109	Estimating the Degrees of Neighboring Nodes in Online Social Networks. <i>Lecture Notes in Computer Science</i> , 2014, , 42-56.	1.0	4
18112	Harnessing WebGL and WebSockets for a Web-Based Collaborative Graph Exploration Tool. <i>Lecture Notes in Computer Science</i> , 2015, , 583-598.	1.0	4
18113	Bottom-Up Proteomics. , 2016, , 155-185.		1
18114	Leveraging Social Media for Health Promotion and Behavior Change: Methods of Analysis and Opportunities for Intervention. <i>Computers in Health Care</i> , 2017, , 315-345.	0.2	6
18115	Use of Mass Spectrometry to Study the Centromere and Kinetochore. <i>Progress in Molecular and Subcellular Biology</i> , 2017, 56, 3-27.	0.9	3
18116	FCA in a Logical Programming Setting for Visualization-Oriented Graph Compression. <i>Lecture Notes in Computer Science</i> , 2017, , 89-105.	1.0	3

#	ARTICLE	IF	CITATIONS
18117	Omics and System Biology Approaches in Plant Stress Research. SpringerBriefs in Systems Biology, 2017, , 21-34.	0.1	35
18118	Refined JST Thesaurus Extended with Data from Other Open Life Science Data Sources. Lecture Notes in Computer Science, 2017, , 35-48.	1.0	3
18119	Revisited Experimental Comparison of Node-Link and Matrix Representations. Lecture Notes in Computer Science, 2018, , 287-302.	1.0	6
18121	Interactive Visualization of Gene Regulatory Networks with Associated Gene Expression Time Series Data. Mathematics and Visualization, 2008, , 293-311.	0.4	5
18122	An Integrated QAP-Based Approach to Visualize Patterns of Gene Expression Similarity. , 2007, , 156-167.		15
18123	Seven Variations of an Alignment Workflow - An Illustration of Agile Process Design and Management in Bio-jETI. , 2008, , 445-456.		30
18124	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 302-320.	1.0	3
18125	Artificial Neural Network Based Algorithm for Biomolecular Interactions Modeling. Lecture Notes in Computer Science, 2009, , 877-885.	1.0	18
18126	Inference and Validation of Networks. Lecture Notes in Computer Science, 2009, , 344-358.	1.0	4
18127	WiGis: A Framework for Scalable Web-Based Interactive Graph Visualizations. Lecture Notes in Computer Science, 2010, , 119-134.	1.0	8
18128	Semi-bipartite Graph Visualization for Gene Ontology Networks. Lecture Notes in Computer Science, 2010, , 244-255.	1.0	9
18129	Modeling without Borders: Creating and Annotating VCell Models Using the Web. Lecture Notes in Computer Science, 2010, , 3-17.	1.0	1
18130	An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity. Lecture Notes in Computer Science, 2010, , 179-191.	1.0	1
18131	SameAs Networks and Beyond: Analyzing Deployment Status and Implications of owl:sameAs in Linked Data. Lecture Notes in Computer Science, 2010, , 145-160.	1.0	44
18132	Explorations into the Provenance of High Throughput Biomedical Experiments. Lecture Notes in Computer Science, 2010, , 120-128.	1.0	2
18133	Discovering Collaborative Cyber Attack Patterns Using Social Network Analysis. Lecture Notes in Computer Science, 2011, , 129-136.	1.0	15
18134	VENLO: Interactive Visual Exploration of Aligned Biological Networks and Their Evolution. Mathematics and Visualization, 2012, , 229-247.	0.4	2
18135	Structure-Dynamics Interplay in Directed Complex Networks with Border Effects. Communications in Computer and Information Science, 2011, , 46-56.	0.4	2

#	ARTICLE	IF	CITATIONS
18137	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Lecture Notes in Computer Science</i> , 2012, , 287-301.	1.0	7
18138	Mid-Ontology Learning from Linked Data. <i>Lecture Notes in Computer Science</i> , 2012, , 112-127.	1.0	6
18139	Supervising Random Forest Using Attribute Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2013, , 104-116.	1.0	3
18142	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. , 2007, 97, 277-307.		7
18143	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
18144	Plant Systems Biology: Insights and Advancements. , 2015, , 791-819.		6
18145	Processing of Mass Spectrometry Data in Clinical Applications. <i>Translational Bioinformatics</i> , 2013, , 207-233.	0.0	1
18146	Construction of Breast Cancer-Based Proteinâ€“Protein Interaction Network Using Multiple Sources of Datasets. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2019, , 11-16.	0.2	1
18147	Advancement in Sustainable Agriculture: Computational and Bioinformatics Tools. , 2019, , 465-547.		4
18148	Systems Biology and Integrated Computational Methods for Cancer-Associated Mutation Analysis. , 2020, , 335-362.		3
18149	L1CAM drives oncogenicity in esophageal squamous cell carcinoma by stimulation of ezrin transcription. <i>Journal of Molecular Medicine</i> , 2017, 95, 1355-1368.	1.7	27
18150	Identification of core biomarkers associated with pathogenesis and prognostic outcomes of laryngeal squamous-cell cancer using bioinformatics analysis. <i>European Archives of Oto-Rhino-Laryngology</i> , 2020, 277, 1397-1408.	0.8	9
18151	A network perspective on genotypeâ€“phenotype mapping in genetic programming. <i>Genetic Programming and Evolvable Machines</i> , 2020, 21, 375-397.	1.5	14
18152	Multidimensional patterns of metabolic response in abiotic stress-induced growth of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2016, 92, 689-699.	2.0	11
18153	Co-occurrence network analyses of rhizosphere soil microbial PLFAs and metabolites over continuous cropping seasons in tobacco. <i>Plant and Soil</i> , 2020, 452, 119-135.	1.8	32
18154	Revealing the Common Mechanisms of Scutellarin in Angina Pectoris and Ischemic Stroke Treatment via a Network Pharmacology Approach. <i>Chinese Journal of Integrative Medicine</i> , 2021, 27, 62-69.	0.7	16
18155	Single-Base Resolution Mapping of 5-Hydroxymethylcytosine Modifications in Hippocampus of Alzheimerâ€™s Disease Subjects. <i>Journal of Molecular Neuroscience</i> , 2017, 63, 185-197.	1.1	28
18156	miRNA-mRNA interaction network in non-small-cell lung cancer. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, , .	2.2	5

#	ARTICLE	IF	CITATIONS
18157	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. <i>Protein and Cell</i> , 2013, 5, 59.	4.8	3
18158	Î±-Glucosidase inhibitors from <i>Duranta repens</i> modulate p53 signaling pathway in diabetes mellitus. <i>Advances in Traditional Medicine</i> , 2020, 20, 427-438.	1.0	23
18159	Glutathione Transferases. , 2010, , 295-321.		6
18160	Vertical Investigations of Enzyme Evolution Using Ancestral Sequence Reconstruction. , 2020, , 640-653.		1
18161	Unusual Suspects in the Twilight Zone Between the Hsp90 Interactome and Carcinogenesis. <i>Advances in Cancer Research</i> , 2016, 129, 1-30.	1.9	39
18162	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , 2020, 181, 1329-1345.e24.	13.5	79
18163	Inverse Data-Driven Modeling and Multiomics Analysis Reveals Phgdh as a Metabolic Checkpoint of Macrophage Polarization and Proliferation. <i>Cell Reports</i> , 2020, 30, 1542-1552.e7.	2.9	52
18164	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
18165	High-Throughput Functional Analysis Distinguishes Pathogenic, Nonpathogenic, and Compensatory Transcriptional Changes in Neurodegeneration. <i>Cell Systems</i> , 2018, 7, 28-40.e4.	2.9	32
18166	<i>Pseudomonas fluorescens</i> accelerates a reverse and long-distance transport of cadmium and sucrose in the hyperaccumulator plant <i>Sedum alfredii</i> . <i>Chemosphere</i> , 2020, 256, 127156.	4.2	21
18167	MicroPhenoDB Associates Metagenomic Data with Pathogenic Microbes, Microbial Core Genes, and Human Disease Phenotypes. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 760-772.	3.0	19
18168	Absence of NLRP3 Inflammasome in Hematopoietic Cells Reduces Adverse Remodeling After Experimental Myocardial Infarction. <i>JACC Basic To Translational Science</i> , 2020, 5, 1210-1224.	1.9	19
18169	Antiseizure potential of the ancient Greek medicinal plant <i>Helleborus odorus</i> subsp. <i>cyclophyllus</i> and identification of its main active principles. <i>Journal of Ethnopharmacology</i> , 2020, 259, 112954.	2.0	10
18170	How tryptophan levels in plant-based aquafeeds affect fish physiology, metabolism and proteome. <i>Journal of Proteomics</i> , 2020, 221, 103782.	1.2	30
18171	Identifying of miR-98-5p/IGF1 axis contributes breast cancer progression using comprehensive bioinformatic analyses methods and experiments validation. <i>Life Sciences</i> , 2020, 261, 118435.	2.0	8
18172	Molecular Connectivity of Mitochondrial Gene Expression and OXPHOS Biogenesis. <i>Molecular Cell</i> , 2020, 79, 1051-1065.e10.	4.5	40
18173	Complete neural stem cell (NSC) neuronal differentiation requires a branched chain amino acids-induced persistent metabolic shift towards energy metabolism. <i>Pharmacological Research</i> , 2020, 158, 104863.	3.1	27
18174	Assessing specialized metabolite diversity of <i>Alnus</i> species by a digitized LC-MS/MS data analysis workflow. <i>Phytochemistry</i> , 2020, 173, 112292.	1.4	15



#	ARTICLE	IF	CITATIONS
18175	Particle-attached riverine bacteriome shifts in a pollutant-resistant and pathogenic community during a Mediterranean extreme storm event. <i>Science of the Total Environment</i> , 2020, 732, 139047.	3.9	7
18176	<i>Ralstonia solanacearum</i> pathogen disrupts bacterial rhizosphere microbiome during an invasion. <i>Soil Biology and Biochemistry</i> , 2018, 118, 8-17.	4.2	120
18177	Zearalenone exposure triggered porcine granulosa cells apoptosis via microRNAs-mediated focal adhesion pathway. <i>Toxicology Letters</i> , 2020, 330, 80-89.	0.4	18
18178	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. <i>Water Research</i> , 2020, 178, 115815.	5.3	40
18179	Persistence of HIV-1 Env-Specific Plasmablast Lineages in Plasma Cells after Vaccination in Humans. <i>Cell Reports Medicine</i> , 2020, 1, 100015.	3.3	10
18180	Single-cell RNA-seq reveals different subsets of non-specific cytotoxic cells in teleost. <i>Genomics</i> , 2020, 112, 5170-5179.	1.3	42
18181	Mapping Chemical Respiratory Sensitization: How Useful Are Our Current Computational Tools?. <i>Chemical Research in Toxicology</i> , 2021, 34, 473-482.	1.7	11
18182	Will a Non-antibiotic Metalloid Enhance the Spread of Antibiotic Resistance Genes: The Selenate Story. <i>Environmental Science &amp; Technology</i> , 2021, 55, 1004-1014.	4.6	42
18183	A tutorial on regularized partial correlation networks.. <i>Psychological Methods</i> , 2018, 23, 617-634.	2.7	1,157
18184	N6-methyladenosine (m6A) recruits and repels proteins to regulate mRNA homeostasis. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 870-878.	3.6	432
18185	Longitudinal transcriptome analyses show robust T cell immunity during recovery from COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 294.	7.1	62
18186	Environmental heterogeneity determines the ecological processes that govern bacterial metacommunity assembly in a floodplain river system. <i>ISME Journal</i> , 2020, 14, 2951-2966.	4.4	104
18187	Leukemic stem cell signatures identify novel therapeutics targeting acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2018, 8, 52.	2.8	55
18188	Elevated T cell levels in peripheral blood predict poor clinical response following rituximab treatment in new-onset type 1 diabetes. <i>Genes and Immunity</i> , 2019, 20, 293-307.	2.2	41
18189	Quantitative SUMO proteomics identifies PIAS1 substrates involved in cell migration and motility. <i>Nature Communications</i> , 2020, 11, 834.	5.8	47
18190	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , 2017, 3, 715-723.	4.7	98
18191	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020, 6, 3.	2.0	14
18192	Spatial metabolomics of in situ host-microbe interactions at the micrometre scale. <i>Nature Microbiology</i> , 2020, 5, 498-510.	5.9	144

#	ARTICLE	IF	CITATIONS
18193	Structural basis of ligand recognition and self-activation of orphan GPR52. <i>Nature</i> , 2020, 579, 152-157.	13.7	97
18194	Analysis of wild tomato introgression lines elucidates the genetic basis of transcriptome and metabolome variation underlying fruit traits and pathogen response. <i>Nature Genetics</i> , 2020, 52, 1111-1121.	9.4	103
18195	Transcriptomics analysis reveals new insights in E171-induced molecular alterations in a mouse model of colon cancer. <i>Scientific Reports</i> , 2018, 8, 9738.	1.6	16
18196	Novel genes exhibiting DNA methylation alterations in Korean patients with chronic lymphocytic leukaemia: a methyl-CpG-binding domain sequencing study. <i>Scientific Reports</i> , 2020, 10, 1085.	1.6	3
18197	Wheat dwarfing influences selection of the rhizosphere microbiome. <i>Scientific Reports</i> , 2020, 10, 1452.	1.6	62
18198	Cell-specific metabolomic responses to injury: novel insights into blood-brain barrier modulation. <i>Scientific Reports</i> , 2020, 10, 7760.	1.6	12
18199	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. <i>Scientific Reports</i> , 2020, 10, 8436.	1.6	10
18200	Cerina: systematic circRNA functional annotation based on integrative analysis of ceRNA interactions. <i>Scientific Reports</i> , 2020, 10, 22165.	1.6	17
18201	Impact of individual demographic and social factors on human-wildlife interactions: a comparative study of three macaque species. <i>Scientific Reports</i> , 2020, 10, 21991.	1.6	23
18202	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. <i>Scientific Data</i> , 2018, 5, 180114.	2.4	26
18203	Dissecting the regulation rules of cancer-related miRNAs based on network analysis. <i>Scientific Reports</i> , 2016, 6, 34172.	1.6	9
18204	Chapter 11. Strategies for Building Protein-Glycosaminoglycan Interaction Networks Combining SPRi, SPR, and BLI. , 0, , 398-414.		5
18205	Investigation of a common gene expression signature in gastrointestinal cancers using systems biology approaches. <i>Molecular BioSystems</i> , 2017, 13, 2277-2288.	2.9	4
18206	Systematic bioinformatic analysis of nutrigenomic data of flavanols in cell models of cardiometabolic disease. <i>Food and Function</i> , 2020, 11, 5040-5064.	2.1	13
18207	An allosteric hot spot in the tandem-SH2 domain of ZAP-70 regulates T-cell signaling. <i>Biochemical Journal</i> , 2020, 477, 1287-1308.	1.7	13
18208	Cytoskeleton regulators CAPZA2 and INF2 associate with CFTR to control its plasma membrane levels under EPAC1 activation. <i>Biochemical Journal</i> , 2020, 477, 2561-2580.	1.7	13
18209	Identification of potential plasma biomarkers and metabolic dysfunction for unstable angina pectoris and its complication based on global metabolomics. <i>Bioscience Reports</i> , 2019, 39, .	1.1	4
18210	Regulatory networks of circRNAs related to transcription factors in <i>Populus euphratica</i> Oliv. heteromorphic leaves. <i>Bioscience Reports</i> , 2019, 39, .	1.1	8

#	ARTICLE	IF	CITATIONS
18211	Bioinformatics analysis of circulating miRNAs related to cancer following spinal cord injury. Bioscience Reports, 2019, 39, .	1.1	3
18212	HPO-Shuffle: an associated gene prioritization strategy and its application in drug repurposing for the treatment of canine epilepsy. Bioscience Reports, 2019, 39, .	1.1	10
18213	Time series expression pattern of key genes reveals the molecular process of esophageal cancer. Bioscience Reports, 2020, 40, .	1.1	2
18214	KRT8 and KRT19, associated with EMT, are hypomethylated and overexpressed in lung adenocarcinoma and link to unfavorable prognosis. Bioscience Reports, 2020, 40, .	1.1	27
18215	Identification of prognostic significance of <i>BIRC5</i> in breast cancer using integrative bioinformatics analysis. Bioscience Reports, 2020, 40, .	1.1	39
18216	MiR-489 aggravates H2O2-induced apoptosis of cardiomyocytes via inhibiting IGF1. Bioscience Reports, 2020, 40, .	1.1	9
18217	Mining TCGA database for tumor mutation burden and their clinical significance in bladder cancer. Bioscience Reports, 2020, 40, .	1.1	79
18218	Identification of cell division cycle 20 as a candidate biomarker and potential therapeutic target in bladder cancer using bioinformatics analysis. Bioscience Reports, 2020, 40, .	1.1	4
18219	The construction and analysis of tumor-infiltrating immune cells and ceRNA networks in metastatic adrenal cortical carcinoma. Bioscience Reports, 2020, 40, .	1.1	11
18220	Association between SNAP25 and human glioblastoma multiform: a comprehensive bioinformatic analysis. Bioscience Reports, 2020, 40, .	1.1	5
18221	Construction of a novel prognostic-predicting model correlated to ovarian cancer. Bioscience Reports, 2020, 40, .	1.1	4
18222	Identification prognosis-associated immune genes in colon adenocarcinoma. Bioscience Reports, 2020, 40, .	1.1	17
18223	Network pharmacology evaluation of the active ingredients and potential targets of XiaoLuoWan for application to uterine fibroids. Bioscience Reports, 2020, 40, .	1.1	7
18224	Immune-associated biomarkers for early diagnosis of Parkinson's disease based on hematological lncRNA-mRNA co-expression. Bioscience Reports, 2020, 40, .	1.1	11
18225	Diurnal rhythms across the human dorsal and ventral striatum. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	27
18226	Recent advances in the application of metabolomics for food safety control and food quality analyses. Critical Reviews in Food Science and Nutrition, 2021, 61, 1448-1469.	5.4	186
18227	Mouse Embryonic Fibroblast Adipogenic Potential: A Comprehensive Transcriptome Analysis. Adipocyte, 2021, 10, 1-20.	1.3	7
18228	Dendritic cells in tumor microenvironment promoted the neuropathic pain via paracrine inflammatory and growth factors. Bioengineered, 2020, 11, 661-678.	1.4	26

#	ARTICLE	IF	CITATIONS
18229	Rescaling the complex network of low-temperature plasma chemistry through graph-theoretical analysis. <i>Plasma Sources Science and Technology</i> , 2020, 29, 115018.	1.3	13
18230	Plasma Metabolomic Signatures of Chronic Obstructive Pulmonary Disease and the Impact of Genetic Variants on Phenotype-Driven Modules. <i>Network and Systems Medicine</i> , 2020, 3, 159-181.	2.7	22
18231	<i>Atlas</i>: automatic modeling of regulation of bacterial gene expression and metabolism using rule-based languages. <i>Bioinformatics</i> , 2021, 36, 5473-5480.	1.8	7
18232	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. <i>Brain</i> , 2021, 144, 450-461.	3.7	16
18233	The protein interaction network of the inherited central nervous system diseases reveals new gene candidates for molecularly unclassified myelin disorders. <i>Journal of Complex Networks</i> , 2020, 8, .	1.1	1
18234	The IMEx coronavirus interactome: an evolving map of<i>Coronaviridae</i>“host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	34
18235	The cytosolic invertase NI6 affects vegetative growth, flowering, fruit set, and yield in tomato. <i>Journal of Experimental Botany</i> , 2021, 72, 2525-2543.	2.4	16
18236	Cis- and Trans-Regulatory Variations in the Domestication of the Chili Pepper Fruit. <i>Molecular Biology and Evolution</i> , 2020, 37, 1593-1603.	3.5	19
18237	Bidirectional Genetic Control of Phenotypic Heterogeneity and Its Implication for Cancer Drug Resistance. <i>Molecular Biology and Evolution</i> , 2021, 38, 1874-1887.	3.5	5
18238	BRENDA, the ELIXIR core data resource in 2021: new developments and updates. <i>Nucleic Acids Research</i> , 2021, 49, D498-D508.	6.5	347
18239	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. <i>Nucleic Acids Research</i> , 2021, 49, e3-e3.	6.5	5
18240	A topologically distinct class of photolyases specific for UV lesions within single-stranded DNA. <i>Nucleic Acids Research</i> , 2020, 48, 12845-12857.	6.5	9
18241	A systems genetics approach to deciphering the effect of dosage variation on leaf morphology in <i>Populus</i>. <i>Plant Cell</i> , 2021, 33, 940-960.	3.1	10
18242	Kingdom-wide analysis of the evolution of the plant type III polyketide synthase superfamily. <i>Plant Physiology</i> , 2021, 185, 857-875.	2.3	20
18243	Transcriptome analysis of gynoceium morphogenesis uncovers the chronology of gene regulatory network activity. <i>Plant Physiology</i> , 2021, 185, 1076-1090.	2.3	11
18244	Aryl Hydrocarbon Receptor Mediates Larval Zebrafish Fin Duplication Following Exposure to Benzofluoranthenes. <i>Toxicological Sciences</i> , 2020, 176, 46-64.	1.4	5
18245	Construction and analysis of an aberrant lncRNA-miRNA-mRNA network associated with papillary thyroid cancer. <i>Medicine (United States)</i> , 2020, 99, e22705.	0.4	12
18246	Mesenchymal Stem/Stromal Cells Increase Cardiac MIR-187-3P Expression in Polymicrobial Animal Model of Sepsis. <i>Shock</i> , 2020, Publish Ahead of Print, 133-141.	1.0	12

#	ARTICLE	IF	CITATIONS
18247	Phylogenomic analysis of <i>Haemophilus parasuis</i> and proposed reclassification to <i>Glaesserella parasuis</i> , gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 180-186.	0.8	51
18248	First insight into the faecal microbiota of the high Arctic muskoxen ( <i>Ovibos moschatus</i> ). <i>Microbial Genomics</i> , 2016, 2, e000066.	1.0	18
18249	Analysis of the diversity of the glycoside hydrolase family 130 in mammal gut microbiomes reveals a novel mannoside-phosphorylase function. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
18250	Evidence that COG0325 proteins are involved in PLP homeostasis. <i>Microbiology (United Kingdom)</i> , 2016, 162, 694-706.	0.7	47
18251	The intestinal proteome of diabetic and control children is enriched with different microbial and host proteins. <i>Microbiology (United Kingdom)</i> , 2017, 163, 161-174.	0.7	46
18252	Systems and synthetic biology perspective of the versatile plant-pathogenic and polysaccharide-producing bacterium <i>Xanthomonas campestris</i> . <i>Microbiology (United Kingdom)</i> , 2017, 163, 1117-1144.	0.7	7
18253	Dissecting the protein architecture of DNA-binding transcription factors in bacteria and archaea. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1167-1178.	0.7	13
18254	Analysis of essential gene dynamics under antibiotic stress in <i>Streptococcus sanguinis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 173-185.	0.7	9
18664	Susceptible individuals drive active social contagion. <i>Physical Review Research</i> , 2019, 1, .	1.3	3
18665	DyNetVis - An interactive software to visualize structure and epidemics on temporal networks. , 2020, , .		4
18666	PopPhy-CNN: A Phylogenetic Tree Embedded Architecture for Convolutional Neural Networks to Predict Host Phenotype From Metagenomic Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 2993-3001.	3.9	55
18667	Exosomes mediate intercellular transfer of non- $\alpha$ autonomous tolerance to proteasome inhibitors in mixed-lineage leukemia. <i>Cancer Science</i> , 2020, 111, 1279-1290.	1.7	28
18668	Shotgun mitogenomics across body size classes in a local assemblage of tropical Diptera: Phylogeny, species diversity and mitochondrial abundance spectrum. <i>Molecular Ecology</i> , 2017, 26, 5086-5098.	2.0	17
18669	The modulation of the burn wound environment by negative pressure wound therapy: Insights from the proteome. <i>Wound Repair and Regeneration</i> , 2021, 29, 288-297.	1.5	10
18670	Distance canonical correlation analysis with application to an imaging-genetic study. <i>Journal of Medical Imaging</i> , 2019, 6, 1.	0.8	8
18671	Protein interaction networks revealed by proteome coevolution. <i>Science</i> , 2019, 365, 185-189.	6.0	208
18672	A Genome Epidemiological Study of SARS-CoV-2 Introduction into Japan. <i>MSphere</i> , 2020, 5, .	1.3	42
18673	Global Network Analysis of <i>Neisseria gonorrhoeae</i> Identifies Coordination between Pathways, Processes, and Regulators Expressed during Human Infection. <i>MSystems</i> , 2020, 5, .	1.7	8

#	ARTICLE	IF	CITATIONS
18674	Building associations between markers of environmental stressors and adverse human health impacts using frequent itemset mining. , 2014, , .		9
18675	CHALKBOARD: ONTOLOGY-BASED PATHWAY MODELING AND QUALITATIVE INFERENCE OF DISEASE MECHANISMS. , 2006, , .		2
18676	DIACHRONIC PROCESSES IN LANGUAGE AS SIGNALING UNDER CONFLICTING INTERESTS. , 2014, , .		1
18677	SYNTACTIC DEVELOPMENT IN PHENOTYPIC SPACE. , 2014, , .		2
18679	Active Pathways. , 2016, , .		32
18680	DyNetVis. , 2017, , .		23
18682	Constructing Reliable Protein-Protein Interaction (PPI) Networks. , 2017, , 15.		4
18683	JGraphTâ€”A Java Library for Graph Data Structures and Algorithms. ACM Transactions on Mathematical Software, 2020, 46, 1-29.	1.6	65
18684	Bioinformatic Tools for Inferring Functional Information from Plant Microarray Data II: Analysis Beyond Single Gene. International Journal of Plant Genomics, 2008, 2008, 1-13.	2.2	12
18685	Network Pharmacology Approach to Explore the Potential Mechanisms of Jieduan-Niwan Formula Treating Acute-on-Chronic Liver Failure. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-16.	0.5	7
18686	Gender Differences in Rheumatoid Arthritis: Interleukin-4 Plays an Important Role. Journal of Immunology Research, 2020, 2020, 1-12.	0.9	10
18687	Assessing the Anti-inflammatory Mechanism of Reduning Injection by Network Pharmacology. BioMed Research International, 2020, 2020, 1-13.	0.9	11
18688	Exploring the Antitumor Mechanisms of Zingiberis Rhizoma Combined with Coptidis Rhizoma Using a Network Pharmacology Approach. BioMed Research International, 2020, 2020, 1-18.	0.9	2
18689	Gene network analysis: from heart development to cardiac therapy. Thrombosis and Haemostasis, 2015, 113, 521-531.	1.8	7
18690	Wilmsâ€™ tumor 1 drives fibroproliferation and myofibroblast transformation in severe fibrotic lung disease. JCI Insight, 2018, 3, .	2.3	32
18691	WIPI1 is a conserved mediator of right ventricular failure. JCI Insight, 2019, 4, .	2.3	16
18692	Cell typeâ€™specific immune phenotypes predict loss of insulin secretion in new-onset type 1 diabetes. JCI Insight, 2019, 4, .	2.3	38
18693	B lymphocyte alterations accompany abatacept resistance in new-onset type 1 diabetes. JCI Insight, 2019, 4, .	2.3	39



#	ARTICLE	IF	CITATIONS
18694	Integrative study of the upper and lower airway microbiome and transcriptome in asthma. JCI Insight, 2020, 5, .	2.3	44
18695	Regulator combinations identify systemic sclerosis patients with more severe disease. JCI Insight, 2020, 5, .	2.3	2
18696	In utero human intestine harbors unique metabolome, including bacterial metabolites. JCI Insight, 2020, 5, .	2.3	33
18697	Hsp90 regulation of fibroblast activation in pulmonary fibrosis. JCI Insight, 2017, 2, e91454.	2.3	73
18698	Clonal relationships of CSF B cells in treatment-naive multiple sclerosis patients. JCI Insight, 2017, 2, .	2.3	84
18699	Pediatric dilated cardiomyopathy hearts display a unique gene expression profile. JCI Insight, 2017, 2, .	2.3	46
18700	A BAG3 chaperone complex maintains cardiomyocyte function during proteotoxic stress. JCI Insight, 2017, 2, .	2.3	81
18701	IRS2 mutations linked to invasion in pleomorphic invasive lobular carcinoma. JCI Insight, 2018, 3, .	2.3	18
18702	A peripheral blood transcriptomic signature predicts autoantibody development in infants at risk of type 1 diabetes. JCI Insight, 2018, 3, .	2.3	18
18703	Whole-exome sequencing uncovers oxidoreductases DHTKD1 and OGDHL as linkers between mitochondrial dysfunction and eosinophilic esophagitis. JCI Insight, 2018, 3, .	2.3	39
18704	Sphingosine kinase 2 restricts T cell immunopathology but permits viral persistence. Journal of Clinical Investigation, 2020, 130, 6523-6538.	3.9	17
18705	Norrin mediates tumor-promoting and -suppressive effects in glioblastoma via Notch and Wnt. Journal of Clinical Investigation, 2020, 130, 3069-3086.	3.9	15
18706	Machine learning reveals serum sphingolipids as cholesterol-independent biomarkers of coronary artery disease. Journal of Clinical Investigation, 2020, 130, 1363-1376.	3.9	141
18707	Epithelial splicing regulatory protein 2-mediated alternative splicing reprograms hepatocytes in severe alcoholic hepatitis. Journal of Clinical Investigation, 2020, 130, 2129-2145.	3.9	49
18708	Graft-versus-host disease reduces lymph node display of tissue-restricted self-antigens and promotes autoimmunity. Journal of Clinical Investigation, 2020, 130, 1896-1911.	3.9	27
18709	Filgotinib suppresses HIV-1-driven gene transcription by inhibiting HIV-1 splicing and T cell activation. Journal of Clinical Investigation, 2020, 130, 4969-4984.	3.9	26
18710	Glioma escape signature and clonal development under immune pressure. Journal of Clinical Investigation, 2020, 130, 5257-5271.	3.9	21
18711	Bicc1 is a genetic determinant of osteoblastogenesis and bone mineral density. Journal of Clinical Investigation, 2014, 124, 2736-2749.	3.9	51

#	ARTICLE	IF	CITATIONS
18712	Cardiomyocyte proliferation prevents failure in pressure overload but not volume overload. <i>Journal of Clinical Investigation</i> , 2017, 127, 4285-4296.	3.9	31
18713	Cancer-associated fibroblast-derived annexin A6+ extracellular vesicles support pancreatic cancer aggressiveness. <i>Journal of Clinical Investigation</i> , 2016, 126, 4140-4156.	3.9	169
18714	Loss-of-function mutations in co-chaperone BAG3 destabilize small HSPs and cause cardiomyopathy. <i>Journal of Clinical Investigation</i> , 2017, 127, 3189-3200.	3.9	107
18715	Transcription factor Fra-1 targets arginase-1 to enhance macrophage-mediated inflammation in arthritis. <i>Journal of Clinical Investigation</i> , 2019, 129, 2669-2684.	3.9	51
18716	CD28 blockade controls T cell activation to prevent graft-versus-host disease in primates. <i>Journal of Clinical Investigation</i> , 2018, 128, 3991-4007.	3.9	42
18717	Identifications of Candidate Genes Significantly Associated With Rectal Cancer by Integrated Bioinformatics Analysis. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382097327.	0.8	9
18718	A Competing Endogenous RNA Network Reveals Novel lncRNA, miRNA and mRNA Biomarkers With Diagnostic and Prognostic Value for Early Breast Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382098329.	0.8	15
18719	Enrichment of genomic pathways based on differential DNA methylation profiles associated with chronic musculoskeletal pain in older adults: An exploratory study. <i>Molecular Pain</i> , 2020, 16, 174480692096690.	1.0	7
18720	Alteration of RNA Splicing by Small-Molecule Inhibitors of the Interaction between NHP2L1 and U4. <i>SLAS Discovery</i> , 2018, 23, 164-173.	1.4	14
18721	An integrated multiomic and quantitative label-free microscopy-based approach to study pro-fibrotic signalling in <i>ex vivo</i> human precision-cut lung slices. <i>European Respiratory Journal</i> , 2021, 58, 2000221.	3.1	21
18723	Transcriptome Sequencing and iTRAQ of Different Rice Cultivars Provide Insight into Molecular Mechanisms of Cold-Tolerance Response in Japonica Rice. <i>Rice</i> , 2020, 13, 43.	1.7	19
18724	ModelExplorer - software for visual inspection and inconsistency correction of genome-scale metabolic reconstructions. <i>BMC Bioinformatics</i> , 2019, 20, 56.	1.2	10
18725	Coexpression and Transcriptome analyses identify active Apomixis-related genes in <i>Paspalum notatum</i> leaves. <i>BMC Genomics</i> , 2020, 21, 78.	1.2	12
18726	Tuberomics: a molecular profiling for the adaption of edible fungi ( <i>Tuber magnatum</i> Pico) to different natural environments. <i>BMC Genomics</i> , 2020, 21, 90.	1.2	15
18727	Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans. <i>BMC Biology</i> , 2020, 18, 51.	1.7	26
18728	miR-124 and miR-203 synergistically inactivate EMT pathway via coregulation of ZEB2 in clear cell renal cell carcinoma (ccRCC). <i>Journal of Translational Medicine</i> , 2020, 18, 69.	1.8	48
18729	Expression profiling of spinal cord dorsal horn in a rat model of complex regional pain syndrome type-1 uncovers potential mechanisms mediating pain and neuroinflammation responses. <i>Journal of Neuroinflammation</i> , 2020, 17, 162.	3.1	31
18730	Potentially adaptive SARS-CoV-2 mutations discovered with novel spatiotemporal and explainable AI models. <i>Genome Biology</i> , 2020, 21, 304.	3.8	55

#	ARTICLE	IF	CITATIONS
18731	Identification of key genes and pathways in syphilis combined with diabetes: a bioinformatics study. <i>AMB Express</i> , 2020, 10, 83.	1.4	2
18732	Contrasting bacterial and archaeal distributions reflecting different geochemical processes in a sediment core from the Pearl River Estuary. <i>AMB Express</i> , 2020, 10, 16.	1.4	18
18733	Root ethylene mediates rhizosphere microbial community reconstruction when chemically detecting cyanide produced by neighbouring plants. <i>Microbiome</i> , 2020, 8, 4.	4.9	102
18734	The microbiome as a biosensor: functional profiles elucidate hidden stress in hosts. <i>Microbiome</i> , 2020, 8, 71.	4.9	24
18735	Linking belowground microbial network changes to different tolerance level towards <i>Verticillium</i> wilt of olive. <i>Microbiome</i> , 2020, 8, 11.	4.9	78
18736	Transcriptional profiling of leukocytes in critically ill COVID19 patients: implications for interferon response and coagulation. <i>Intensive Care Medicine Experimental</i> , 2020, 8, 75.	0.9	37
18739	Systems Pharmacology Dissection of Mechanisms of Dengzhan Xixin Injection against Cardiovascular Diseases. <i>Chemical and Pharmaceutical Bulletin</i> , 2020, 68, 837-847.	0.6	6
18740	Identification of CD20, ECM, and ITGA as Biomarkers for Osteosarcoma by Integrating Transcriptome Analysis. <i>Medical Science Monitor</i> , 2016, 22, 2075-2085.	0.5	11
18741	Clinical Value of miR-101-3p and Biological Analysis of its Prospective Targets in Breast Cancer: A Study Based on The Cancer Genome Atlas (TCGA) and Bioinformatics. <i>Medical Science Monitor</i> , 2017, 23, 1857-1871.	0.5	25
18742	RNA Sequencing Uncovers Molecular Mechanisms Underlying Pathological Complete Response to Chemotherapy in Patients with Operable Breast Cancer. <i>Medical Science Monitor</i> , 2017, 23, 4321-4327.	0.5	19
18743	Identification of Novel Target for Osteosarcoma by Network Analysis. <i>Medical Science Monitor</i> , 2018, 24, 5914-5924.	0.5	3
18744	Distinct Prognostic Values of Alcohol Dehydrogenase Family Members for Non-Small Cell Lung Cancer. <i>Medical Science Monitor</i> , 2018, 24, 3578-3590.	0.5	21
18745	microRNA-205 and microRNA-338-3p Reduces Cell Apoptosis in Prostate Carcinoma Tissue and LNCaP Prostate Carcinoma Cells by Directly Targeting the B-Cell Lymphoma 2 (Bcl-2) Gene. <i>Medical Science Monitor</i> , 2019, 25, 1122-1132.	0.5	12
18746	Both Peripheral Blood and Urinary miR-195-5p, miR-192-3p, miR-328-5p and Their Target Genes PPM1A, RAB1A and BRSK1 May Be Potential Biomarkers for Membranous Nephropathy. <i>Medical Science Monitor</i> , 2019, 25, 1903-1916.	0.5	16
18747	Network Pharmacology-Based Pharmacological Mechanism of the Chinese Medicine <i>Rhizoma drynariae</i> Against Osteoporosis. <i>Medical Science Monitor</i> , 2019, 25, 5700-5716.	0.5	46
18748	Construction of a Competitive Endogenous RNA Network in Uterine Corpus Endometrial Carcinoma. <i>Medical Science Monitor</i> , 2019, 25, 7998-8010.	0.5	13
18749	Weighted Gene Coexpression Network Analysis Identifies Key Genes and Pathways Associated with Idiopathic Pulmonary Fibrosis. <i>Medical Science Monitor</i> , 2019, 25, 4285-4304.	0.5	12
18750	Identification of a 5-Gene Signature Predicting Progression and Prognosis of Clear Cell Renal Cell Carcinoma. <i>Medical Science Monitor</i> , 2019, 25, 4401-4413.	0.5	26

#	ARTICLE	IF	CITATIONS
18751	Establishment of the Prognosis Predicting Signature for Endometrial Cancer Patient. Medical Science Monitor, 2019, 25, 8248-8259.	0.5	6
18752	Identification of Key Genes in Thyroid Cancer Microenvironment. Medical Science Monitor, 2019, 25, 9602-9608.	0.5	20
18753	Identification and Integrated Analysis of Key Biomarkers for Diagnosis and Prognosis of Non-Small Cell Lung Cancer. Medical Science Monitor, 2019, 25, 9280-9289.	0.5	16
18754	Combined Use of Three Machine Learning Modeling Methods to Develop a Ten-Genes Signature for the Diagnosis of Ventilator-Associated Pneumonia. Medical Science Monitor, 2020, 26, e919035.	0.5	4
18755	Bioinformatics Analysis Identifies Hub Genes and Molecular Pathways Involved in Sepsis-Induced Myopathy. Medical Science Monitor, 2020, 26, e919665.	0.5	5
18756	Comprehensive Analysis of Differential Gene Expression to Identify Common Gene Signatures in Multiple Cancers. Medical Science Monitor, 2020, 26, e919953.	0.5	26
18757	Integrated Analysis of Three Publicly Available Gene Expression Profiles Identified Genes and Pathways Associated with Clear Cell Renal Cell Carcinoma. Medical Science Monitor, 2020, 26, e919965.	0.5	2
18758	Identification of Genes with Prognostic Value in the Breast Cancer Microenvironment Using Bioinformatics Analysis. Medical Science Monitor, 2020, 26, e920212.	0.5	9
18759	Identification of Hub Genes and Pathways in Gastric Adenocarcinoma Based on Bioinformatics Analysis. Medical Science Monitor, 2020, 26, e920261.	0.5	18
18760	Identification of Hub Genes and Pathways in a Rat Model of Renal Ischemia-Reperfusion Injury Using Bioinformatics Analysis of the Gene Expression Omnibus (GEO) Dataset and Integration of Gene Expression Profiles. Medical Science Monitor, 2019, 25, 8403-8411.	0.5	20
18761	Identification of 2 Potential Core Genes for Influence of Gut Probiotics on Formation of Intracranial Aneurysms by Bioinformatics Analysis. Medical Science Monitor, 2020, 26, e920754.	0.5	4
18762	Bioinformatics Analysis for Multiple Gene Expression Profiles in Sepsis. Medical Science Monitor, 2020, 26, e920818.	0.5	16
18763	Anticancer Effect of Radix Astragali on Cholangiocarcinoma In Vitro and Its Mechanism via Network Pharmacology. Medical Science Monitor, 2020, 26, e921162.	0.5	8
18764	POLE2 Serves as a Prognostic Biomarker and Is Associated with Immune Infiltration in Squamous Cell Lung Cancer. Medical Science Monitor, 2020, 26, e921430.	0.5	11
18765	Bioinformatics Analysis Identifies the Estrogen Receptor 1 (ESR1) Gene and hsa-miR-26a-5p as Potential Prognostic Biomarkers in Patients with Intrahepatic Cholangiocarcinoma. Medical Science Monitor, 2020, 26, e921815.	0.5	6
18766	Comprehensive Analysis of Candidate Diagnostic and Prognostic Biomarkers Associated with Lung Adenocarcinoma. Medical Science Monitor, 2020, 26, e922070.	0.5	6
18767	Integrated Analysis of Hub Genes and Pathways In Esophageal Carcinoma Based on NCBI's Gene Expression Omnibus (GEO) Database: A Bioinformatics Analysis. Medical Science Monitor, 2020, 26, e923934.	0.5	11
18768	Tomatidine Alleviates Osteoporosis by Downregulation of p53. Medical Science Monitor, 2020, 26, e923996.	0.5	17

#	ARTICLE	IF	CITATIONS
18769	Bioinformatics Analysis and Identification of Underlying Biomarkers Potentially Linking Allergic Rhinitis and Asthma. <i>Medical Science Monitor</i> , 2020, 26, e924934.	0.5	21
18770	A Systematic Pharmacology and In Vitro Study to Identify the Role of the Active Compounds of <i>Achyranthes bidentata</i> in the Treatment of Osteoarthritis. <i>Medical Science Monitor</i> , 2020, 26, e925545.	0.5	4
18771	A Network Pharmacological Approach to Investigate the Mechanism of Action of Active Ingredients of <i>Epimedii Herba</i> and Their Potential Targets in Treatment of Alzheimer's Disease. <i>Medical Science Monitor</i> , 2020, 26, e926295.	0.5	3
18772	Identification of Potential Biomarkers of Prognosis-Related Long Non-Coding RNA (lncRNA) in Pediatric Rhabdoid Tumor of the Kidney Based on ceRNA Networks. <i>Medical Science Monitor</i> , 2020, 26, e927725.	0.5	9
18773	Functional Analysis of Estrogen Receptor 1 in Diabetic Wound Healing: A Knockdown Cell-Based and Bioinformatic Study. <i>Medical Science Monitor</i> , 2020, 26, e928788.	0.5	3
18774	Maize Phyllosphere Microbial Community Niche Development Across Stages of Host Leaf Growth. <i>F1000Research</i> , 0, 6, 1698.	0.8	3
18775	Maize Phyllosphere Microbial Community Niche Development Across Stages of Host Leaf Growth. <i>F1000Research</i> , 2017, 6, 1698.	0.8	15
18776	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	0.8	6
18777	CellMap visualizes protein-protein interactions and subcellular localization. <i>F1000Research</i> , 2017, 6, 1824.	0.8	5
18778	Identification of diverse defense mechanisms in trout red blood cells in response to VHSV halted viral replication. <i>F1000Research</i> , 2017, 6, 1958.	0.8	33
18779	Identification of diverse defense mechanisms in rainbow trout red blood cells in response to halted replication of VHS virus. <i>F1000Research</i> , 2017, 6, 1958.	0.8	32
18780	Comparing protein structures with RINspecter automation in Cytoscape. <i>F1000Research</i> , 2018, 7, 563.	0.8	9
18781	Comparing protein structures with RINspecter automation in Cytoscape. <i>F1000Research</i> , 2018, 7, 563.	0.8	15
18782	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. <i>F1000Research</i> , 2018, 7, 743.	0.8	26
18783	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. <i>F1000Research</i> , 2018, 7, 743.	0.8	18
18784	Identifier Mapping in Cytoscape. <i>F1000Research</i> , 2018, 7, 725.	0.8	6
18785	autoHGPEC: Automated prediction of novel disease-gene and disease-disease associations and evidence collection based on a random walk on heterogeneous network. <i>F1000Research</i> , 0, 7, 658.	0.8	3
18786	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 2018, 7, 1346.	0.8	1

#	ARTICLE	IF	CITATIONS
18787	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. F1000Research, 2018, 7, 1906.	0.8	4
18788	Enhancing gene set enrichment using networks. F1000Research, 2019, 8, 129.	0.8	11
18789	Network-based Observability and Controllability Analysis of Dynamical Systems: the NOCAD toolbox. F1000Research, 2019, 8, 646.	0.8	4
18790	Visualization of drug target interactions in the contexts of pathways and networks with ReactomeFIViz. F1000Research, 2019, 8, 908.	0.8	20
18791	Cyrface: An interface from Cytoscape to R that provides a user interface to R packages. F1000Research, 2013, 2, 192.	0.8	3
18792	ANGDelMut â€“ a web-based tool for predicting and analyzing functional loss mechanisms of amyotrophic lateral sclerosis-associated angiogenin mutations. F1000Research, 0, 2, 227.	0.8	1
18793	ANGDelMut â€“ a web-based tool for predicting and analyzing functional loss mechanisms of amyotrophic lateral sclerosis-associated angiogenin mutations. F1000Research, 2013, 2, 227.	0.8	4
18794	RCy3: Network biology using Cytoscape from within R. F1000Research, 2019, 8, 1774.	0.8	39
18795	RCy3: Network biology using Cytoscape from within R. F1000Research, 0, 8, 1774.	0.8	101
18796	RCy3: Network biology using Cytoscape from within R. F1000Research, 2019, 8, 1774.	0.8	80
18797	Precision medicine in inflammatory bowel disease: concept, progress and challenges. F1000Research, 2020, 9, 54.	0.8	59
18798	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	54
18799	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	35
18800	Prediction of repurposed drugs for treating lung injury in COVID-19. F1000Research, 2020, 9, 609.	0.8	21
18801	Prediction of repurposed drugs for treating lung injury in COVID-19. F1000Research, 2020, 9, 609.	0.8	26
18802	PPI layouts: BioJS components for the display of Protein-Protein Interactions. F1000Research, 2014, 3, 50.	0.8	9
18803	BioJS DAGViewer: A reusable JavaScript component for displaying directed graphs. F1000Research, 2014, 3, 51.	0.8	5
18804	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. F1000Research, 0, 3, 152.	0.8	5



#	ARTICLE	IF	CITATIONS
18805	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. F1000Research, 2014, 3, 152.	0.8	57
18806	setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	14
18807	enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014, 3, 147.	0.8	45
18808	Cytoscape tools for the web age: D3.js and Cytoscape.js exporters. F1000Research, 2014, 3, 143.	0.8	44
18809	BridgeDb app: unifying identifier mapping services for Cytoscape. F1000Research, 2014, 3, 148.	0.8	11
18810	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
18811	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10
18812	GeneMANIA: Fast gene network construction and function prediction for Cytoscape. F1000Research, 2014, 3, 153.	0.8	242
18813	Development and use of the Cytoscape app GFD-Net for measuring semantic dissimilarity of gene networks. F1000Research, 2014, 3, 142.	0.8	11
18814	The Cytoscape app article collection. F1000Research, 2014, 3, 138.	0.8	10
18815	Visualisation of BioPAX Networks using BioLayout Express3D. F1000Research, 2014, 3, 246.	0.8	16
18816	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 2015, 4, 103.	0.8	32
18817	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 2015, 4, 103.	0.8	29
18818	PSFC: a Pathway Signal Flow Calculator App for Cytoscape. F1000Research, 2015, 4, 480.	0.8	12
18819	PSFC: a Pathway Signal Flow Calculator App for Cytoscape. F1000Research, 2015, 4, 480.	0.8	13
18820	CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful API. F1000Research, 2015, 4, 478.	0.8	81
18821	Finding the shortest path with PesCa: a tool for network reconstruction. F1000Research, 2015, 4, 484.	0.8	28
18822	Finding the shortest path with PesCa: a tool for network reconstruction. F1000Research, 2015, 4, 484.	0.8	21

#	ARTICLE	IF	CITATIONS
18823	SLiMScape 3.x: a Cytoscape 3 app for discovery of Short Linear Motifs in protein interaction networks. F1000Research, 2015, 4, 477.	0.8	1
18824	CySpanningTree: Minimal Spanning Tree computation in Cytoscape. F1000Research, 0, 4, 476.	0.8	12
18825	Social Network: a Cytoscape app for visualizing co-authorship networks. F1000Research, 2015, 4, 481.	0.8	12
18826	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	11
18827	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485.	0.8	8
18828	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	11
18829	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	10
18830	Integrated analysis of oral tongue squamous cell carcinoma identifies key variants and pathways linked to risk habits, HPV, clinical parameters and tumor recurrence. F1000Research, 2015, 4, 1215.	0.8	23
18831	FlyOde - a platform for community curation and interactive visualization of dynamic gene regulatory networks in Drosophila eye development. F1000Research, 2015, 4, 1484.	0.8	4
18832	BioTapestry now provides a web application and improved drawing and layout tools. F1000Research, 2016, 5, 39.	0.8	25
18833	CyLineUp: A Cytoscape app for visualizing data in network small multiples. F1000Research, 2016, 5, 635.	0.8	3
18834	Contextual Hub Analysis Tool (CHAT): A Cytoscape app for identifying contextually relevant hubs in biological networks. F1000Research, 0, 5, 1745.	0.8	39
18835	Contextual Hub Analysis Tool (CHAT): A Cytoscape app for identifying contextually relevant hubs in biological networks. F1000Research, 2016, 5, 1745.	0.8	18
18836	cy3sabiork: A Cytoscape app for visualizing kinetic data from SABIO-RK. F1000Research, 0, 5, 1736.	0.8	2
18837	Predicted protein interactions of IFITMs which inhibit Zika virus infection. F1000Research, 2016, 5, 1919.	0.8	7
18838	Predicted protein interactions of IFITMs may shed light on mechanisms of Zika virus-induced microcephaly and host invasion. F1000Research, 2016, 5, 1919.	0.8	7
18839	dot-app: a Graphviz-Cytoscape conversion plug-in. F1000Research, 2016, 5, 2543.	0.8	2
18840	ANIMA: Association network integration for multiscale analysis. Wellcome Open Research, 2018, 3, 27.	0.9	6

#	ARTICLE	IF	CITATIONS
18841	Single-cell transcriptome analysis of CD8+ T-cell memory inflation. Wellcome Open Research, 2019, 4, 78.	0.9	6
18842	Differential expression of skeletal muscle mitochondrial proteins in yak, dzo, and cattle: a proteomics-based study. Journal of Veterinary Medical Science, 2020, 82, 1178-1186.	0.3	10
18845	Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. PLoS Biology, 2015, 13, e1002307.	2.6	54
18846	ELF5 Drives Lung Metastasis in Luminal Breast Cancer through Recruitment of Gr1+ CD11b+ Myeloid-Derived Suppressor Cells. PLoS Biology, 2015, 13, e1002330.	2.6	59
18847	Evolution of High Cellulolytic Activity in Symbiotic Streptomyces through Selection of Expanded Gene Content and Coordinated Gene Expression. PLoS Biology, 2016, 14, e1002475.	2.6	68
18848	Single-Cell-Based Analysis Highlights a Surge in Cell-to-Cell Molecular Variability Preceding Irreversible Commitment in a Differentiation Process. PLoS Biology, 2016, 14, e1002585.	2.6	220
18849	Distinct populations of crypt-associated fibroblasts act as signaling hubs to control colon homeostasis. PLoS Biology, 2020, 18, e3001032.	2.6	53
18850	Disease-Aging Network Reveals Significant Roles of Aging Genes in Connecting Genetic Diseases. PLoS Computational Biology, 2009, 5, e1000521.	1.5	74
18851	Coordinating Role of RXR $\alpha$ in Downregulating Hepatic Detoxification during Inflammation Revealed by Fuzzy-Logic Modeling. PLoS Computational Biology, 2016, 12, e1004431.	1.5	27
18852	Connectivity Homology Enables Inter-Species Network Models of Synthetic Lethality. PLoS Computational Biology, 2015, 11, e1004506.	1.5	30
18853	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. PLoS Computational Biology, 2015, 11, e1004613.	1.5	89
18854	QuIN: A Web Server for Querying and Visualizing Chromatin Interaction Networks. PLoS Computational Biology, 2016, 12, e1004809.	1.5	10
18855	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. PLoS Computational Biology, 2016, 12, e1004879.	1.5	123
18856	A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. PLoS Computational Biology, 2016, 12, e1004884.	1.5	5
18857	Conservation in Mammals of Genes Associated with Aggression-Related Behavioral Phenotypes in Honey Bees. PLoS Computational Biology, 2016, 12, e1004921.	1.5	14
18858	Reactome from a WikiPathways Perspective. PLoS Computational Biology, 2016, 12, e1004941.	1.5	35
18859	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. PLoS Computational Biology, 2017, 13, e1005221.	1.5	31
18860	The Multilayer Connectome of Caenorhabditis elegans. PLoS Computational Biology, 2016, 12, e1005283.	1.5	170

#	ARTICLE	IF	CITATIONS
18861	Solving the influence maximization problem reveals regulatory organization of the yeast cell cycle. PLoS Computational Biology, 2017, 13, e1005591.	1.5	12
18862	A data-driven modeling approach to identify disease-specific multi-organ networks driving physiological dysregulation. PLoS Computational Biology, 2017, 13, e1005627.	1.5	8
18863	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. PLoS Computational Biology, 2017, 13, e1005700.	1.5	14
18864	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. PLoS Computational Biology, 2017, 13, e1005807.	1.5	147
18865	Insight into glucocorticoid receptor signalling through interactome model analysis. PLoS Computational Biology, 2017, 13, e1005825.	1.5	7
18866	An evolutionary learning and network approach to identifying key metabolites for osteoarthritis. PLoS Computational Biology, 2018, 14, e1005986.	1.5	30
18867	Model-based analysis of competing-endogenous pathways (MACPath) in human cancers. PLoS Computational Biology, 2018, 14, e1006074.	1.5	11
18868	Multiscale community detection in Cytoscape. PLoS Computational Biology, 2020, 16, e1008239.	1.5	34
18869	Bacteria use structural imperfect mimicry to hijack the host interactome. PLoS Computational Biology, 2020, 16, e1008395.	1.5	9
18870	Long-Term Persistence of Bi-functionality Contributes to the Robustness of Microbial Life through Exaptation. PLoS Genetics, 2016, 12, e1005836.	1.5	18
18871	Conservation of Distinct Genetically-Mediated Human Cortical Pattern. PLoS Genetics, 2016, 12, e1006143.	1.5	15
18872	Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. PLoS Genetics, 2018, 14, e1007376.	1.5	65
18873	SmCL3, a Gastrodermal Cysteine Protease of the Human Blood Fluke Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2009, 3, e449.	1.3	45
18874	Early Regulation of Profibrotic Genes in Primary Human Cardiac Myocytes by Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2016, 10, e0003747.	1.3	42
18875	Phenotypic Features of Circulating Leukocytes from Non-human Primates Naturally Infected with Trypanosoma cruzi Resemble the Major Immunological Findings Observed in Human Chagas Disease. PLoS Neglected Tropical Diseases, 2016, 10, e0004302.	1.3	15
18876	Cynomolgus macaques naturally infected with Trypanosoma cruzi-I exhibit an overall mixed pro-inflammatory/modulated cytokine signature characteristic of human Chagas disease. PLoS Neglected Tropical Diseases, 2017, 11, e0005233.	1.3	17
18877	Different genotypes of Trypanosoma cruzi produce distinctive placental environment genetic response in chronic experimental infection. PLoS Neglected Tropical Diseases, 2017, 11, e0005436.	1.3	16
18878	The introduction of dengue follows transportation infrastructure changes in the state of Acre, Brazil: A network-based analysis. PLoS Neglected Tropical Diseases, 2017, 11, e0006070.	1.3	46

#	ARTICLE	IF	CITATIONS
18879	Trypanosoma cruzi vaccine candidate antigens Tc24 and TSA-1 recall memory immune response associated with HLA-A and -B supertypes in Chagasic chronic patients from Mexico. PLoS Neglected Tropical Diseases, 2018, 12, e0006240.	1.3	31
18880	Experimental Chagas disease-induced perturbations of the fecal microbiome and metabolome. PLoS Neglected Tropical Diseases, 2018, 12, e0006344.	1.3	39
18881	miRNAs may play a major role in the control of gene expression in key pathobiological processes in Chagas disease cardiomyopathy. PLoS Neglected Tropical Diseases, 2020, 14, e0008889.	1.3	31
18882	Rich-Club Phenomenon in the Interactome of P. falciparum—Artifact or Signature of a Parasitic Life Style?. PLoS ONE, 2007, 2, e335.	1.1	15
18883	Linking Gene Expression and Functional Network Data in Human Heart Failure. PLoS ONE, 2007, 2, e1347.	1.1	40
18884	Sequence Evidence in the Archaeal Genomes that tRNAs Emerged Through the Combination of Ancestral Genes as 5â€² and 3â€² tRNA Halves. PLoS ONE, 2008, 3, e1622.	1.1	39
18885	A Visual Data Mining Tool that Facilitates Reconstruction of Transcription Regulatory Networks. PLoS ONE, 2008, 3, e1717.	1.1	23
18886	Mapping Genetically Compensatory Pathways from Synthetic Lethal Interactions in Yeast. PLoS ONE, 2008, 3, e1922.	1.1	41
18887	Targeted Development of Registries of Biological Parts. PLoS ONE, 2008, 3, e2671.	1.1	63
18888	The Evolving Transcriptome of Head and Neck Squamous Cell Carcinoma: A Systematic Review. PLoS ONE, 2008, 3, e3215.	1.1	61
18889	SLEPR: A Sample-Level Enrichment-Based Pathway Ranking Method — Seeking Biological Themes through Pathway-Level Consistency. PLoS ONE, 2008, 3, e3288.	1.1	18
18890	Human Gene Coexpression Landscape: Confident Network Derived from Tissue Transcriptomic Profiles. PLoS ONE, 2008, 3, e3911.	1.1	213
18891	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
18892	A Sequence and Structure Based Method to Predict Putative Substrates, Functions and Regulatory Networks of Endo Proteases. PLoS ONE, 2009, 4, e5700.	1.1	8
18893	Layered Functional Network Analysis of Gene Expression in Human Heart Failure. PLoS ONE, 2009, 4, e6288.	1.1	16
18894	Mining Biological Pathways Using WikiPathways Web Services. PLoS ONE, 2009, 4, e6447.	1.1	100
18895	Inferring the Transcriptional Landscape of Bovine Skeletal Muscle by Integrating Co-Expression Networks. PLoS ONE, 2009, 4, e7249.	1.1	63
18896	VitisNet: —Omics—Integration through Grapevine Molecular Networks. PLoS ONE, 2009, 4, e8365.	1.1	153

#	ARTICLE	IF	CITATIONS
18897	Covariation of Branch Lengths in Phylogenies of Functionally Related Genes. PLoS ONE, 2009, 4, e8487.	1.1	5
18898	Application of Gene Network Analysis Techniques Identifies AXIN1/PDIA2 and Endoglin Haplotypes Associated with Bicuspid Aortic Valve. PLoS ONE, 2010, 5, e8830.	1.1	52
18899	A PubMed-Wide Associational Study of Infectious Diseases. PLoS ONE, 2010, 5, e9535.	1.1	11
18900	Evidence for Large Complex Networks of Plant Short Silencing RNAs. PLoS ONE, 2010, 5, e9901.	1.1	44
18901	Connecting Mutations of the RNA Polymerase II C-Terminal Domain to Complex Phenotypic Changes Using Combined Gene Expression and Network Analyses. PLoS ONE, 2010, 5, e11386.	1.1	2
18902	Transcription Profiling of Epstein-Barr Virus Nuclear Antigen (EBNA)-1 Expressing Cells Suggests Targeting of Chromatin Remodeling Complexes. PLoS ONE, 2010, 5, e12052.	1.1	23
18903	DEGAS: De Novo Discovery of Dysregulated Pathways in Human Diseases. PLoS ONE, 2010, 5, e13367.	1.1	113
18904	Yeast Biological Networks Unfold the Interplay of Antioxidants, Genome and Phenotype, and Reveal a Novel Regulator of the Oxidative Stress Response. PLoS ONE, 2010, 5, e13606.	1.1	14
18905	QAPgrid: A Two Level QAP-Based Approach for Large-Scale Data Analysis and Visualization. PLoS ONE, 2011, 6, e14468.	1.1	22
18906	Gene Expression Meta-Analysis Identifies VDAC1 as a Predictor of Poor Outcome in Early Stage Non-Small Cell Lung Cancer. PLoS ONE, 2011, 6, e14635.	1.1	60
18907	MicroRNA Expression Analysis: Clinical Advantage of Propranolol Reveals Key MicroRNAs in Myocardial Infarction. PLoS ONE, 2011, 6, e14736.	1.1	36
18908	The PluriNetWork: An Electronic Representation of the Network Underlying Pluripotency in Mouse, and Its Applications. PLoS ONE, 2010, 5, e15165.	1.1	67
18909	Integrated Profiling of MicroRNAs and mRNAs: MicroRNAs Located on Xq27.3 Associate with Clear Cell Renal Cell Carcinoma. PLoS ONE, 2010, 5, e15224.	1.1	573
18910	Using Regulatory and Epistatic Networks to Extend the Findings of a Genome Scan: Identifying the Gene Drivers of Pigmentation in Merino Sheep. PLoS ONE, 2011, 6, e21158.	1.1	52
18911	HelmCoP: An Online Resource for Helminth Functional Genomics and Drug and Vaccine Targets Prioritization. PLoS ONE, 2011, 6, e21832.	1.1	17
18912	ChIP-seq Defined Genome-Wide Map of TGF $\beta$ 2/SMAD4 Targets: Implications with Clinical Outcome of Ovarian Cancer. PLoS ONE, 2011, 6, e22606.	1.1	27
18913	Global and Local Features of Semantic Networks: Evidence from the Hebrew Mental Lexicon. PLoS ONE, 2011, 6, e23912.	1.1	84
18914	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. PLoS ONE, 2011, 6, e24442.	1.1	87



#	ARTICLE	IF	CITATIONS
18915	Defining the Molecular Character of the Developing and Adult Kidney Podocyte. PLoS ONE, 2011, 6, e24640.	1.1	116
18916	A Targeted Association Study of Immunity Genes and Networks Suggests Novel Associations with Placental Malaria Infection. PLoS ONE, 2011, 6, e24996.	1.1	6
18917	Biochemical and Computational Analysis Of LNX1 Interacting Proteins. PLoS ONE, 2011, 6, e26248.	1.1	22
18918	Prediction of Disease and Phenotype Associations from Genome-Wide Association Studies. PLoS ONE, 2011, 6, e27175.	1.1	37
18919	Comparing Statistical Methods for Constructing Large Scale Gene Networks. PLoS ONE, 2012, 7, e29348.	1.1	156
18920	Composite Structural Motifs of Binding Sites for Delineating Biological Functions of Proteins. PLoS ONE, 2012, 7, e31437.	1.1	8
18921	Network Analysis of Epidermal Growth Factor Signaling Using Integrated Genomic, Proteomic and Phosphorylation Data. PLoS ONE, 2012, 7, e34515.	1.1	37
18922	Regulation of Motility of Myogenic Cells in Filling Limb Muscle Anlagen by Pitx2. PLoS ONE, 2012, 7, e35822.	1.1	17
18923	Identification and Validation of Ifit1 as an Important Innate Immune Bottleneck. PLoS ONE, 2012, 7, e36465.	1.1	28
18924	Integrative Gene Regulatory Network Analysis Reveals Light-Induced Regional Gene Expression Phase Shift Programs in the Mouse Suprachiasmatic Nucleus. PLoS ONE, 2012, 7, e37833.	1.1	15
18925	Transcriptome Kinetics of Circulating Neutrophils during Human Experimental Endotoxemia. PLoS ONE, 2012, 7, e38255.	1.1	38
18926	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. PLoS ONE, 2012, 7, e38571.	1.1	190
18927	Systemic Biomarkers of Neutrophilic Inflammation, Tissue Injury and Repair in COPD Patients with Differing Levels of Disease Severity. PLoS ONE, 2012, 7, e38629.	1.1	86
18928	A Non-Targeted Approach Unravels the Volatile Network in Peach Fruit. PLoS ONE, 2012, 7, e38992.	1.1	63
18929	Modulation of Lactobacillus plantarum Gastrointestinal Robustness by Fermentation Conditions Enables Identification of Bacterial Robustness Markers. PLoS ONE, 2012, 7, e39053.	1.1	56
18930	Proteomic and Systems Biology Analysis of Monocytes Exposed to Securinine, a GABAA Receptor Antagonist and Immune Adjuvant. PLoS ONE, 2012, 7, e41278.	1.1	12
18931	FunSAV: Predicting the Functional Effect of Single Amino Acid Variants Using a Two-Stage Random Forest Model. PLoS ONE, 2012, 7, e43847.	1.1	43
18932	Novel Genes and Pathways Modulated by Syndecan-1: Implications for the Proliferation and Cell-Cycle Regulation of Malignant Mesothelioma Cells. PLoS ONE, 2012, 7, e48091.	1.1	41

#	ARTICLE	IF	CITATIONS
18933	Prediction of <i>C. elegans</i> Longevity Genes by Human and Worm Longevity Networks. PLoS ONE, 2012, 7, e48282.	1.1	49
18934	An Approach for the Identification of Targets Specific to Bone Metastasis Using Cancer Genes Interactome and Gene Ontology Analysis. PLoS ONE, 2012, 7, e49401.	1.1	16
18935	Expression Profile in Rice Panicle: Insights into Heat Response Mechanism at Reproductive Stage. PLoS ONE, 2012, 7, e49652.	1.1	110
18936	Expression-Based Functional Investigation of the Organ-Specific MicroRNAs in Arabidopsis. PLoS ONE, 2012, 7, e50870.	1.1	16
18937	Pronounced Effects of Acute Endurance Exercise on Gene Expression in Resting and Exercising Human Skeletal Muscle. PLoS ONE, 2012, 7, e51066.	1.1	107
18938	Power-Laws and the Use of Pluripotent Stem Cell Lines. PLoS ONE, 2013, 8, e52068.	1.1	6
18939	In Captive Rhesus Macaques, Cervicovaginal Inflammation Is Common but Not Associated with the Stable Polymicrobial Microbiome. PLoS ONE, 2012, 7, e52992.	1.1	16
18940	The Transcriptional and Gene Regulatory Network of <i>Lactococcus lactis</i> MG1363 during Growth in Milk. PLoS ONE, 2013, 8, e53085.	1.1	23
18941	Identification of Novel Protein-Protein Interactions of <i>Yersinia pestis</i> Type III Secretion System by Yeast Two Hybrid System. PLoS ONE, 2013, 8, e54121.	1.1	15
18942	Equal Opportunity for Low-Degree Network Nodes: A PageRank-Based Method for Protein Target Identification in Metabolic Graphs. PLoS ONE, 2013, 8, e54204.	1.1	36
18943	Human 14-3-3 Paralogs Differences Uncovered by Cross-Talk of Phosphorylation and Lysine Acetylation. PLoS ONE, 2013, 8, e55703.	1.1	45
18944	N-Glycoproteome of E14.Tg2a Mouse Embryonic Stem Cells. PLoS ONE, 2013, 8, e55722.	1.1	18
18945	Pharmacometabolomics Reveals Racial Differences in Response to Atenolol Treatment. PLoS ONE, 2013, 8, e57639.	1.1	68
18946	Gene Expression Profile Analysis of Type 2 Diabetic Mouse Liver. PLoS ONE, 2013, 8, e57766.	1.1	37
18947	The Properties of Genome Conformation and Spatial Gene Interaction and Regulation Networks of Normal and Malignant Human Cell Types. PLoS ONE, 2013, 8, e58793.	1.1	35
18948	Modulation of the Metabiome by Rifaximin in Patients with Cirrhosis and Minimal Hepatic Encephalopathy. PLoS ONE, 2013, 8, e60042.	1.1	340
18949	Worldwide Spread of Dengue Virus Type 1. PLoS ONE, 2013, 8, e62649.	1.1	69
18950	Genome-Scale Modeling of the Protein Secretory Machinery in Yeast. PLoS ONE, 2013, 8, e63284.	1.1	71

#	ARTICLE	IF	CITATIONS
18951	Medullospheres from DAOY, UW228 and ONS-76 Cells: Increased Stem Cell Population and Proteomic Modifications. PLoS ONE, 2013, 8, e63748.	1.1	35
18952	Genome-Wide Identification, Phylogenetic and Co-Expression Analysis of OsSET Gene Family in Rice. PLoS ONE, 2013, 8, e65426.	1.1	29
18953	Analysis and Prediction of Pathways in HeLa Cells by Integrating Biological Levels of Organization with Systems-Biology Approaches. PLoS ONE, 2013, 8, e65433.	1.1	8
18954	Comparative Network Analysis of Preterm vs. Full-Term Infant-Mother Interactions. PLoS ONE, 2013, 8, e67183.	1.1	5
18955	The Cardiac Acetyl-Lysine Proteome. PLoS ONE, 2013, 8, e67513.	1.1	86
18956	Transcriptomic Analysis of Insulin-Sensitive Tissues from Anti-Diabetic Drug Treated ZDF Rats, a T2DM Animal Model. PLoS ONE, 2013, 8, e69624.	1.1	4
18957	Biphasic Functional Regulation in Hippocampus of Rat with Chronic Cerebral Hypoperfusion Induced by Permanent Occlusion of Bilateral Common Carotid Artery. PLoS ONE, 2013, 8, e70093.	1.1	34
18958	Detection of Deregulated Modules Using Deregulatory Linked Path. PLoS ONE, 2013, 8, e70412.	1.1	4
18959	Short-Chain Fructo-Oligosaccharides Modulate Intestinal Microbiota and Metabolic Parameters of Humanized Gnotobiotic Diet Induced Obesity Mice. PLoS ONE, 2013, 8, e71026.	1.1	75
18960	Evaluating the Pharmacological Mechanism of Chinese Medicine Si-Wu-Tang through Multi-Level Data Integration. PLoS ONE, 2013, 8, e72334.	1.1	39
18961	Gene Regulatory Networks Elucidating Huanglongbing Disease Mechanisms. PLoS ONE, 2013, 8, e74256.	1.1	106
18962	Specific Extracellular Matrix Remodeling Signature of Colon Hepatic Metastases. PLoS ONE, 2013, 8, e74599.	1.1	46
18963	Bacterial Community Mapping of the Mouse Gastrointestinal Tract. PLoS ONE, 2013, 8, e74957.	1.1	363
18964	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	1.1	24
18965	Identification of Candidate B-Lymphoma Genes by Cross-Species Gene Expression Profiling. PLoS ONE, 2013, 8, e76889.	1.1	13
18966	Quantitative Phosphoproteome Analysis Unveils LAT as a Modulator of CD3 $\zeta$ and ZAP-70 Tyrosine Phosphorylation. PLoS ONE, 2013, 8, e77423.	1.1	27
18967	Reconstruction and Analysis of Transcription Factor $\mu$ miRNA Co-Regulatory Feed-Forward Loops in Human Cancers Using Filter-Wrapper Feature Selection. PLoS ONE, 2013, 8, e78197.	1.1	20
18968	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	1.1	7

#	ARTICLE	IF	CITATIONS
18969	Deciphering Genomic Alterations in Colorectal Cancer through Transcriptional Subtype-Based Network Analysis. PLoS ONE, 2013, 8, e79282.	1.1	15
18970	A Genome-Wide Screen Identifies Yeast Genes Required for Tolerance to Technical Toxaphene, an Organochlorinated Pesticide Mixture. PLoS ONE, 2013, 8, e81253.	1.1	12
18971	Mycophenolic Acid Inhibits Migration and Invasion of Gastric Cancer Cells via Multiple Molecular Pathways. PLoS ONE, 2013, 8, e81702.	1.1	38
18972	Analysis of Time-Resolved Gene Expression Measurements across Individuals. PLoS ONE, 2013, 8, e82340.	1.1	7
18973	Fyn-Dependent Gene Networks in Acute Ethanol Sensitivity. PLoS ONE, 2013, 8, e82435.	1.1	40
18974	The Anti-Tumor Histone Deacetylase Inhibitor SAHA and the Natural Flavonoid Curcumin Exhibit Synergistic Neuroprotection against Amyloid-Beta Toxicity. PLoS ONE, 2014, 9, e85570.	1.1	35
18975	MALDI-TOF Identification of the Human Gut Microbiome in People with and without Diarrhea in Senegal. PLoS ONE, 2014, 9, e87419.	1.1	50
18976	A Network Based Method for Analysis of lncRNA-Disease Associations and Prediction of lncRNAs Implicated in Diseases. PLoS ONE, 2014, 9, e87797.	1.1	150
18977	Systems Genetics of Liver Fibrosis: Identification of Fibrogenic and Expression Quantitative Trait Loci in the BXD Murine Reference Population. PLoS ONE, 2014, 9, e89279.	1.1	20
18978	A Selected Core Microbiome Drives the Early Stages of Three Popular Italian Cheese Manufactures. PLoS ONE, 2014, 9, e89680.	1.1	1,195
18979	Modulation of Neuronal Proteome Profile in Response to Japanese Encephalitis Virus Infection. PLoS ONE, 2014, 9, e90211.	1.1	27
18980	Transcriptomic Profile Reveals Gender-Specific Molecular Mechanisms Driving Multiple Sclerosis Progression. PLoS ONE, 2014, 9, e90482.	1.1	46
18981	Pathway Based Analysis of Genes and Interactions Influencing Porcine Testis Samples from Boars with Divergent Androstenone Content in Back Fat. PLoS ONE, 2014, 9, e91077.	1.1	9
18982	Mapping the Structure and Dynamics of Genomics-Related MeSH Terms Complex Networks. PLoS ONE, 2014, 9, e92639.	1.1	11
18983	RNA-Seq and Microarrays Analyses Reveal Global Differential Transcriptomes of Mesorhizobium huakuii 7653R between Bacteroids and Free-Living Cells. PLoS ONE, 2014, 9, e93626.	1.1	24
18984	Identification of the Critical Sites of NNRTI-Resistance in Reverse Transcriptase of HIV-1 CRF_BC Strains. PLoS ONE, 2014, 9, e93804.	1.1	8
18985	Interaction Networks of Prion, Prionogenic and Prion-Like Proteins in Budding Yeast, and Their Role in Gene Regulation. PLoS ONE, 2014, 9, e100615.	1.1	18
18986	HCV Genome-Wide Genetic Analyses in Context of Disease Progression and Hepatocellular Carcinoma. PLoS ONE, 2014, 9, e103748.	1.1	3

#	ARTICLE	IF	CITATIONS
18987	GIANT: A Cytoscape Plugin for Modular Networks. PLoS ONE, 2014, 9, e105001.	1.1	39
18988	Analysis of Papaya Cell Wall-Related Genes during Fruit Ripening Indicates a Central Role of Polygalacturonases during Pulp Softening. PLoS ONE, 2014, 9, e105685.	1.1	68
18989	A Multienzyme Complex Channels Substrates and Electrons through Acetyl-CoA and Methane Biosynthesis Pathways in Methanosarcina. PLoS ONE, 2014, 9, e107563.	1.1	22
18990	17 $\beta$ -Estradiol Modulates Gene Expression in the Female Mouse Cerebral Cortex. PLoS ONE, 2014, 9, e111975.	1.1	18
18991	Finding Needles in a Haystack: Application of Network Analysis and Target Enrichment Studies for the Identification of Potential Anti-Diabetic Phytochemicals. PLoS ONE, 2014, 9, e112911.	1.1	10
18992	Transcriptional Evidence for the Role of Chronic Venlafaxine Treatment in Neurotrophic Signaling and Neuroplasticity Including also Glutamate- and Insulin-Mediated Neuronal Processes. PLoS ONE, 2014, 9, e113662.	1.1	52
18993	Transcriptome Analysis Reveals Genes Commonly Induced by Botrytis cinerea Infection, Cold, Drought and Oxidative Stresses in Arabidopsis. PLoS ONE, 2014, 9, e113718.	1.1	73
18994	A Co-Association Network Analysis of the Genetic Determination of Pig Conformation, Growth and Fatness. PLoS ONE, 2014, 9, e114862.	1.1	36
18995	The Transcriptomic and Proteomic Landscapes of Bone Marrow and Secondary Lymphoid Tissues. PLoS ONE, 2014, 9, e115911.	1.1	13
18996	Acute and Chronic Plasma Metabolomic and Liver Transcriptomic Stress Effects in a Mouse Model with Features of Post-Traumatic Stress Disorder. PLoS ONE, 2015, 10, e0117092.	1.1	36
18997	Genome-Wide Identification of Small RNAs in Bifidobacterium animalis subsp. lactis KLDS 2.0603 and Their Regulation Role in the Adaption to Gastrointestinal Environment. PLoS ONE, 2015, 10, e0117373.	1.1	11
18998	Classification of Beta-Lactamases and Penicillin Binding Proteins Using Ligand-Centric Network Models. PLoS ONE, 2015, 10, e0117874.	1.1	41
18999	Proteomic Analysis of Mitochondrial-Associated ER Membranes (MAM) during RNA Virus Infection Reveals Dynamic Changes in Protein and Organelle Trafficking. PLoS ONE, 2015, 10, e0117963.	1.1	91
19000	Identifying Prognostic Features by Bottom-Up Approach and Correlating to Drug Repositioning. PLoS ONE, 2015, 10, e0118672.	1.1	12
19001	Functional Analysis of the Molecular Interactions of TATA Box-Containing Genes and Essential Genes. PLoS ONE, 2015, 10, e0120848.	1.1	35
19002	Abundant Genetic Overlap between Blood Lipids and Immune-Mediated Diseases Indicates Shared Molecular Genetic Mechanisms. PLoS ONE, 2015, 10, e0123057.	1.1	40
19003	Quorum-Sensing Dysbiotic Shifts in the HIV-Infected Oral Metabiome. PLoS ONE, 2015, 10, e0123880.	1.1	9
19004	Systems Biology Analysis Merging Phenotype, Metabolomic and Genomic Data Identifies Non-SMC Condensin I Complex, Subunit G (NCAPG) and Cellular Maintenance Processes as Major Contributors to Genetic Variability in Bovine Feed Efficiency. PLoS ONE, 2015, 10, e0124574.	1.1	62

#	ARTICLE	IF	CITATIONS
19005	TMREC: A Database of Transcription Factor and MiRNA Regulatory Cascades in Human Diseases. PLoS ONE, 2015, 10, e0125222.	1.1	22
19006	A Ranking-Based Meta-Analysis Reveals Let-7 Family as a Meta-Signature for Grade Classification in Breast Cancer. PLoS ONE, 2015, 10, e0126837.	1.1	15
19007	Natural Selection and Functional Potentials of Human Noncoding Elements Revealed by Analysis of Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0129023.	1.1	7
19008	Defining the Human Brain Proteome Using Transcriptomics and Antibody-Based Profiling with a Focus on the Cerebral Cortex. PLoS ONE, 2015, 10, e0130028.	1.1	44
19009	Tissue-Specific Evolution of Protein Coding Genes in Human and Mouse. PLoS ONE, 2015, 10, e0131673.	1.1	40
19010	Systematic Analysis of the Molecular Mechanism Underlying Decidualization Using a Text Mining Approach. PLoS ONE, 2015, 10, e0134585.	1.1	15
19011	CoGA: An R Package to Identify Differentially Co-Expressed Gene Sets by Analyzing the Graph Spectra. PLoS ONE, 2015, 10, e0135831.	1.1	25
19012	Intermediate Tyrosyl Radical and Amyloid Structure in Peroxide-Activated Cytochrome b5. PLoS ONE, 2015, 10, e0136554.	1.1	9
19013	Meta-Analysis of Large-Scale Toxicogenomic Data Finds Neuronal Regeneration Related Protein and Cathepsin D to Be Novel Biomarkers of Drug-Induced Toxicity. PLoS ONE, 2015, 10, e0136698.	1.1	16
19014	Transcriptomic Characterization of Innate and Acquired Immune Responses in Red-Legged Partridges ( <i>Alectoris rufa</i> ): A Resource for Immunoecology and Robustness Selection. PLoS ONE, 2015, 10, e0136776.	1.1	6
19015	Discovery of Intermediary Genes between Pathways Using Sparse Regression. PLoS ONE, 2015, 10, e0137222.	1.1	1
19016	Gene Co-Expression Analysis Inferring the Crosstalk of Ethylene and Gibberellin in Modulating the Transcriptional Acclimation of Cassava Root Growth in Different Seasons. PLoS ONE, 2015, 10, e0137602.	1.1	12
19017	The Relationship of Immune Cell Signatures to Patient Survival Varies within and between Tumor Types. PLoS ONE, 2015, 10, e0138726.	1.1	24
19018	Bioinformatics Analyses of the Role of Vascular Endothelial Growth Factor in Patients with Non-Small Cell Lung Cancer. PLoS ONE, 2015, 10, e0139285.	1.1	13
19019	Predicting Abdominal Aortic Aneurysm Target Genes by Level-2 Protein-Protein Interaction. PLoS ONE, 2015, 10, e0140888.	1.1	2
19020	Bringing Down Cancer Aircraft: Searching for Essential Hypomutated Proteins in Skin Melanoma. PLoS ONE, 2015, 10, e0142819.	1.1	14
19021	Dysregulated Immune Activation in Second-Line HAART HIV+ Patients Is Similar to That of Untreated Patients. PLoS ONE, 2015, 10, e0145261.	1.1	16
19022	Origin and Evolution of Rickettsial Plasmids. PLoS ONE, 2016, 11, e0147492.	1.1	26



#	ARTICLE	IF	CITATIONS
19023	Genome-Wide Analysis of Acute Endurance Exercise-Induced Translational Regulation in Mouse Skeletal Muscle. PLoS ONE, 2016, 11, e0148311.	1.1	14
19024	Network Analysis of a Comprehensive Knowledge Repository Reveals a Dual Role for Ceramide in Alzheimer's Disease. PLoS ONE, 2016, 11, e0148431.	1.1	14
19025	Transcriptomics Modeling of the Late-Gestation Fetal Pituitary Response to Transient Hypoxia. PLoS ONE, 2016, 11, e0148465.	1.1	6
19026	Identification of Interactions in the NMD Complex Using Proximity-Dependent Biotinylation (BioID). PLoS ONE, 2016, 11, e0150239.	1.1	31
19027	Microglia Transcriptome Changes in a Model of Depressive Behavior after Immune Challenge. PLoS ONE, 2016, 11, e0150858.	1.1	35
19028	Nuclear Localization of the Autism Candidate Gene Neurobeachin and Functional Interaction with the NOTCH1 Intracellular Domain Indicate a Role in Regulating Transcription. PLoS ONE, 2016, 11, e0151954.	1.1	20
19029	Identification of Gene Networks for Residual Feed Intake in Angus Cattle Using Genomic Prediction and RNA-seq. PLoS ONE, 2016, 11, e0152274.	1.1	106
19030	GUIdock: Using Docker Containers with a Common Graphics User Interface to Address the Reproducibility of Research. PLoS ONE, 2016, 11, e0152686.	1.1	40
19031	Bacterial Diversity and Community Structure in Korean Ginseng Field Soil Are Shifted by Cultivation Time. PLoS ONE, 2016, 11, e0155055.	1.1	26
19032	Data-Driven Identification of Risk Factors of Patient Satisfaction at a Large Urban Academic Medical Center. PLoS ONE, 2016, 11, e0156076.	1.1	20
19033	Comprehensive RNA-Seq Analysis on the Regulation of Tomato Ripening by Exogenous Auxin. PLoS ONE, 2016, 11, e0156453.	1.1	44
19034	Computational Identification of Novel Stage-Specific Biomarkers in Colorectal Cancer Progression. PLoS ONE, 2016, 11, e0156665.	1.1	60
19035	NrdR Transcription Regulation: Global Proteome Analysis and Its Role in Escherichia coli Viability and Virulence. PLoS ONE, 2016, 11, e0157165.	1.1	13
19036	Differential Transcriptome Networks between IDO1-Knockout and Wild-Type Mice in Brain Microglia and Macrophages. PLoS ONE, 2016, 11, e0157727.	1.1	15
19037	Sequence- and Structure-Based Analysis of Tissue-Specific Phosphorylation Sites. PLoS ONE, 2016, 11, e0157896.	1.1	10
19038	Gene-Expression Profiling Suggests Impaired Signaling via the Interferon Pathway in Cstb <sup>-/-</sup> Microglia. PLoS ONE, 2016, 11, e0158195.	1.1	9
19039	Erythropoietin Levels Increase during Cerebral Malaria and Correlate with Heme, Interleukin-10 and Tumor Necrosis Factor-Alpha in India. PLoS ONE, 2016, 11, e0158420.	1.1	6
19040	Co-Expression of Cancer Stem Cell Markers Corresponds to a Pro-Tumorigenic Expression Profile in Pancreatic Adenocarcinoma. PLoS ONE, 2016, 11, e0159255.	1.1	32

#	ARTICLE	IF	CITATIONS
19041	Phenome-Wide Association Study to Explore Relationships between Immune System Related Genetic Loci and Complex Traits and Diseases. PLoS ONE, 2016, 11, e0160573.	1.1	23
19042	Whole Transcriptome Profiling Identifies CD93 and Other Plasma Cell Survival Factor Genes Associated with Measles-Specific Antibody Response after Vaccination. PLoS ONE, 2016, 11, e0160970.	1.1	20
19043	Sensitivity Analysis of the NPM-ALK Signalling Network Reveals Important Pathways for Anaplastic Large Cell Lymphoma Combination Therapy. PLoS ONE, 2016, 11, e0163011.	1.1	14
19044	Exploring the Inflammatory Metabolomic Profile to Predict Response to TNF- $\alpha$ Inhibitors in Rheumatoid Arthritis. PLoS ONE, 2016, 11, e0163087.	1.1	43
19045	Heat Stress and Lipopolysaccharide Stimulation of Chicken Macrophage-Like Cell Line Activates Expression of Distinct Sets of Genes. PLoS ONE, 2016, 11, e0164575.	1.1	46
19046	Identification of Binding Targets of a Pyrrole-Imidazole Polyamide KR12 in the LS180 Colorectal Cancer Genome. PLoS ONE, 2016, 11, e0165581.	1.1	11
19047	The Human Kinome Targeted by FDA Approved Multi-Target Drugs and Combination Products: A Comparative Study from the Drug-Target Interaction Network Perspective. PLoS ONE, 2016, 11, e0165737.	1.1	51
19048	An Integrative Analysis of Preeclampsia Based on the Construction of an Extended Composite Network Featuring Protein-Protein Physical Interactions and Transcriptional Relationships. PLoS ONE, 2016, 11, e0165849.	1.1	13
19049	From Proteomic Analysis to Potential Therapeutic Targets: Functional Profile of Two Lung Cancer Cell Lines, A549 and SW900, Widely Studied in Pre-Clinical Research. PLoS ONE, 2016, 11, e0165973.	1.1	33
19050	Disease Type- and Status-Specific Alteration of CSF Metabolome Coordinated with Clinical Parameters in Inflammatory Demyelinating Diseases of CNS. PLoS ONE, 2016, 11, e0166277.	1.1	24
19051	Transcriptomic Analysis Shows Decreased Cortical Expression of NR4A1, NR4A2 and RXRB in Schizophrenia and Provides Evidence for Nuclear Receptor Dysregulation. PLoS ONE, 2016, 11, e0166944.	1.1	22
19052	The rs3957357C>T SNP in GSTA1 Is Associated with a Higher Risk of Occurrence of Hepatocellular Carcinoma in European Individuals. PLoS ONE, 2016, 11, e0167543.	1.1	21
19053	A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. PLoS ONE, 2016, 11, e0167788.	1.1	46
19054	Gene Co-Expression Network Analysis Unraveling Transcriptional Regulation of High-Altitude Adaptation of Tibetan Pig. PLoS ONE, 2016, 11, e0168161.	1.1	32
19055	Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist <i>Poteroiochromonas malhamensis</i> . PLoS ONE, 2017, 12, e0168183.	1.1	8
19056	Exploring Identity-By-Descent Segments and Putative Functions Using Different Foundation Parents in Maize. PLoS ONE, 2016, 11, e0168374.	1.1	18
19057	MicroRNA and Transcription Factor Gene Regulatory Network Analysis Reveals Key Regulatory Elements Associated with Prostate Cancer Progression. PLoS ONE, 2016, 11, e0168760.	1.1	44
19058	Drug Repositioning for Alzheimer's Disease Based on Systematic $\epsilon$ -omics Data Mining. PLoS ONE, 2016, 11, e0168812.	1.1	95

#	ARTICLE	IF	CITATIONS
19059	Comprehensive RNA-Seq Profiling to Evaluate the Sheep Mammary Gland Transcriptome in Response to Experimental Mycoplasma agalactiae Infection. PLoS ONE, 2017, 12, e0170015.	1.1	16
19060	Polymorphisms and Mutational Covariation Associated with Death in a Prospective Cohort of HIV/AIDS Patients Receiving Long-Term ART in China. PLoS ONE, 2017, 12, e0170139.	1.1	8
19061	MEDICI: Mining Essentiality Data to Identify Critical Interactions for Cancer Drug Target Discovery and Development. PLoS ONE, 2017, 12, e0170339.	1.1	4
19062	IL-22R Ligands IL-20, IL-22, and IL-24 Promote Wound Healing in Diabetic db/db Mice. PLoS ONE, 2017, 12, e0170639.	1.1	74
19063	Metabox: A Toolbox for Metabolomic Data Analysis, Interpretation and Integrative Exploration. PLoS ONE, 2017, 12, e0171046.	1.1	85
19064	Exploring Team Passing Networks and Player Movement Dynamics in Youth Association Football. PLoS ONE, 2017, 12, e0171156.	1.1	95
19065	Deep-proteome mapping of WM-266-4 human metastatic melanoma cells: From oncogenic addiction to druggable targets. PLoS ONE, 2017, 12, e0171512.	1.1	21
19066	Dissecting nutrient-related co-expression networks in phosphate starved poplars. PLoS ONE, 2017, 12, e0171958.	1.1	41
19067	Whole exome sequencing implicates eye development, the unfolded protein response and plasma membrane homeostasis in primary open-angle glaucoma. PLoS ONE, 2017, 12, e0172427.	1.1	8
19068	Targeted proteome analysis of single-gene deletion strains of Saccharomyces cerevisiae lacking enzymes in the central carbon metabolism. PLoS ONE, 2017, 12, e0172742.	1.1	18
19069	Influence of a pre-stimulation with chronic low-dose UVB on stress response mechanisms in human skin fibroblasts. PLoS ONE, 2017, 12, e0173740.	1.1	8
19070	Mapping the N-linked glycosites of rice (Oryza sativa L.) germinating embryos. PLoS ONE, 2017, 12, e0173853.	1.1	15
19071	Integrated network analysis reveals potentially novel molecular mechanisms and therapeutic targets of refractory epilepsies. PLoS ONE, 2017, 12, e0174964.	1.1	13
19072	Development of a forecasting model for brucellosis spreading in the Italian cattle trade network aimed to prioritise the field interventions. PLoS ONE, 2017, 12, e0177313.	1.1	14
19073	Identification of key contributors in complex population structures. PLoS ONE, 2017, 12, e0177638.	1.1	13
19074	Different adaptation strategies of two citrus scion/rootstock combinations in response to drought stress. PLoS ONE, 2017, 12, e0177993.	1.1	28
19075	Properties of genes essential for mouse development. PLoS ONE, 2017, 12, e0178273.	1.1	17
19076	AlzhCPI: A knowledge base for predicting chemical-protein interactions towards Alzheimer's disease. PLoS ONE, 2017, 12, e0178347.	1.1	15

#	ARTICLE	IF	CITATIONS
19077	Identification of key microRNAs and genes in preeclampsia by bioinformatics analysis. PLoS ONE, 2017, 12, e0178549.	1.1	45
19078	Genome-wide association study provides strong evidence of genes affecting the reproductive performance of Nellore beef cows. PLoS ONE, 2017, 12, e0178551.	1.1	36
19079	Proteome-wide profiling of protein lysine acetylation in <i>Aspergillus flavus</i> . PLoS ONE, 2017, 12, e0178603.	1.1	27
19080	De novo assembly and annotation of the retinal transcriptome for the Nile grass rat ( <i>Arvicantis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 11	1.1	2
19081	Genome wide host gene expression analysis in mice experimentally infected with <i>Pasteurella multocida</i> . PLoS ONE, 2017, 12, e0179420.	1.1	23
19082	Circulating microRNAs and association with methacholine PC20 in the Childhood Asthma Management Program (CAMP) cohort. PLoS ONE, 2017, 12, e0180329.	1.1	38
19083	Netlang: A software for the linguistic analysis of corpora by means of complex networks. PLoS ONE, 2017, 12, e0181341.	1.1	9
19084	Exploring the cross talk between ER stress and inflammation in age-related macular degeneration. PLoS ONE, 2017, 12, e0181667.	1.1	19
19085	The <i>Bos taurus</i> "Bos indicus balance in fertility and milk related genes. PLoS ONE, 2017, 12, e0181930.	1.1	33
19086	A data mining approach for identifying pathway-gene biomarkers for predicting clinical outcome: A case study of erlotinib and sorafenib. PLoS ONE, 2017, 12, e0181991.	1.1	2
19087	High hydrostatic pressure induces pro-osteoarthritic changes in cartilage precursor cells: A transcriptome analysis. PLoS ONE, 2017, 12, e0183226.	1.1	30
19088	Protein complex prediction via dense subgraphs and false positive analysis. PLoS ONE, 2017, 12, e0183460.	1.1	10
19089	A systems medicine approach for finding target proteins affecting treatment outcomes in patients with non-Hodgkin lymphoma. PLoS ONE, 2017, 12, e0183969.	1.1	12
19090	Three-way interaction model to trace the mechanisms involved in Alzheimer's disease transgenic mice. PLoS ONE, 2017, 12, e0184697.	1.1	13
19091	Network modeling of kinase inhibitor polypharmacology reveals pathways targeted in chemical screens. PLoS ONE, 2017, 12, e0185650.	1.1	3
19092	Examining word association networks: A cross-country comparison of women's perceptions of HPV testing and vaccination. PLoS ONE, 2017, 12, e0185669.	1.1	1
19093	Transcriptome analysis of sheep oral mucosa response to Orf virus infection. PLoS ONE, 2017, 12, e0186681.	1.1	14
19094	Biological substantiation of antipsychotic-associated pneumonia: Systematic literature review and computational analyses. PLoS ONE, 2017, 12, e0187034.	1.1	20

#	ARTICLE	IF	CITATIONS
19095	Systems genomics study reveals expression quantitative trait loci, regulator genes and pathways associated with boar taint in pigs. PLoS ONE, 2018, 13, e0192673.	1.1	22
19096	Cross-species multiple environmental stress responses: An integrated approach to identify candidate genes for multiple stress tolerance in sorghum ( <i>Sorghum bicolor</i> (L.) Moench) and related model species. PLoS ONE, 2018, 13, e0192678.	1.1	24
19097	Sex- and brain region-specific patterns of gene expression associated with socially-mediated puberty in a eusocial mammal. PLoS ONE, 2018, 13, e0193417.	1.1	24
19098	The benzodiazepine-like natural product tilivalline is produced by the entomopathogenic bacterium <i>Xenorhabdus eapokensis</i> . PLoS ONE, 2018, 13, e0194297.	1.1	13
19099	Microbial diversity in two traditional bacterial douchi from Gansu province in northwest China using Illumina sequencing. PLoS ONE, 2018, 13, e0194876.	1.1	26
19100	In silico identification and characterization of AGO, DCL and RDR gene families and their associated regulatory elements in sweet orange ( <i>Citrus sinensis</i> L.). PLoS ONE, 2020, 15, e0228233.	1.1	12
19101	Innate immune gene expression in <i>Acropora palmata</i> is consistent despite variance in yearly disease events. PLoS ONE, 2020, 15, e0228514.	1.1	12
19102	RNA-seq analysis identifies cytoskeletal structural genes and pathways for meat quality in beef. PLoS ONE, 2020, 15, e0240895.	1.1	9
19103	Transcriptomic and proteomic intra-tumor heterogeneity of colorectal cancer varies depending on tumor location within the colorectum. PLoS ONE, 2020, 15, e0241148.	1.1	13
19104	Serum miRNAs associated with tumor-promoting cytokines in non-small cell lung cancer. PLoS ONE, 2020, 15, e0241593.	1.1	6
19105	Lipopolysaccharide triggers different transcriptional signatures in taurine and indicine cattle macrophages: Reactive oxygen species and potential outcomes to the development of immune response to infections. PLoS ONE, 2020, 15, e0241861.	1.1	5
19106	Mycobiome changes in the vitreous of post fever retinitis patients. PLoS ONE, 2020, 15, e0242138.	1.1	12
19107	Identification of potential target genes and crucial pathways in small cell lung cancer based on bioinformatic strategy and human samples. PLoS ONE, 2020, 15, e0242194.	1.1	7
19108	Coupling of autism genes to tissue-wide expression and dysfunction of synapse, calcium signalling and transcriptional regulation. PLoS ONE, 2020, 15, e0242773.	1.1	15
19109	Gut mycobiomes are altered in people with type 2 Diabetes Mellitus and Diabetic Retinopathy. PLoS ONE, 2020, 15, e0243077.	1.1	60
19110	CoMA – an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. PLoS ONE, 2020, 15, e0243241.	1.1	15
19111	The transcriptomic profiling of SARS-CoV-2 compared to SARS, MERS, EBOV, and H1N1. PLoS ONE, 2020, 15, e0243270.	1.1	27
19112	Metabolomic study of marine <i>Streptomyces</i> sp.: Secondary metabolites and the production of potential anticancer compounds. PLoS ONE, 2020, 15, e0244385.	1.1	28

#	ARTICLE	IF	CITATIONS
19113	Strain Dependent Genetic Networks for Antibiotic-Sensitivity in a Bacterial Pathogen with a Large Pan-Genome. <i>PLoS Pathogens</i> , 2016, 12, e1005869.	2.1	66
19114	Transcriptomic Analysis Implicates the p53 Signaling Pathway in the Establishment of HIV-1 Latency in Central Memory CD4 T Cells in an In Vitro Model. <i>PLoS Pathogens</i> , 2016, 12, e1006026.	2.1	28
19115	Regulation of NF- $\kappa$ B by the p105-ABIN2-TPL2 complex and RelA $\kappa$ 43 during rabies virus infection. <i>PLoS Pathogens</i> , 2017, 13, e1006697.	2.1	32
19116	<i>Sclerotinia sclerotiorum</i> utilizes host-derived copper for ROS detoxification and infection. <i>PLoS Pathogens</i> , 2020, 16, e1008919.	2.1	23
19117	Dynamic metabolic reprogramming in dendritic cells: An early response to influenza infection that is essential for effector function. <i>PLoS Pathogens</i> , 2020, 16, e1008957.	2.1	13
19118	Longitudinal analysis reveals characteristically high proportions of bacterial vaginosis-associated bacteria and temporal variability of vaginal microbiota in northern pig-tailed macaques ( <i>Macaca</i> ) Tj ETQq1 1 0.784314 rgBT /@verlock	1.4	10
19119	Network Pharmacology Analysis Uncovers the Potential Anti-Hypertensive Mechanisms of Xia Sang Ju Granule. <i>Journal of Exploratory Research in Pharmacology</i> , 2020, 000, 1-10.	0.2	6
19120	PPAR $\alpha$ -Target Gene Expression Requires TIS21 Gene in Liver of the C57BL/6 Mice under Fasting Condition. <i>Molecules and Cells</i> , 2018, 41, 140-149.	1.0	2
19121	Co-Authorship Networks among DRDO Life Science Scientists. <i>Defence Life Science Journal</i> , 2016, 1, 188.	0.1	3
19122	ARNetMiT R Package: association rules based gene co-expression networks of miRNA targets. <i>Cellular and Molecular Biology</i> , 2017, 63, 18.	0.3	6
19123	Identifying potential therapeutic targets of a natural product Jujuboside B for insomnia through network pharmacology. <i>Plant Science Today</i> , 2014, 1, 69-79.	0.4	13
19124	Possible key microRNAs and corresponding molecular mechanisms for atrial fibrillation. <i>Anatolian Journal of Cardiology</i> , 2020, 23, 324-333.	0.5	4
19125	Superclusteroid: a Web tool dedicated to data processing of protein-protein interaction networks. <i>EMBnet Journal</i> , 2011, 17, 10.	0.2	1,728
19126	Plant Growth Promoting Rhizobacteria (PGPR) Regulated Phyto and Microbial Beneficial Protein Interactions. <i>Open Life Sciences</i> , 2020, 15, 68-78.	0.6	12
19127	Role of phase partitioning in coordinating DNA damage response: focus on the Apurinic Apyrimidinic Endonuclease 1 interactome. <i>Biomolecular Concepts</i> , 2020, 11, 209-220.	1.0	15
19128	Diversity of GPI-anchored fungal adhesins. <i>Biological Chemistry</i> , 2020, 401, 1389-1405.	1.2	17
19129	Functional expression and impact of testis-specific gene antigen 10 in breast cancer: a combined in vitro and in silico analysis. <i>BiolImpacts</i> , 2019, 9, 145-159.	0.7	10
19130	Evaluation of Skin Response After Erbium:Yttrium-Aluminum-Garnet Laser Irradiation: A Network Analysis Approach. <i>Journal of Lasers in Medical Sciences</i> , 2019, 10, 194-199.	0.4	23



#	ARTICLE	IF	CITATIONS
19131	The Structure of Negative Social Ties in Rural Village Networks. <i>Sociological Science</i> , 2019, 6, 197-218.	2.0	74
19132	High-Content Genome-Wide RNAi Screen Reveals <i>CCR3</i> as a Key Mediator of Neuronal Cell Death. <i>ENeuro</i> , 2016, 3, ENEURO.0185-16.2016.	0.9	15
19133	Noninvasive Brain Stimulation Enhances Memory Acquisition and Is Associated with Synaptoneurosome Modification in the Rat Hippocampus. <i>ENeuro</i> , 2019, 6, ENEURO.0311-19.2019.	0.9	7
19134	Deciphering the regulatory landscape of fetal and adult $\beta$ cell development at single-cell resolution. <i>EMBO Journal</i> , 2020, 39, e104159.	3.5	48
19135	Phosphoproteomics reveals novel modes of function and interrelationships among PIKKs in response to genotoxic stress. <i>EMBO Journal</i> , 2021, 40, e104400.	3.5	28
19136	Pharmacological reversal of synaptic and network pathology in human <i>MECP2</i> $\alpha$ KO neurons and cortical organoids. <i>EMBO Molecular Medicine</i> , 2021, 13, e12523.	3.3	53
19137	Integrated regulatory models for inference of subtype-specific susceptibilities in glioblastoma. <i>Molecular Systems Biology</i> , 2020, 16, e9506.	3.2	5
19138	A single cell atlas of the human liver tumor microenvironment. <i>Molecular Systems Biology</i> , 2020, 16, e9682.	3.2	99
19139	<i>CEN</i> tools: an integrative platform to identify the contexts of essential genes. <i>Molecular Systems Biology</i> , 2020, 16, e9698.	3.2	14
19140	Effect of Substrate Topography and Chemistry on Human Mesenchymal Stem Cell Markers: A Transcriptome Study. <i>International Journal of Stem Cells</i> , 2019, 12, 84-94.	0.8	18
19141	Uterine fluid proteome changes during diapause and resumption of embryo development in roe deer ( <i>Capreolus capreolus</i> ). <i>Reproduction</i> , 2019, 158, 13-24.	1.1	15
19142	Regulation of Secondary Metabolism by the Velvet Complex Is Temperature-Responsive in <i>Aspergillus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4023-4033.	0.8	58
19143	DEVELOPMENT OF METHODS FOR AUTOMATIC EXTRACTION OF KNOWLEDGE FROM TEXTS OF SCIENTIFIC PUBLICATIONS FOR THE CREATION OF A KNOWLEDGE BASE SOLANUM TUBEROSUM. <i>Sel'skokhozyaistvennaya Biologiya</i> , 2017, 52, 63-74.	0.1	4
19144	Cheminformatics and Computational Approaches in Metabolomics. , 0, , 143-159.		2
19145	Development of a technique for the reconstruction and validation of gene network models based on gene expression profiles. <i>Eastern-European Journal of Enterprise Technologies</i> , 2018, 1, 19-32.	0.3	17
19146	Construction and evaluation of yeast expression networks by database-guided predictions. <i>Microbial Cell</i> , 2016, 3, 236-247.	1.4	7
19147	Genome-wide analysis of yeast expression data based on a priori generated co-regulation cliques. <i>Microbial Cell</i> , 2019, 6, 160-176.	1.4	2
19148	POLYMORPHISMS OF EXTRACELLULAR CONNECTIVE TISSUE REMODELING PROTEINASES AND <i>MMP2</i> , <i>MMP3</i> , <i>MMP9</i> GENES, AND NEOANGIOGENESIS <i>VEGF</i> GENE IN RETINAL MICROANGIOPATHY IN THE PATIENTS WITH TYPE 2 DIABETES MELLITUS. <i>Medical Immunology (Russia)</i> , 2019, 21, 441-450.	0.1	1

#	ARTICLE	IF	CITATIONS
19149	G-language System as a platform for large-scale analysis of high-throughput omics data. <i>Journal of Pesticide Sciences</i> , 2006, 31, 282-288.	0.8	31
19150	System-Pharmacology Dissection of Traditional Chinese herbs SINI Decoction for Treatment of Cardiovascular Diseases. <i>Anais Da Academia Brasileira De Ciencias</i> , 2019, 91, e20180424.	0.3	11
19151	Prioritisation of potential drug targets against <i>Bartonella bacilliformis</i> by an integrative in-silico approach. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e200184.	0.8	7
19152	Screening potential prognostic biomarkers of long non-coding RNAs for predicting the risk of chronic kidney disease. <i>Brazilian Journal of Medical and Biological Research</i> , 2019, 52, e8333.	0.7	13
19153	Integrated analysis of lncRNA-associated ceRNA network identified potential regulatory interactions in osteosarcoma. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190090.	0.6	4
19154	Cooperation and interplay between base and nucleotide excision repair pathways: From DNA lesions to proteins. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190104.	0.6	47
19155	Systems chemo-biology analysis of DNA damage response and cell cycle effects induced by coal exposure. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190134.	0.6	8
19156	Identification of differentially expressed microRNAs in middle-size ovarian follicles of Meishan and Duroc sows. <i>Revista Brasileira De Zootecnia</i> , 0, 48, .	0.3	1
19157	Export Diversification in a Transitioning Economy: The Case of Syria. <i>Policy Research Working Papers</i> , 2011, , .	1.4	9
19158	Computational Biology of Genome Expression and Regulation—A Review of Microarray Bioinformatics. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2008, 27, 157-179.	0.6	22
19159	Bionformatics analysis reveals TSPAN1 as a candidate biomarker of progression and prognosis in pancreatic cancer. <i>Bosnian Journal of Basic Medical Sciences</i> , 2021, 21, 47-60.	0.6	6
19160	In Silico Cell: Challenges and Perspectives. <i>Mathematical Biology and Bioinformatics</i> , 2013, 8, 295-315.	0.1	7
19161	Interaction Design for Complex Cognitive Activities with Visual Representations: A Pattern-Based Approach. <i>AIS Transactions on Human-Computer Interaction</i> , 2013, 5, 84-133.	1.1	91
19163	2018 Update on Protein-Protein Interaction Data in WormBase. <i>MicroPublication Biology</i> , 2018, 2018, .	0.1	3
19164	Identification of microRNA-mRNA regulatory networks and pathways related to retinoblastoma across human and mouse. <i>International Journal of Ophthalmology</i> , 2020, 13, 535-544.	0.5	3
19165	Red de interacci3n prote3na-prote3na de fosfatidilinositol 4,5-bifosfato 5-fosfatasa relacionada con el s3ndrome de Lowe. <i>Revista De La Academia Colombiana De Ciencias Exactas, Fisicas Y Naturales</i> , 2016, 40, 559.	0.0	1
19166	Computational Systems Biology Approach for the Study of Rheumatoid Arthritis: From a Molecular Map to a Dynamical Model. <i>Genomics and Computational Biology</i> , 2017, 4, 100050.	0.7	20
19167	Molecular links between cellular senescence, longevity and age-related diseases “ a systems biology perspective. <i>Aging</i> , 2011, 3, 1178-1191.	1.4	119

#	ARTICLE	IF	CITATIONS
19168	Altered lipid metabolism in the aging kidney identified by three layered omic analysis. <i>Aging</i> , 2016, 8, 441-454.	1.4	46
19169	Central role of the p53 pathway in the noncoding-RNA response to oxidative stress. <i>Aging</i> , 2017, 9, 2559-2586.	1.4	54
19170	Mining TCGA database for genes of prognostic value in glioblastoma microenvironment. <i>Aging</i> , 2018, 10, 592-605.	1.4	311
19171	SNCA overexpression disturbs hippocampal gene expression trajectories in midlife. <i>Aging</i> , 2018, 10, 4024-4041.	1.4	10
19172	Integrated DNA methylation and gene expression analysis in the pathogenesis of coronary artery disease. <i>Aging</i> , 2019, 11, 1486-1500.	1.4	33
19173	The acute transcriptional response to resistance exercise: impact of age and contraction mode. <i>Aging</i> , 2019, 11, 2111-2126.	1.4	14
19174	Analysis of transcription factor- and ncRNA-mediated potential pathogenic gene modules in Alzheimer's disease. <i>Aging</i> , 2019, 11, 6109-6119.	1.4	15
19175	miR-125a-5p inhibits tumorigenesis in hepatocellular carcinoma. <i>Aging</i> , 2019, 11, 7639-7662.	1.4	28
19176	Systematic profiling of alternative splicing events and splicing factors in left- and right-sided colon cancer. <i>Aging</i> , 2019, 11, 8270-8293.	1.4	25
19177	CircUBAP2-mediated competing endogenous RNA network modulates tumorigenesis in pancreatic adenocarcinoma. <i>Aging</i> , 2019, 11, 8484-8501.	1.4	59
19178	Association of a novel seven-gene expression signature with the disease prognosis in colon cancer patients. <i>Aging</i> , 2019, 11, 8710-8727.	1.4	25
19179	Identifying hub genes of clear cell renal cell carcinoma associated with the proportion of regulatory T cells by weighted gene co-expression network analysis. <i>Aging</i> , 2019, 11, 9478-9491.	1.4	13
19180	Circular RNA circGRAMD1B inhibits gastric cancer progression by sponging miR-130a-3p and regulating PTEN and p21 expression. <i>Aging</i> , 2019, 11, 9689-9708.	1.4	41
19181	The construction and analysis of tumor-infiltrating immune cell and ceRNA networks in recurrent soft tissue sarcoma. <i>Aging</i> , 2019, 11, 10116-10143.	1.4	35
19182	Prognostic genes in the tumor microenvironment in cervical squamous cell carcinoma. <i>Aging</i> , 2019, 11, 10154-10166.	1.4	43
19183	Long non-coding RNA RNF7 promotes the cardiac fibrosis in rat model via miR-543/THBS1 axis and TGF $\beta$ 21 activation. <i>Aging</i> , 2020, 12, 996-1010.	1.4	16
19184	Identification of prognostic genes in the acute myeloid leukemia microenvironment. <i>Aging</i> , 2019, 11, 10557-10580.	1.4	34
19185	Identification of molecular correlations of RBM8A with autophagy in Alzheimer's disease. <i>Aging</i> , 2019, 11, 11673-11685.	1.4	43

#	ARTICLE	IF	CITATIONS
19186	System level characterization of small molecule drugs and their affected long noncoding RNAs. <i>Aging</i> , 2019, 11, 12428-12451.	1.4	8
19187	CeRNA regulatory network-based analysis to study the roles of noncoding RNAs in the pathogenesis of intrahepatic cholangiocellular carcinoma. <i>Aging</i> , 2020, 12, 1047-1086.	1.4	27
19188	Network analysis of human muscle adaptation to aging and contraction. <i>Aging</i> , 2020, 12, 740-755.	1.4	14
19189	The whole transcriptome regulation as a function of mitochondrial polymorphisms and aging in <i>Caenorhabditis elegans</i> . <i>Aging</i> , 2020, 12, 2453-2470.	1.4	12
19190	Identification of prognostic immune-related genes in the tumor microenvironment of endometrial cancer. <i>Aging</i> , 2020, 12, 3371-3387.	1.4	83
19191	Identification of biomarkers related to CD8+ T cell infiltration with gene co-expression network in clear cell renal cell carcinoma. <i>Aging</i> , 2020, 12, 3694-3712.	1.4	51
19192	Comprehensive analysis of circular RNA profiles in skeletal muscles of aging mice and after aerobic exercise intervention. <i>Aging</i> , 2020, 12, 5071-5090.	1.4	20
19193	Development of a prognostic index and screening of potential biomarkers based on immunogenomic landscape analysis of colorectal cancer. <i>Aging</i> , 2020, 12, 5832-5857.	1.4	34
19194	USP22 promotes development of lung adenocarcinoma through ubiquitination and immunosuppression. <i>Aging</i> , 2020, 12, 6990-7005.	1.4	16
19195	Identification of HMG-box family establishes the significance of SOX6 in the malignant progression of glioblastoma. <i>Aging</i> , 2020, 12, 8084-8106.	1.4	14
19196	The shared KEGG pathways between icariin-targeted genes and osteoporosis. <i>Aging</i> , 2020, 12, 8191-8201.	1.4	17
19197	Tomatidine suppresses inflammation in primary articular chondrocytes and attenuates cartilage degradation in osteoarthritic rats. <i>Aging</i> , 2020, 12, 12799-12811.	1.4	11
19198	MiR-16-5p regulates postmenopausal osteoporosis by directly targeting VEGFA. <i>Aging</i> , 2020, 12, 9500-9514.	1.4	32
19199	MiR-1908/EXO1 and MiR-203a/FOS, regulated by <i>scd1</i> , are associated with fracture risk and bone health in postmenopausal diabetic women. <i>Aging</i> , 2020, 12, 9549-9584.	1.4	28
19200	Cytoplasmic PCNA is located in the actin belt and involved in osteoclast differentiation. <i>Aging</i> , 2020, 12, 13297-13317.	1.4	10
19201	Quantitative proteomics analysis of young and elderly skin with DIA mass spectrometry reveals new skin aging-related proteins. <i>Aging</i> , 2020, 12, 13529-13554.	1.4	21
19202	Constructing a global transcriptional regulatory landscape for early non-small cell lung cancer to identify hub genes and key pathways. <i>Aging</i> , 2020, 12, 17948-17957.	1.4	5
19203	FGF2-induced PI3K/Akt signaling evokes greater proliferation and adipogenic differentiation of human adipose stem cells from breast than from abdomen or thigh. <i>Aging</i> , 2020, 12, 14830-14848.	1.4	5

#	ARTICLE	IF	CITATIONS
19204	Analysis of plasma metabolic profile, characteristics and enzymes in the progression from chronic hepatitis B to hepatocellular carcinoma. <i>Aging</i> , 2020, 12, 14949-14965.	1.4	27
19205	Identification of a new pseudogenes/lncRNAs-hsa-miR-26b-5p-COL12A1 competing endogenous RNA network associated with prognosis of pancreatic cancer using bioinformatics analysis. <i>Aging</i> , 2020, 12, 19107-19128.	1.4	12
19206	Gene expression profiles during postnatal development of the liver and pancreas in giant pandas. <i>Aging</i> , 2020, 12, 15705-15729.	1.4	3
19207	&lt;i>TRIM28&lt;/i> is a distinct prognostic biomarker that worsens the tumor immune microenvironment in lung adenocarcinoma. <i>Aging</i> , 2020, 12, 20308-20331.	1.4	12
19208	Identification of a hippocampal lncRNA-regulating network in cognitive dysfunction caused by chronic cerebral hypoperfusion. <i>Aging</i> , 2020, 12, 19520-19538.	1.4	5
19209	Integrated analysis of transcriptomic and metabolomic data demonstrates the significant role of pyruvate carboxylase in the progression of ovarian cancer. <i>Aging</i> , 2020, 12, 21874-21889.	1.4	9
19210	Prognostic risk signature based on the expression of three m6A RNA methylation regulatory genes in kidney renal papillary cell carcinoma. <i>Aging</i> , 2020, 12, 22078-22094.	1.4	23
19211	SMARCD3 is a potential prognostic marker and therapeutic target in CAFs. <i>Aging</i> , 2020, 12, 20835-20861.	1.4	14
19212	Integrated analysis of a competing endogenous RNA network reveals an 11-lncRNA prognostic signature in ovarian cancer. <i>Aging</i> , 2020, 12, 25153-25171.	1.4	4
19213	Vascular endothelial growth factor receptor-2 and its association with tumor immune regulatory gene expression in hepatocellular carcinoma. <i>Aging</i> , 2020, 12, 25172-25188.	1.4	5
19214	Exploring diagnostic m6A regulators in endometriosis. <i>Aging</i> , 2020, 12, 25916-25938.	1.4	45
19215	Tumor-associated macrophage polarization promotes the progression of esophageal carcinoma. <i>Aging</i> , 2021, 13, 2049-2072.	1.4	26
19216	Biological characteristics of aging in human acute myeloid leukemia cells: the possible importance of aldehyde dehydrogenase, the cytoskeleton and altered transcriptional regulation. <i>Aging</i> , 2020, 12, 24734-24777.	1.4	13
19217	MicroRNA-messenger RNA interactions involving JAK-STAT signaling genes in colorectal cancer. <i>Genes and Cancer</i> , 2018, 9, 232-246.	0.6	6
19218	A meta-analysis to evaluate the cellular processes regulated by the interactome of endogenous and over-expressed estrogen receptor alpha. <i>Oncoscience</i> , 2015, 2, 487-496.	0.9	4
19219	Quantitative proteomics reveals molecular mechanism of gamabufotalin and its potential inhibition on Hsp90 in lung cancer. <i>Oncotarget</i> , 2016, 7, 76551-76564.	0.8	24
19220	MALDI imaging reveals NCOA7 as a potential biomarker in oral squamous cell carcinoma arising from oral submucous fibrosis. <i>Oncotarget</i> , 2016, 7, 59987-60004.	0.8	27
19221	The gain and loss of long noncoding RNA associated-competing endogenous RNAs in prostate cancer. <i>Oncotarget</i> , 2016, 7, 57228-57238.	0.8	43

#	ARTICLE	IF	CITATIONS
19222	Proteomic identification of cyclophilin A as a potential biomarker and therapeutic target in oral submucous fibrosis. <i>Oncotarget</i> , 2016, 7, 60348-60365.	0.8	18
19223	Association mining of mutated cancer genes in different clinical stages across 11 cancer types. <i>Oncotarget</i> , 2016, 7, 68270-68277.	0.8	9
19224	Molecular differences between cerebral blood volume and vessel size in glioblastoma multiforme. <i>Oncotarget</i> , 2017, 8, 11083-11093.	0.8	18
19225	Secretome proteomics reveals candidate non-invasive biomarkers of <i>BRCA1</i> deficiency in breast cancer. <i>Oncotarget</i> , 2016, 7, 63537-63548.	0.8	14
19226	Blood RNA expression profiles undergo major changes during the seventh decade. <i>Oncotarget</i> , 2016, 7, 71353-71361.	0.8	1
19227	Proteomic analysis reveals diverse proline hydroxylation-mediated oxygen-sensing cellular pathways in cancer cells. <i>Oncotarget</i> , 2016, 7, 79154-79169.	0.8	26
19228	Personalized anticancer therapy selection using molecular landscape topology and thermodynamics. <i>Oncotarget</i> , 2017, 8, 18735-18745.	0.8	21
19229	Altered expression of miRNAs and methylation of their promoters are correlated in neuroblastoma. <i>Oncotarget</i> , 2016, 7, 83330-83341.	0.8	28
19230	Differentiated regulation of immune-response related genes between LUAD and LUSC subtypes of lung cancers. <i>Oncotarget</i> , 2017, 8, 133-144.	0.8	54
19231	Identification of differentially expressed genes in the development of osteosarcoma using RNA-seq. <i>Oncotarget</i> , 2016, 7, 87194-87205.	0.8	13
19232	Pan-organ transcriptome variation across 21 cancer types. <i>Oncotarget</i> , 2017, 8, 6809-6818.	0.8	6
19233	A potential prognostic lncRNA signature for predicting survival in patients with bladder urothelial carcinoma. <i>Oncotarget</i> , 2017, 8, 10485-10497.	0.8	39
19234	Comprehensive proteome analysis of lysosomes reveals the diverse function of macrophages in immune responses. <i>Oncotarget</i> , 2017, 8, 7420-7440.	0.8	28
19235	Aberrant methylation patterns in colorectal cancer: a meta-analysis. <i>Oncotarget</i> , 2017, 8, 12820-12830.	0.8	15
19236	Identification of microRNAs implicated in the late differentiation stages of normal B cells suggests a central role for miRNA targets ZEB1 and TP53. <i>Oncotarget</i> , 2017, 8, 11809-11826.	0.8	11
19237	Systematic analysis of molecular mechanisms for HCC metastasis via text mining approach. <i>Oncotarget</i> , 2017, 8, 13909-13916.	0.8	6
19238	SATB1 plays an oncogenic role in esophageal cancer by up-regulation of FN1 and PDGFRB. <i>Oncotarget</i> , 2017, 8, 17771-17784.	0.8	37
19239	Comparative transcriptomic analysis of mice liver treated with different AMPK activators in a mice model of atherosclerosis. <i>Oncotarget</i> , 2017, 8, 16594-16604.	0.8	6



#	ARTICLE	IF	CITATIONS
19240	Comprehensive analysis of PD-L1 expression in glioblastoma multiforme. <i>Oncotarget</i> , 2017, 8, 42214-42225.	0.8	81
19241	The long non-coding RNA NONHSAG026900 predicts prognosis as a favorable biomarker in patients with diffuse large B-cell lymphoma. <i>Oncotarget</i> , 2017, 8, 34374-34386.	0.8	17
19242	Targeting the PIM protein kinases for the treatment of a T-cell acute lymphoblastic leukemia subset. <i>Oncotarget</i> , 2017, 8, 30199-30216.	0.8	32
19243	Personalizing Chinese medicine by integrating molecular features of diseases and herb ingredient information: application to acute myeloid leukemia. <i>Oncotarget</i> , 2017, 8, 43579-43591.	0.8	3
19244	Identification of the miRNA-mRNA regulatory network of small cell osteosarcoma based on RNA-seq. <i>Oncotarget</i> , 2017, 8, 42525-42536.	0.8	22
19245	Identification of aberrantly expressed long non-coding RNAs in stomach adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 49201-49216.	0.8	55
19246	The highly expressed COL4A1 genes contributes to the proliferation and migration of the invasive ductal carcinomas. <i>Oncotarget</i> , 2017, 8, 58172-58183.	0.8	33
19247	A five-long non-coding RNA signature to improve prognosis prediction of clear cell renal cell carcinoma. <i>Oncotarget</i> , 2017, 8, 58699-58708.	0.8	29
19248	Increased transcriptional and metabolic capacity for lipid metabolism in the peripheral zone of the prostate may underpin its increased susceptibility to cancer. <i>Oncotarget</i> , 2017, 8, 84902-84916.	0.8	14
19249	Identification of dysregulated long non-coding RNAs/microRNAs/mRNAs in TNM I stage lung adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 51703-51718.	0.8	36
19250	microRNA-148a dysregulation discriminates poor prognosis of hepatocellular carcinoma in association with USP4 overexpression. <i>Oncotarget</i> , 2014, 5, 2792-2806.	0.8	85
19251	Identification of hub genes involved in the development of hepatocellular carcinoma by transcriptome sequencing. <i>Oncotarget</i> , 2017, 8, 60358-60367.	0.8	8
19252	Quantitative network mapping of the human kinome interactome reveals new clues for rational kinase inhibitor discovery and individualized cancer therapy. <i>Oncotarget</i> , 2014, 5, 3697-3710.	0.8	96
19253	Identification of microRNA differentially expressed in three subtypes of non-small cell lung cancer and in silico functional analysis. <i>Oncotarget</i> , 2017, 8, 74554-74566.	0.8	20
19254	Identification of the PAK4 interactome reveals PAK4 phosphorylation of N-WASP and promotion of Arp2/3-dependent actin polymerization. <i>Oncotarget</i> , 2017, 8, 77061-77074.	0.8	23
19255	Inference of time-delayed gene regulatory networks based on dynamic Bayesian network hybrid learning method. <i>Oncotarget</i> , 2017, 8, 80373-80392.	0.8	14
19256	Unique expression signatures of circular RNAs in response to DNA tumor virus SV40 infection. <i>Oncotarget</i> , 2017, 8, 98609-98622.	0.8	19
19257	MicroRNA co-expression networks exhibit increased complexity in pancreatic ductal compared to Vater's papilla adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 105320-105339.	0.8	9

#	ARTICLE	IF	CITATIONS
19258	Genetic identification and molecular modeling characterization reveal a novel <i>PROM1</i> mutation in Stargardt4-like macular dystrophy. <i>Oncotarget</i> , 2018, 9, 122-141.	0.8	32
19259	Systemic bioinformatics analysis of recurrent aphthous stomatitis gene expression profiles. <i>Oncotarget</i> , 2017, 8, 111064-111072.	0.8	29
19260	Integrative molecular network analysis identifies emergent enzalutamide resistance mechanisms in prostate cancer. <i>Oncotarget</i> , 2017, 8, 111084-111095.	0.8	11
19261	Domain retention in transcription factor fusion genes and its biological and clinical implications: a pan-cancer study. <i>Oncotarget</i> , 2017, 8, 110103-110117.	0.8	15
19262	Identification of bladder cancer prognostic biomarkers using an ageing gene-related competitive endogenous RNA network. <i>Oncotarget</i> , 2017, 8, 111742-111753.	0.8	7
19263	Comprehensive analysis of gene expression and DNA methylation datasets identify valuable biomarkers for rheumatoid arthritis progression. <i>Oncotarget</i> , 2018, 9, 2977-2983.	0.8	11
19264	Dihydroartemisinin-regulated mRNAs and lncRNAs in chronic myeloid leukemia. <i>Oncotarget</i> , 2018, 9, 2543-2552.	0.8	5
19265	Construction of key signal regulatory network in metastatic colorectal cancer. <i>Oncotarget</i> , 2018, 9, 6086-6094.	0.8	13
19266	Competitive endogenous RNA networks: integrated analysis of non-coding RNA and mRNA expression profiles in infantile hemangioma. <i>Oncotarget</i> , 2018, 9, 11948-11963.	0.8	11
19267	Discovery and validation of a glioblastoma co-expressed gene module. <i>Oncotarget</i> , 2018, 9, 10995-11008.	0.8	15
19268	Whole exome sequencing identifies mTOR and KEAP1 as potential targets for radiosensitization of HNSCC cells refractory to EGFR and $\Gamma$ 21 integrin inhibition. <i>Oncotarget</i> , 2018, 9, 18099-18114.	0.8	18
19269	GSTM3 and GSTP1: novel players driving tumor progression in cervical cancer. <i>Oncotarget</i> , 2018, 9, 21696-21714.	0.8	34
19270	A TRPV2 interactome-based signature for prognosis in glioblastoma patients. <i>Oncotarget</i> , 2018, 9, 18400-18409.	0.8	18
19271	UniPR1331, a small molecule targeting Eph/ephrin interaction, prolongs survival in glioblastoma and potentiates the effect of antiangiogenic therapy in mice. <i>Oncotarget</i> , 2018, 9, 24347-24363.	0.8	28
19272	Aberration hubs in protein interaction networks highlight actionable targets in cancer. <i>Oncotarget</i> , 2018, 9, 25166-25180.	0.8	6
19273	An NF $\kappa$ B-dependent mechanism of tumor cell plasticity and lateral transmission of aggressive features. <i>Oncotarget</i> , 2018, 9, 26679-26700.	0.8	14
19274	Global metabolite profiling analysis of lipotoxicity in HER2/neu-positive breast cancer cells. <i>Oncotarget</i> , 2018, 9, 27133-27150.	0.8	8
19275	Transcriptome profiling of anti-m $\mu$ 4 allergic hormone treated preantral/small antral mouse ovary follicles. <i>Oncotarget</i> , 2018, 9, 30253-30267.	0.8	3

#	ARTICLE	IF	CITATIONS
19276	MYC-related microRNAs signatures in non-Hodgkin B-cell lymphomas and their relationships with core cellular pathways. <i>Oncotarget</i> , 2018, 9, 29753-29771.	0.8	13
19277	Distinct urinary glycoprotein signatures in prostate cancer patients. <i>Oncotarget</i> , 2018, 9, 33077-33097.	0.8	33
19278	Integrated copy number and miRNA expression analysis in triple negative breast cancer of Latin American patients. <i>Oncotarget</i> , 2019, 10, 6184-6203.	0.8	15
19279	RNA sequencing analyses reveal differentially expressed genes and pathways as Notch2 targets in B-cell lymphoma. <i>Oncotarget</i> , 2020, 11, 4527-4540.	0.8	3
19280	Identification of novel prognostic markers of survival time in high-risk neuroblastoma using gene expression profiles. <i>Oncotarget</i> , 2020, 11, 4293-4305.	0.8	7
19281	New insights into the genetics of glioblastoma multiforme by familial exome sequencing. <i>Oncotarget</i> , 2015, 6, 5918-5931.	0.8	28
19282	Prognostic value of a 92-probe signature in breast cancer. <i>Oncotarget</i> , 2015, 6, 15662-15680.	0.8	14
19283	Long non-coding RNA expression profiles of hepatitis C virus-related dysplasia and hepatocellular carcinoma. <i>Oncotarget</i> , 2015, 6, 43770-43778.	0.8	79
19284	RNA-binding protein CELF1 promotes tumor growth and alters gene expression in oral squamous cell carcinoma. <i>Oncotarget</i> , 2015, 6, 43620-43634.	0.8	29
19285	Sense-antisense gene-pairs in breast cancer and associated pathological pathways. <i>Oncotarget</i> , 2015, 6, 42197-42221.	0.8	20
19286	Identification of the BRAF V600E mutation in gastroenteropancreatic neuroendocrine tumors. <i>Oncotarget</i> , 2016, 7, 4024-4035.	0.8	36
19287	The drug target genes show higher evolutionary conservation than non-target genes. <i>Oncotarget</i> , 2016, 7, 4961-4971.	0.8	16
19288	Identification of ovarian cancer subtype-specific network modules and candidate drivers through an integrative genomics approach. <i>Oncotarget</i> , 2016, 7, 4298-4309.	0.8	20
19289	Histone H3 lysine 4 acetylation and methylation dynamics define breast cancer subtypes. <i>Oncotarget</i> , 2016, 7, 5094-5109.	0.8	89
19290	G protein-coupled receptor GPR160 is associated with apoptosis and cell cycle arrest of prostate cancer cells. <i>Oncotarget</i> , 2016, 7, 12823-12839.	0.8	24
19291	Whole transcriptome profiling of patient-derived xenograft models as a tool to identify both tumor and stromal specific biomarkers. <i>Oncotarget</i> , 2016, 7, 20773-20787.	0.8	36
19292	Neuroendocrine immunomodulation network dysfunction in SAMP8 mice and PrP-hA <sup>2</sup> PPswe/PS1 <sup>E9</sup> mice: potential mechanism underlying cognitive impairment. <i>Oncotarget</i> , 2016, 7, 22988-23005.	0.8	17
19293	Reprogramming human A375 amelanotic melanoma cells by catalase overexpression: Upregulation of antioxidant genes correlates with regression of melanoma malignancy and with malignant progression when downregulated. <i>Oncotarget</i> , 0, 7, 41154-41171.	0.8	27

#	ARTICLE	IF	CITATIONS
19294	<i>De novo</i> HAPLN1 expression hallmarks Wnt-induced stem cell and fibrogenic networks leading to aggressive human hepatocellular carcinomas. <i>Oncotarget</i> , 2016, 7, 39026-39043.	0.8	29
19295	Quantitative proteomics reveals that distant recurrence-associated protein R-Ras and Transgelin predict post-surgical survival in patients with Stage III colorectal cancer. <i>Oncotarget</i> , 2016, 7, 43868-43893.	0.8	13
19296	Learning Large-Scale Bayesian Networks with the <b>sparsebn</b> Package. <i>Journal of Statistical Software</i> , 2019, 91, .	1.8	21
19297	The <i>C. elegans</i> pharynx: a model for organogenesis. <i>WormBook</i> , 2007, , 1-26.	5.3	98
19298	Atractyloside targets cancer-associated fibroblasts and inhibits the metastasis of colon cancer. <i>Annals of Translational Medicine</i> , 2020, 8, 1443-1443.	0.7	5
19299	Changes in transcriptome profiling during the acute/subacute phases of contusional spinal cord injury in rats. <i>Annals of Translational Medicine</i> , 2020, 8, 1682-1682.	0.7	19
19300	Intestinal mRNA expression profile and bioinformatics analysis in a methamphetamine-induced mouse model of inflammatory bowel disease. <i>Annals of Translational Medicine</i> , 2020, 8, 1669-1669.	0.7	10
19301	Systematic identification of key genes and pathways in clear cell renal cell carcinoma on bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2019, 7, 89-89.	0.7	17
19302	Genome-wide mutation profiling and related risk signature for prognosis of papillary renal cell carcinoma. <i>Annals of Translational Medicine</i> , 2019, 7, 427-427.	0.7	50
19303	Genetic landscape of prognostic value in pancreatic ductal adenocarcinoma microenvironment. <i>Annals of Translational Medicine</i> , 2019, 7, 645-645.	0.7	26
19304	Screening TCGA database for prognostic genes in lower grade glioma microenvironment. <i>Annals of Translational Medicine</i> , 2020, 8, 209-209.	0.7	35
19305	C3, C3AR1, HLA-DRA, and HLA-E as potential prognostic biomarkers for renal clear cell carcinoma. <i>Translational Andrology and Urology</i> , 2020, 9, 2640-2656.	0.6	9
19306	Circular RNA hsa_circ_0002124 promotes hepatocellular carcinoma cell proliferation through the MAPK pathway. <i>Translational Cancer Research</i> , 2019, 8, 367-378.	0.4	4
19307	Bioinformatic analysis of long non-coding RNA-associated competing endogenous RNA network in adrenocortical carcinoma. <i>Translational Cancer Research</i> , 2019, 8, 2175-2186.	0.4	7
19308	Screening of potential biomarkers and their predictive value in early stage non-small cell lung cancer: a bioinformatics analysis. <i>Translational Lung Cancer Research</i> , 2019, 8, 797-807.	1.3	28
19309	Correlation Trait Loci (CTL) mapping: phenotype network inference subject to genotype. <i>Journal of Open Source Software</i> , 2016, 1, 87.	2.0	3
19310	Netwulf: Interactive visualization of networks in Python. <i>Journal of Open Source Software</i> , 2019, 4, 1425.	2.0	14
19311	webweb: a tool for creating, displaying, and sharing interactive network visualizations on the web. <i>Journal of Open Source Software</i> , 2019, 4, 1458.	2.0	7

#	ARTICLE	IF	CITATIONS
19312	Identification of liver metastasis-associated genes in human colon carcinoma by mRNA profiling. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 2018, 30, 633-646.	0.7	15
19317	Analysis of the Skeletal Muscle Proteome Uncovers Alteration in Splicing, Mitochondria, and Immune Factors with Aging. SSRN Electronic Journal, 0, , .	0.4	1
19318	Harnessing Tumor Immune Ecosystem Dynamics to Personalize Radiation Therapy. SSRN Electronic Journal, 0, , .	0.4	2
19319	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Cholesterol Metabolism in Alzheimer's Disease. SSRN Electronic Journal, 0, , .	0.4	6
19320	Prediction of interacting proteins from homology-modeled complex structures using sequence and structure scores. Biophysics (Nagoya-shi, Japan), 2007, 3, 13-26.	0.4	6
19321	KIF14 and KIF23 Promote Cell Proliferation and Chemoresistance in HCC Cells, and Predict Worse Prognosis of Patients with HCC. Cancer Management and Research, 2020, Volume 12, 13241-13257.	0.9	19
19322	Bioinformatics Analysis of Key Genes and Pathways of Cervical Cancer. OncoTargets and Therapy, 2020, Volume 13, 13275-13283.	1.0	8
19323	Decoding Psoriasis: Integrated Bioinformatics Approach to Understand Hub Genes and Involved Pathways. Current Pharmaceutical Design, 2020, 26, 3619-3630.	0.9	11
19324	High Expression of miR-206 Predicts Adverse Outcomes: A Potential Therapeutic Target for Esophageal Cancer. Combinatorial Chemistry and High Throughput Screening, 2020, 22, 599-611.	0.6	4
19325	Identification of Potential Biomarkers in Neonatal Sepsis by Establishing a Competitive Endogenous RNA Network. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 369-380.	0.6	10
19326	Computational Prediction of Protein-Protein Interaction Networks: Algorithms and Resources. Current Genomics, 2013, 14, 397-414.	0.7	119
19327	Constructing Networks of Organelle Functional Modules in Arabidopsis. Current Genomics, 2016, 17, 427-438.	0.7	16
19328	A Systematic in-silico Analysis of Helicobacter pylori Pathogenic Islands for Identification of Novel Drug Target Candidates. Current Genomics, 2017, 18, 450-465.	0.7	7
19329	Decoding Common Features of Neurodegenerative Disorders: From Differentially Expressed Genes to Pathways. Current Genomics, 2018, 19, 300-312.	0.7	21
19330	CatbNet: A Multi Network Analyzer for Comparing and Analyzing the Topology of Biological Networks. Current Genomics, 2019, 20, 69-75.	0.7	2
19331	Domain-based Comparative Analysis of Bacterial Proteomes: Uniqueness, Interactions, and the Dark Matter. Current Genomics, 2019, 20, 115-123.	0.7	7
19332	Understanding the Mechanism of Cell Death in Gemcitabine Resistant Pancreatic Ductal Adenocarcinoma: A Systems Biology Approach. Current Genomics, 2020, 20, 483-490.	0.7	3
19333	Deciphering the Novel Target Genes Involved in the Epigenetics of Hepatocellular Carcinoma Using Graph Theory Approach. Current Genomics, 2020, 20, 545-555.	0.7	3

#	ARTICLE	IF	CITATIONS
19334	Amino Acid Network for the Discrimination of Native Protein Structures from Decoys. <i>Current Protein and Peptide Science</i> , 2014, 15, 522-528.	0.7	14
19335	Diagnostic Value of MiR-125b as a Potential Biomarker for Stage I Lung Adenocarcinoma. <i>Current Molecular Medicine</i> , 2019, 19, 216-227.	0.6	23
19336	Exploring Shared Pathogenesis of Alzheimer's Disease and Type 2 Diabetes Mellitus via Co-expression Networks Analysis. <i>Current Alzheimer Research</i> , 2020, 17, 566-575.	0.7	25
19337	Molecular Modeling and Ligand Docking for Solute Carrier (SLC) Transporters. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 843-856.	1.0	85
19338	Functional Cross-Talk between Adenosine and Metabotropic Glutamate Receptors. <i>Current Neuropharmacology</i> , 2019, 17, 422-437.	1.4	16
19339	Computational Analysis of Arginine Deiminase Sequences to Provide a Guideline for Protein Engineering. <i>Current Proteomics</i> , 2020, 17, 132-146.	0.1	3
19340	A New Model of Identifying Differentially Expressed Genes via Weighted Network Analysis Based on Dimensionality Reduction Method. <i>Current Bioinformatics</i> , 2019, 14, 762-770.	0.7	1
19341	Integrated In-silico Analysis to Study the Role of microRNAs in the Detection of Chronic Kidney Diseases. <i>Current Bioinformatics</i> , 2020, 15, 144-154.	0.7	10
19342	Integrated System Pharmacology and In Silico Analysis Elucidating Neuropharmacological Actions of <i>Withania somnifera</i> in the Treatment of Alzheimer's Disease. <i>CNS and Neurological Disorders - Drug Targets</i> , 2020, 19, 541-556.	0.8	6
19343	Analysis and Visualization of Long-Range Contacts and Networks in Homologous Families of Proteins. <i>The Open Structural Biology Journal</i> , 2009, 3, 104-125.	0.1	5
19344	Identification of Critical MicroRNA Gene Targets in Cervical Cancer Using Network Properties. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2014, 3, 37-44.	0.6	12
19345	Computational Analysis of miRNA and their Gene Targets Significantly Involved in Colorectal Cancer Progression. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2018, 8, 68-75.	0.6	14
19346	Development of Integrated Visualization Tool for Differentially Expressed Genes and Gene Ontology Analysis. <i>International Journal of Image and Signal Systems Engineering</i> , 2017, 1, 1-6.	0.1	1
19347	Global Analysis of miRNA-mRNA Interaction Network in Breast Cancer with Brain Metastasis. <i>Anticancer Research</i> , 2017, 37, 4455-4468.	0.5	26
19348	Social and Self-Reflective Use of a Web-Based Personally Controlled Health Management System. <i>Journal of Medical Internet Research</i> , 2013, 15, e211.	2.1	16
19349	Recommending Education Materials for Diabetic Questions Using Information Retrieval Approaches. <i>Journal of Medical Internet Research</i> , 2017, 19, e342.	2.1	9
19350	Next Generation Phenotyping Using the Unified Medical Language System. <i>JMIR Medical Informatics</i> , 2014, 2, e5.	1.3	20
19351	Nasopharyngeal Carcinoma Protein Interaction Mapping Analysis via Proteomic Approaches. <i>Asian Pacific Journal of Cancer Prevention</i> , 2018, 19, 845-851.	0.5	11



#	ARTICLE	IF	CITATIONS
19352	Protein-Protein Interaction Network Analysis of Salivary Proteomic Data in Oral Cancer Cases. Asian Pacific Journal of Cancer Prevention, 2018, 19, 1639-1645.	0.5	9
19354	Serum-based metabolic alterations in patients with papillary thyroid carcinoma unveiled by non-targeted <sup>1</sup> H-NMR metabolomics approach. Iranian Journal of Basic Medical Sciences, 2018, 21, 1140-1147.	1.0	12
19356	Identification of Potential Molecular Mechanisms and Candidate Genes Involved in The Acute Phase of Myocardial Infarction. Cell Journal, 2018, 20, 435-442.	0.2	6
19357	Enhancing data integration with text analysis to find proteins implicated in plant stress response. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	8
19358	Blood transcriptome analysis reveals gene expression features of breast-feeding rhesus macaque (<i>Macaca mulatta</i>) infants. Zoological Research, 2020, 41, 431-436.	0.9	10
19359	Identification of Potential Therapeutic Targets of Alzheimer's Disease By Weighted Gene Co-Expression Network Analysis. Chinese Medical Sciences Journal, 2020, 35, 330.	0.2	7
19360	NemoSuite: Web-based Network Motif Analytic Suite. Advances in Science, Technology and Engineering Systems, 2020, 5, 1545-1553.	0.4	2
19361	Enhanced Awareness In Space Operations Using Multipurpose Dynamic Network Analysis. , 2018, , .		3
19362	Chronic platelet-derived growth factor receptor signaling exerts control over initiation of protein translation in glioma. Life Science Alliance, 2018, 1, e201800029.	1.3	5
19363	Rab1b and ARF5 are novel RNA-binding proteins involved in FMDV IRES-driven RNA localization. Life Science Alliance, 2019, 2, e201800131.	1.3	14
19364	A network of human functional gene interactions from knockout fitness screens in cancer cells. Life Science Alliance, 2019, 2, e201800278.	1.3	81
19365	Oxidised metabolites of the omega-6 fatty acid linoleic acid activate dFOXO. Life Science Alliance, 2020, 3, e201900356.	1.3	17
19366	CLIC4 and CLIC1 bridge plasma membrane and cortical actin network for a successful cytokinesis. Life Science Alliance, 2020, 3, e201900558.	1.3	23
19367	Metabolic reprogramming of fibro/adipogenic progenitors facilitates muscle regeneration. Life Science Alliance, 2020, 3, e202000646.	1.3	36
19368	An evolutionary approach to systematic discovery of novel deubiquitinases, applied to <i>Legionella</i>. Life Science Alliance, 2020, 3, e202000838.	1.3	21
19369	FIREWORKS: a bottom-up approach to integrative coessentiality network analysis. Life Science Alliance, 2021, 4, e202000882.	1.3	29
19370	Measles outbreak linked to European B3 outbreaks, Wales, United Kingdom, 2017. Eurosurveillance, 2017, 22, .	3.9	23
19371	Application of Sparse Linear Discriminant Analysis and Elastic Net for Diagnosis of IgA Nephropathy: Statistical and Biological Viewpoints. Iranian Biomedical Journal, 2018, 22, 374-384.	0.4	6

#	ARTICLE	IF	CITATIONS
19372	RNA-Seq Bayesian Network Exploration of Immune System in Bovine. Iranian Journal of Biotechnology, 2019, 17, 9-17.	0.3	3
19373	An In-Silico Study: Interaction of BOR1-type Boron (B) Transporters with A Small Group of Functionally Unidentified Proteins Under Various Stresses in Potato ( <i>Solanum tuberosum</i> ). Commagene Journal of Biology, 0, , 134-139.	0.1	3
19374	The effect of chronic, mild heat stress on metabolic changes of nutrition and adaptations in rumen papillae of lactating dairy cows. Journal of Dairy Science, 2020, 103, 8601-8614.	1.4	19
19375	Construction of Disease Similarity Networks Using Concept Embedding and Ontology. Studies in Health Technology and Informatics, 2019, 264, 442-446.	0.2	7
19376	Research Paper: Serum Proteomic Study of Women With Obsessive-Compulsive Disorder, Washing Subtype. Basic and Clinical Neuroscience, 2018, 9, 337-346.	0.3	4
19377	The Diversity of the Endobiotic Bacterial Communities in the Four Jellyfish Species. Polish Journal of Microbiology, 2019, 68, 465-476.	0.6	1
19378	Bile Ductal Transcriptome Identifies Key Pathways and Hub Genes in <i>Clonorchis sinensis</i> -Infected Sprague-Dawley Rats. Korean Journal of Parasitology, 2020, 58, 513-525.	0.5	2
19379	Marine bacterial, archaeal and eukaryotic diversity and community structure on the continental shelf of the western Antarctic Peninsula. Aquatic Microbial Ecology, 2014, 73, 107-121.	0.9	53
19380	Specific Features of Fibrotic Lung Fibroblasts Highly Sensitive to Fibrotic Processes Mediated via TGF- $\beta$ -ERK5 Interaction. Cellular Physiology and Biochemistry, 2019, 52, 822-837.	1.1	7
19381	Deletion of miRNA-22 Induces Cardiac Hypertrophy in Females but Attenuates Obesogenic Diet-Mediated Metabolic Disorders.. Cellular Physiology and Biochemistry, 2020, 54, 1199-1217.	1.1	7
19382	Relationship Between Mitochondrial Structure and Bioenergetics in <i>Pseudoxanthoma elasticum</i> Dermal Fibroblasts. Frontiers in Cell and Developmental Biology, 2020, 8, 610266.	1.8	12
19383	Dysregulated lncRNA-miRNA-mRNA Network Reveals Patient Survival-Associated Modules and RNA Binding Proteins in Invasive Breast Carcinoma. Frontiers in Genetics, 2019, 10, 1284.	1.1	16
19384	Identification of Novel Genes and Biological Pathways That Overlap in Infectious and Nonallergic Diseases of the Upper and Lower Airways Using Network Analyses. Frontiers in Genetics, 2019, 10, 1352.	1.1	9
19385	Systematically Dissecting the Function of RNA-Binding Proteins During Glioma Progression. Frontiers in Genetics, 2019, 10, 1394.	1.1	6
19386	Transcriptional Profiles of Long Non-coding RNA and mRNA in Sheep Mammary Gland During Lactation Period. Frontiers in Genetics, 2020, 11, 946.	1.1	8
19387	Hub Genes Identification in a Murine Model of Allergic Rhinitis Based on Bioinformatics Analysis. Frontiers in Genetics, 2020, 11, 970.	1.1	5
19388	Development of an Immune-Related Risk Signature for Predicting Prognosis in Lung Squamous Cell Carcinoma. Frontiers in Genetics, 2020, 11, 978.	1.1	43
19389	Identification of Critical Genes and Proteins for Stent Restenosis Induced by Esophageal Benign Hyperplasia in Esophageal Cancer. Frontiers in Genetics, 2020, 11, 563954.	1.1	6

#	ARTICLE	IF	CITATIONS
19390	Silent Witness: Dual-Species Transcriptomics Reveals Epithelial Immunological Quiescence to Helminth Larval Encounter and Fostered Larval Development. <i>Frontiers in Immunology</i> , 2018, 9, 1868.	2.2	13
19391	Small Intestinal Immunopathology Plays a Big Role in Lethal Cytokine Release Syndrome, and Its Modulation by Interferon- $\beta$ , IL-17A, and a Janus Kinase Inhibitor. <i>Frontiers in Immunology</i> , 2020, 11, 1311.	2.2	11
19392	Proteome of the Triatomine Digestive Tract: From Catalytic to Immune Pathways; Focusing on Annexin Expression. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 589435.	1.6	8
19393	A Prognostic Prediction Model Developed Based on Four CpG Sites and Weighted Correlation Network Analysis Identified DNAB1 as a Novel Biomarker for Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 1716.	1.3	12
19394	Semantic organization in children with cochlear implants: computational analysis of verbal fluency. <i>Frontiers in Psychology</i> , 2013, 4, 543.	1.1	60
19395	Identification of Important Proteins and Pathways Affecting Feed Efficiency in DLY Pigs by iTRAQ-Based Proteomic Analysis. <i>Animals</i> , 2020, 10, 189.	1.0	6
19396	The Extracellular Bone Marrow Microenvironment—A Proteomic Comparison of Constitutive Protein Release by In Vitro Cultured Osteoblasts and Mesenchymal Stem Cells. <i>Cancers</i> , 2021, 13, 62.	1.7	16
19397	The Interactome of Cancer-Related Lysyl Oxidase and Lysyl Oxidase-Like Proteins. <i>Cancers</i> , 2021, 13, 71.	1.7	20
19398	Genome-Wide Characterization of Cucumber ( <i>Cucumis sativus</i> L.) GRAS Genes and Their Response to Various Abiotic Stresses. <i>Horticulturae</i> , 2020, 6, 110.	1.2	7
19399	A Network-Based Bioinformatics Approach to Identify Molecular Biomarkers for Type 2 Diabetes that Are Linked to the Progression of Neurological Diseases. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 1035.	1.2	52
19400	The Effect of 3-Hydroxy-3,4,5,4-Tetramethoxy-stilbene, the Metabolite of the Resveratrol Analogue DMU-212, on the Motility and Proliferation of Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1100.	1.8	9
19401	The Proteomic Landscape of Resting and Activated CD4+ T Cells Reveal Insights into Cell Differentiation and Function. <i>International Journal of Molecular Sciences</i> , 2021, 22, 275.	1.8	9
19402	Whole-Transcriptome RNA Sequencing Reveals the Global Molecular Responses and CeRNA Regulatory Network of mRNAs, lncRNAs, miRNAs and circRNAs in Response to Salt Stress in Sugar Beet ( <i>Beta</i> ) Tj ETQq0 0 0 rgB8/Overlook 10 Tf 50		
19403	Global Genome Conformational Programming during Neuronal Development Is Associated with CTCF and Nuclear FGFR1—The Genome Archipelago Model. <i>International Journal of Molecular Sciences</i> , 2021, 22, 347.	1.8	9
19404	Accumulation of the Auxin Precursor Indole-3-Acetamide Curtails Growth through the Repression of Ribosome-Biogenesis and Development-Related Transcriptional Networks. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2040.	1.8	6
19405	Influence of OSMAC-Based Cultivation in Metabolome and Anticancer Activity of Fungi Associated with the Brown Alga <i>Fucus vesiculosus</i> . <i>Marine Drugs</i> , 2019, 17, 67.	2.2	30
19406	Diversity, Bioactivity Profiling and Untargeted Metabolomics of the Cultivable Gut Microbiota of <i>Ciona intestinalis</i> . <i>Marine Drugs</i> , 2021, 19, 6.	2.2	13
19407	Pan-Genome-Based Analysis as a Framework for Demarcating Two Closely Related Methanotroph Genera <i>Methylocystis</i> and <i>Methylosinus</i> . <i>Microorganisms</i> , 2020, 8, 768.	1.6	15

#	ARTICLE	IF	CITATIONS
19408	Vibrio Colonization Is Highly Dynamic in Early Microplastic-Associated Biofilms as Well as on Field-Collected Microplastics. <i>Microorganisms</i> , 2021, 9, 76.	1.6	48
19409	Signalling and Bioactive Metabolites from <i>Streptomyces</i> sp. RK44. <i>Molecules</i> , 2020, 25, 460.	1.7	15
19410	Larvicidal Activity of Cinnamic Acid Derivatives: Investigating Alternative Products for <i>Aedes aegypti</i> L. Control. <i>Molecules</i> , 2021, 26, 61.	1.7	22
19411	Mexican <i>Ganoderma Lucidum</i> Extracts Decrease Lipogenesis Modulating Transcriptional Metabolic Networks and Gut Microbiota in C57BL/6 Mice Fed with a High-Cholesterol Diet. <i>Nutrients</i> , 2021, 13, 38.	1.7	15
19412	Bioinformatics and In vitro Studies Reveal the Importance of p53, PPARG and Notch Signaling Pathway in Inhibition of Breast Cancer Stem Cells by Hesperetin. <i>Advanced Pharmaceutical Bulletin</i> , 2021, 11, 351-360.	0.6	7
19413	Genome-wide Analysis of $\mu$ DR-related Transposable Elements Insertion Population in Maize. <i>Acta Agronomica Sinica</i> (China), 2011, 37, 772-777.	0.1	1
19414	$\mu$ MetaGen: a Promising Tool for Modeling Metabolic Networks From KEGG*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 63-68.	0.3	3
19415	Discovering Active Subnetwork in Protein Interaction Network*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 208-217.	0.3	2
19416	Human Protein Structural Interaction Network: Domain Effects on Network Topology and Protein Function*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 517-526.	0.3	2
19418	Natural taurine promotes apoptosis of human hepatic stellate cells in proteomics analysis. <i>World Journal of Gastroenterology</i> , 2010, 16, 1916.	1.4	18
19419	Exploring pathogenesis of primary biliary cholangitis by proteomics: A pilot study. <i>World Journal of Gastroenterology</i> , 2017, 23, 8489-8499.	1.4	2
19420	Long noncoding RNA NALT1-induced gastric cancer invasion and metastasis via NOTCH signaling pathway. <i>World Journal of Gastroenterology</i> , 2019, 25, 6508-6526.	1.4	15
19421	Comprehensive multi-omics analysis identified core molecular processes in esophageal cancer and revealed GNGT2 as a potential prognostic marker. <i>World Journal of Gastroenterology</i> , 2019, 25, 6890-6901.	1.4	8
19422	Promising key genes associated with tumor microenvironments and prognosis of hepatocellular carcinoma. <i>World Journal of Gastroenterology</i> , 2020, 26, 789-803.	1.4	26
19424	Comparison of Fecal Microbial Communities between White and Black Pigs. <i>Journal of Applied Biological Chemistry</i> , 2015, 58, 369-375.	0.2	8
19425	Identification of key miRNAs in papillary thyroid carcinoma based on data mining and bioinformatics methods. <i>Biomedical Reports</i> , 2020, 12, 11-16.	0.9	5
19426	Identification of potential key genes in gastric cancer using bioinformatics analysis. <i>Biomedical Reports</i> , 2020, 12, 178-192.	0.9	18
19427	Identification of the miRNA-target gene regulatory network in intracranial aneurysm based on microarray expression data. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 3239-3248.	0.8	5

#	ARTICLE	IF	CITATIONS
19428	TOB1â€™AS1 suppresses nonâ€™small cell lung cancer cell migration and invasion through a ceRNA network. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4249-4258.	0.8	19
19429	LncRNA ZFAS1 serves as a prognostic biomarker to predict the survival of patients with ovarian cancer. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4673-4681.	0.8	5
19430	A fiveâ€™long nonâ€™coding RNA signature with the ability to predict overall survival of patients with lung adenocarcinoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4852-4864.	0.8	11
19431	Identification of differentially expressed genes in the endothelial precursor cells of patients with type 2 diabetes mellitus by bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 499-510.	0.8	7
19432	Integrative module analysis of HCC gene expression landscapes. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 1779-1788.	0.8	20
19433	ETS2 and microRNAâ€™155 regulate the pathogenesis of heart failure through targeting and regulating GPR18 expression. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 3469-3478.	0.8	8
19434	Identification of a lncRNAâ€™miRNAâ€™mRNA network based on competitive endogenous RNA theory reveals functional lncRNAs in hypertrophic cardiomyopathy. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 1176-1190.	0.8	10
19435	Comprehensive evaluation of differential long nonâ€™coding RNA and gene expression in patients with cartilaginous endplate degeneration of cervical vertebra. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 1-1.	0.8	10
19436	Antiâ€™inflammatory activity of <i>Radix Angelicae biseratae</i> in the treatment of osteoarthritis determined by systematic pharmacology and inâ€™vitro experiments. <i>Experimental and Therapeutic Medicine</i> , 2020, 21, 5.	0.8	5
19437	Weighted gene coâ€™expression network analysis to identify key modules and hub genes associated with atrial fibrillation. <i>International Journal of Molecular Medicine</i> , 2020, 45, 401-416.	1.8	23
19438	Genomeâ€™wide DNA methylation regulation analysis of long nonâ€™coding RNAs in glioblastoma. <i>International Journal of Molecular Medicine</i> , 2020, 46, 224-238.	1.8	10
19439	p53 and ANXA4/NFâ€™B p50 complexes regulate cell proliferation, apoptosis and tumor progression in ovarian clear cell carcinoma. <i>International Journal of Molecular Medicine</i> , 2020, 46, 2102-2114.	1.8	9
19440	Transcriptomic landscaping of core genes andâ€™pathways of mild and severe psoriasis vulgaris. <i>International Journal of Molecular Medicine</i> , 2020, 47, 219-231.	1.8	17
19441	Novel circRNA_0071196/miRNAâ€™19bâ€™3p/CIT axis is associated with proliferation and migration of bladder cancer. <i>International Journal of Oncology</i> , 2020, 57, 767-779.	1.4	17
19442	Networkâ€™based identification of signature genes KLF6 and SPOCK1 associated with oral submucous fibrosis. <i>Molecular and Clinical Oncology</i> , 2020, 12, 299-310.	0.4	7
19443	Screening of the prognostic targets for breast cancer based co-expression modules analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 4038-4044.	1.1	20
19444	Comprehensive expression profiles and bioinformatics analysis reveal special circular RNA expression and potential predictability in the peripheral blood of humans with idiopathic membranous nephropathy. <i>Molecular Medicine Reports</i> , 2019, 20, 4125-4139.	1.1	6
19445	Identification of aberrantly methylatedâ€™differentially expressed genes and gene ontology in prostate cancer. <i>Molecular Medicine Reports</i> , 2020, 21, 744-758.	1.1	5

#	ARTICLE	IF	CITATIONS
19446	Integrated analysis of DNA methylation and transcriptome profiling of polycystic ovary syndrome. <i>Molecular Medicine Reports</i> , 2020, 21, 2138-2150.	1.1	11
19447	Application of weighted gene co-expression network analysis to explore the potential diagnostic biomarkers for colorectal cancer. <i>Molecular Medicine Reports</i> , 2020, 21, 2533-2543.	1.1	8
19448	A novel plasma lncRNA ENST00000416361 is upregulated in coronary artery disease and is related to inflammation and lipid metabolism. <i>Molecular Medicine Reports</i> , 2020, 21, 2375-2384.	1.1	12
19449	Circular RNA Circ100084 functions as sponge of miR-23a-5p to regulate IGF2 expression in hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2020, 21, 2395-2404.	1.1	14
19450	Comprehensive analysis of aberrantly expressed long non-coding RNAs, microRNAs, and mRNAs associated with the competitive endogenous RNA network in cervical cancer. <i>Molecular Medicine Reports</i> , 2020, 22, 405-415.	1.1	10
19451	Identification of potential crucial genes and molecular mechanisms in glioblastoma multiforme by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 859-869.	1.1	17
19452	Identification of prognostic biomarkers and drug target prediction for colon cancer according to a competitive endogenous RNA network. <i>Molecular Medicine Reports</i> , 2020, 22, 620-632.	1.1	24
19453	Identification of co-expression modules and hub genes of retinoblastoma via co-expression analysis and protein-protein interaction networks. <i>Molecular Medicine Reports</i> , 2020, 22, 1155-1168.	1.1	8
19454	Key miRNAs associated with memory and learning disorder upon exposure to sevoflurane determined by RNA sequencing. <i>Molecular Medicine Reports</i> , 2020, 22, 1567-1575.	1.1	6
19455	Expression profiling of circular RNAs and their potential role in early-stage diabetic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2020, 22, 1958-1968.	1.1	12
19456	Identification of potential markers for type 2 diabetes mellitus via bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 1868-1882.	1.1	18
19457	Uncovering potential differentially expressed miRNAs and targeted mRNAs in myocardial infarction based on integrating analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 4383-4395.	1.1	6
19458	Identification of inflammation-associated circulating long non-coding RNAs and genes in intracranial aneurysm rupture-induced subarachnoid hemorrhage. <i>Molecular Medicine Reports</i> , 2020, 22, 4541-4550.	1.1	9
19459	Identification of circulating hub long noncoding RNAs associated with hypertrophic cardiomyopathy using weighted correlation network analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 4637-4644.	1.1	9
19460	Co-expression network analysis identified specific miRNAs and genes in association with slow-transit constipation. <i>Molecular Medicine Reports</i> , 2020, 22, 4696-4706.	1.1	6
19461	Differentially expressed circular RNAs in a murine asthma model. <i>Molecular Medicine Reports</i> , 2020, 22, 5412-5422.	1.1	11
19462	Survival-related risk score of lung adenocarcinoma identified by weight gene co-expression network analysis. <i>Oncology Letters</i> , 2019, 18, 4441-4448.	0.8	5
19463	Identification of cancer/testis antigen 12 gene as a potential hepatocellular carcinoma therapeutic target by hub gene screening with topological analysis. <i>Oncology Letters</i> , 2019, 18, 4778-4788.	0.8	6



#	ARTICLE	IF	CITATIONS
19464	Four targeted genes for predicting the prognosis of colorectal cancer: A bioinformatics analysis case. <i>Oncology Letters</i> , 2019, 18, 5043-5054.	0.8	18
19465	Identification of the lncRNA-miRNA-mRNA network associated with gastric cancer via integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 5769-5784.	0.8	9
19466	Identification of key genes and evaluation of clinical outcomes in lung squamous cell carcinoma using integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 5859-5870.	0.8	13
19467	The core genes involved in the promotion of depression in patients with ovarian cancer. <i>Oncology Letters</i> , 2019, 18, 5995-6007.	0.8	10
19468	Identification of biomarkers and construction of a microRNA-mRNA regulatory network for ependymoma using integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 6079-6089.	0.8	4
19469	Screening of core genes and pathways in breast cancer development via comprehensive analysis of multi gene expression datasets. <i>Oncology Letters</i> , 2019, 18, 5821-5830.	0.8	9
19470	Cathepsin $\beta$ 1/2L interacts with CDK2-AP1 as a potential predictor of prognosis in patients with breast cancer. <i>Oncology Letters</i> , 2020, 19, 167-176.	0.8	7
19471	Identification of key genes involved in the development and progression of early-onset colorectal cancer by co-expression network analysis. <i>Oncology Letters</i> , 2020, 19, 177-186.	0.8	46
19472	FNDC3B is associated with ER stress and poor prognosis in cervical cancer. <i>Oncology Letters</i> , 2020, 19, 406-414.	0.8	12
19473	Integrated bioinformatics analysis to screen hub genes in the lymph node metastasis of thyroid cancer. <i>Oncology Letters</i> , 2020, 19, 1375-1383.	0.8	3
19474	Overexpression of miR-206 in osteosarcoma and its associated molecular mechanisms as assessed through TCGA and GEO databases. <i>Oncology Letters</i> , 2020, 19, 1751-1758.	0.8	7
19475	Identification of crucial genes and pathways associated with colorectal cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2020, 19, 1881-1889.	0.8	13
19476	Identification of candidate RNA signatures in triple-negative breast cancer by the construction of a competing endogenous RNA network with integrative analyses of Gene Expression Omnibus and The Cancer Genome Atlas data. <i>Oncology Letters</i> , 2020, 19, 1915-1927.	0.8	5
19477	Identification of hub genes associated with outcome of clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2020, 19, 2846-2860.	0.8	6
19478	Upregulation of ASPM, BUB1B and SPDL1 in tumor tissues predicts poor survival in patients with pancreatic ductal adenocarcinoma. <i>Oncology Letters</i> , 2020, 19, 3307-3315.	0.8	10
19479	Comprehensive gene and pathway analysis of cervical cancer progression. <i>Oncology Letters</i> , 2020, 19, 3316-3332.	0.8	49
19480	Clinical and prognostic significance of MYH11 in lung cancer. <i>Oncology Letters</i> , 2020, 19, 3899-3906.	0.8	13
19481	A putative competing endogenous RNA network in cisplatin-resistant lung adenocarcinoma cells identifying potentially rewarding research targets. <i>Oncology Letters</i> , 2020, 19, 4040-4052.	0.8	4

#	ARTICLE	IF	CITATIONS
19482	Comprehensive characterization of driver genes in diffuse large B-cell lymphoma. <i>Oncology Letters</i> , 2020, 20, 382-390.	0.8	11
19483	Bioinformatics analysis of prognosis-related long non-coding RNAs in invasive breast carcinoma. <i>Oncology Letters</i> , 2020, 20, 113-122.	0.8	3
19484	Prognostic and predictive value of immune/stromal-related gene biomarkers in renal cell carcinoma. <i>Oncology Letters</i> , 2020, 20, 308-316.	0.8	5
19485	Identification of key genes associated with the progression of intrahepatic cholangiocarcinoma using weighted gene co-expression network analysis. <i>Oncology Letters</i> , 2020, 20, 483-494.	0.8	7
19486	Long non-coding RNA LINC00460 predicts poor survival and promotes cell viability in pancreatic cancer. <i>Oncology Letters</i> , 2020, 20, 1369-1375.	0.8	9
19487	Elevated CELSR3 expression is associated with hepatocarcinogenesis and poor prognosis. <i>Oncology Letters</i> , 2020, 20, 1083-1092.	0.8	6
19488	Identification and validation of tumor microenvironment-related genes of prognostic value in lung adenocarcinoma. <i>Oncology Letters</i> , 2020, 20, 1772-1780.	0.8	12
19489	Circular RNA profiling in plasma exosomes from patients with gastric cancer. <i>Oncology Letters</i> , 2020, 20, 2199-2208.	0.8	14
19490	Identification of the association between HMMR expression and progression of hepatocellular carcinoma via construction of a co-expression network. <i>Oncology Letters</i> , 2020, 20, 2645-2654.	0.8	10
19491	Analysis of key genes and pathways in breast ductal carcinoma <i>in situ</i> . <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	2
19492	Identification of diagnostic and prognostic biomarkers, and candidate targeted agents for hepatitis B virus-associated early stage hepatocellular carcinoma based on RNA sequencing data. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	4
19493	Overexpression of Rho GTPase-binding protein 2 promotes hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	7
19494	Polyphyllin VII suppresses cell proliferation, the cell cycle and cell migration in colorectal cancer. <i>Oncology Letters</i> , 2020, 21, 1-1.	0.8	7
19495	Îlelemin inhibits the generation of peritoneum effusion in pancreatic cancer via suppression of the HIF1-VEGFA pathway based on network pharmacology. <i>Oncology Reports</i> , 2019, 42, 2561-2571.	1.2	20
19496	Comprehensive analysis of the lncRNA-associated competing endogenous RNA network in breast cancer. <i>Oncology Reports</i> , 2019, 42, 2572-2582.	1.2	27
19497	Integrative analysis of mRNA and miRNA expression profiles reveals seven potential diagnostic biomarkers for non-small cell lung cancer. <i>Oncology Reports</i> , 2020, 43, 99-112.	1.2	20
19498	METTL14 promotes the migration and invasion of breast cancer cells by modulating N6-methyladenosine and hsa-miR-146a-5p expression. <i>Oncology Reports</i> , 2020, 43, 1375-1386.	1.2	65
19499	Identification of lung adenocarcinoma biomarkers based on bioinformatic analysis and human samples. <i>Oncology Reports</i> , 2020, 43, 1437-1450.	1.2	18

#	ARTICLE	IF	CITATIONS
19500	Identification of a prognosis-associated signature associated with energy metabolism in triple-negative breast cancer. <i>Oncology Reports</i> , 2020, 44, 819-837.	1.2	14
19501	Minichromosome maintenance 6 complex component identified by bioinformatics analysis and experimental validation in esophageal squamous cell carcinoma. <i>Oncology Reports</i> , 2020, 44, 987-1002.	1.2	5
19502	m6A methyltransferase METTL3 maintains colon cancer tumorigenicity by suppressing SOCS2 to promote cell proliferation. <i>Oncology Reports</i> , 2020, 44, 973-986.	1.2	61
19503	High expression levels of DEF6 predicts a poor prognosis for patients with clear cell renal cell carcinoma. <i>Oncology Reports</i> , 2020, 44, 2056-2066.	1.2	3
19504	Identification of Target Genes in Breast Cancer Pathway using Protein-Protein Interaction Network. <i>International Journal of Cancer Research</i> , 2017, 13, 51-58.	0.2	3
19505	Algebraic and topological indices of molecular pathway networks in human cancers. <i>Mathematical Biosciences and Engineering</i> , 2015, 12, 1289-1302.	1.0	15
19506	Identification of circulating miRNAs as novel prognostic biomarkers for bladder cancer. <i>Mathematical Biosciences and Engineering</i> , 2020, 17, 834-844.	1.0	19
19507	A microRNA disease signature associated with lymph node metastasis of lung adenocarcinoma. <i>Mathematical Biosciences and Engineering</i> , 2020, 17, 2557-2568.	1.0	4
19508	Current insights into the molecular systems pharmacology of lncRNA-miRNA regulatory interactions and implications in cancer translational medicine. <i>AIMS Molecular Science</i> , 2016, 3, 104-124.	0.3	17
19509	Cloud Computing for Cytopathologists. <i>Advances in Healthcare Information Systems and Administration Book Series</i> , 2014, , 250-271.	0.2	18
19510	Modelling and Simulating Complex Systems in Biology. <i>Advances in Computational Intelligence and Robotics Book Series</i> , 2017, , 128-158.	0.4	1
19511	Mass Informatics in Differential Proteomics. , 2009, , 1176-1181.		1
19512	Module Finding Approaches for Protein Interaction Networks. , 2009, , 335-353.		3
19513	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
19514	Pleiotropic Roles of VEGF in the Microenvironment of the Developing Thymus. <i>Journal of Immunology</i> , 2020, 205, 2423-2436.	0.4	2
19515	Effect of co-administration of <i>Angelicae gigantis radix</i> and <i>Lithospermi radix</i> on rat hepatic injury induced by carbon tetrachloride. <i>Pharmacognosy Magazine</i> , 2015, 11, 395.	0.3	2
19516	Transcription factor networks involved in cell death in the dorsal root ganglia following peripheral nerve injury. <i>Neural Regeneration Research</i> , 2018, 13, 1622.	1.6	7
19517	Novel circular RNAs expressed in brain microvascular endothelial cells after oxygen-glucose deprivation/recovery. <i>Neural Regeneration Research</i> , 2019, 14, 2104.	1.6	21

#	ARTICLE	IF	CITATIONS
19518	Bioinformatic identification of key candidate genes and pathways in axon regeneration after spinal cord injury in zebrafish. <i>Neural Regeneration Research</i> , 2020, 15, 103.	1.6	5
19519	MicroRNA regulatory pattern in spinal cord ischemia-reperfusion injury. <i>Neural Regeneration Research</i> , 2020, 15, 2123.	1.6	21
19520	Gene set enrichment analysis of alpha-glucosidase inhibitors from <i>Ficus benghalensis</i> . <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2019, 9, 263.	0.5	30
19521	A bioinformatics analysis of exosomal microRNAs released following mycobacterial infection. <i>International Journal of Mycobacteriology</i> , 2019, 8, 218.	0.3	6
19522	Network pharmacology-based study on the mechanism of <i>Schisandra chinensis</i> for treating Alzheimer's disease. <i>Indian Journal of Pharmacology</i> , 2020, 52, 94.	0.4	6
19523	Omics data-driven analysis identifies laminin-integrin-mediated signaling pathway as a determinant for cell differentiation in oral squamous cell carcinoma. <i>Indian Journal of Pathology and Microbiology</i> , 2019, 62, 529.	0.1	3
19524	A systematic integrative approach reveals novel microRNAs in diabetic nephropathy. <i>Journal of Research in Medical Sciences</i> , 2020, 25, 1.	0.4	10
19525	Chemical profiling, free radical scavenging and anti-acetylcholinesterase activities of essential oil from <i>curcuma caesia</i> of Arunachal Pradesh, India. <i>Pharmacognosy Research (discontinued)</i> , 2020, 12, 76.	0.3	7
19526	Strategy of systems biology for visualizing the "Black box" of traditional Chinese medicine. <i>World Journal of Traditional Chinese Medicine</i> , 2020, 6, 260.	0.9	8
19527	Network pharmacology approach to determine active compounds and potential targets associated with the anti-abortion effects of <i>scutellariae radix</i> . <i>World Journal of Traditional Chinese Medicine</i> , 2020, 6, 341.	0.9	9
19528	The mechanisms of <i>pei-yuan-tong-nao</i> capsule as a therapeutic agent against cerebrovascular disease. <i>World Journal of Traditional Chinese Medicine</i> , 2020, 6, 331.	0.9	5
19529	Designing a resilient supply chain: An approach to reduce drug shortages in epidemic outbreaks. <i>EAI Endorsed Transactions on Pervasive Health and Technology</i> , 2020, 6, 164260.	0.7	30
19530	Sulfur Amino Acid Metabolic Process Pathway may Modulate Bipolar Disorder with Alcohol Dependence Comorbidity. <i>Journal of Addiction Research &amp; Therapy</i> , 2014, 05, .	0.2	1
19531	Identification of Stress Related Molecular Biomarkers in Zebrafish Employing an In-Silico Approach to Access Toxicity based Risks in Aquaculture. <i>Poultry Fisheries &amp; Wildlife Sciences</i> , 2015, 03, .	0.1	3
19532	Role of a Web-based Software Platform for Systems Biology. <i>Journal of Computer Science and Systems Biology</i> , 2011, 04, .	0.0	9
19533	Integration and Prediction of PPI Using Multiple Resources from Public Databases. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 166-187.	0.4	9
19534	A Comprehensive Curated Reaction Map of Leptin Signaling Pathway. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, .	0.4	17
19535	Improved Functional Enrichment Analysis of Biological Networks using Scalable Modularity Based Clustering. <i>Journal of Proteomics and Bioinformatics</i> , 2016, 9, .	0.4	10

#	ARTICLE	IF	CITATIONS
19536	The TLA+ Toolbox. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 310, 50-62.	0.8	21
19537	Predicate Oriented Pattern Analysis for Biomedical Knowledge Discovery. Intelligent Information Management, 2016, 08, 66-85.	0.3	13
19538	Constrain-based analysis of gene deletion on the metabolic flux redistribution of Saccharomyces Cerevisiae. Journal of Biomedical Science and Engineering, 2008, 01, 121-126.	0.2	3
19539	Adult and neonatal astrocytes exhibit diverse gene expression profiles in response to beta amyloid &lt;i>in vivo&lt;/i>. World Journal of Neuroscience, 2012, 02, 57-67.	0.1	5
19540	Transcriptome network-based method to identify genes associated with unruptured intracranial aneurysms. Genetics and Molecular Research, 2013, 12, 3263-3273.	0.3	4
19541	CARMEN - Comparative Analysis and in silico Reconstruction of organism-specific MEtabolic Networks. Genetics and Molecular Research, 2010, 9, 1660-1672.	0.3	21
19542	Up-regulation of tumor necrosis factor- $\alpha$ pathway survival genes and of the receptor TNFR2 in gastric cancer. World Journal of Gastrointestinal Oncology, 2019, 11, 281-294.	0.8	23
19543	Identification of candidate biomarkers correlated with pathogenesis of postoperative peritoneal adhesion by using microarray analysis. World Journal of Gastrointestinal Oncology, 2020, 12, 54-65.	0.8	8
19544	Connexions: a Social and Successful Anomaly among Learning Object Repositories. Journal of Emerging Technologies in Web Intelligence, 2010, 2, .	0.6	14
19545	Asserted and neglected issues linking evidence-based and Chinese medicines for cardiac rehabilitation. World Journal of Cardiology, 2014, 6, 295.	0.5	3
19546	"Stop Ne(c)king around": How interactomics contributes to functionally characterize Nek family kinases. World Journal of Biological Chemistry, 2014, 5, 141-60.	1.7	52
19547	Integrative Analysis of Microarray Data to Reveal Regulation Patterns in the Pathogenesis of Hepatocellular Carcinoma. Gut and Liver, 2017, 11, 112-120.	1.4	32
19548	Transcript Abundance Responses of Resistance Pathways of Arabidopsis thaliana to Deoxynivalenol. Atlas Journal of Biology, 2013, 2, 154-161.	0.1	1
19550	Is stool frequency associated with the richness and community composition of gut microbiota?. Intestinal Research, 2019, 17, 419-426.	1.0	26
19551	The NOESIS Open Source Framework for Network Data Mining. , 2015, , .		1
19553	Identifying novel biomarkers of gastric cancer through integration analysis of single nucleotide polymorphisms and gene expression profile. International Journal of Biological Markers, 2015, 30, 321-326.	0.7	15
19554	Identification of Potential Drug Targets Implicated in Parkinson's Disease from Human Genome: Insights of Using Fused Domains in Hypothetical Proteins as Probes. ISRN Neurology, 2011, 2011, 1-10.	1.5	1
19555	From proteomics toward systems biology: integration of different types of proteomics data into network models. BMB Reports, 2008, 41, 184-193.	1.1	25

#	ARTICLE	IF	CITATIONS
19556	A replication study of genome-wide CNV association for hepatic biomarkers identifies nine genes associated with liver function. <i>BMB Reports</i> , 2011, 44, 578-583.	1.1	7
19557	Identification of key genes involved in post-traumatic stress disorder: Evidence from bioinformatics analysis. <i>World Journal of Psychiatry</i> , 2020, 10, 286-298.	1.3	3
19558	Visualization of metabolite identifier information. <i>Plant Biotechnology</i> , 2009, 26, 479-483.	0.5	6
19559	Mimosa pudica Modulates Neuroactive Ligand- Receptor Interaction in Parkinson's Disease. <i>Indian Journal of Pharmaceutical Education and Research</i> , 2020, 54, 732-739.	0.3	12
19560	Gene expression profiling reveals key genes and pathways related to the development of non-alcoholic fatty liver disease. <i>Annals of Hepatology</i> , 2016, 15, 190-9.	0.6	28
19561	Differential gene expression analysis of human cumulus cells. <i>Clinical and Experimental Reproductive Medicine</i> , 2019, 46, 76-86.	0.5	18
19562	Computational Prediction of Alzheimer's and Parkinson's Disease MicroRNAs in Domestic Animals. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 782-792.	2.4	3
19563	The Prediction of the Expected Current Selection Coefficient of Single Nucleotide Polymorphism Associated with Holstein Milk Yield, Fat and Protein Contents. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 36-42.	2.4	15
19564	Pathway enrichment and protein interaction network analysis for milk yield, fat yield and age at first calving in a Thai multibreed dairy population. <i>Asian-Australasian Journal of Animal Sciences</i> , 2019, 32, 508-518.	2.4	8
19565	Prediction of hub genes of Alzheimer's disease using a protein interaction network and functional enrichment analysis. <i>Genomics and Informatics</i> , 2020, 18, e39.	0.4	9
19566	Transcriptional regulatory networks in response to salt and drought stress in <i>Arabidopsis thaliana</i> . <i>Journal of Medicinal Plants Research</i> , 2012, 6, .	0.2	26
19567	Microarray Data Analysis and Mining Tools. <i>Bioinformatics</i> , 2011, 6, 95-99.	0.2	36
19568	A systems biological study on the comorbidity of autism spectrum disorders and bipolar disorder. <i>Bioinformatics</i> , 2011, 7, 102-106.	0.2	17
19569	Identification of drought responsive proteins using gene ontology hierarchy. <i>Bioinformatics</i> , 2012, 8, 595-599.	0.2	7
19570	A two-step drug repositioning method based on a protein-protein interaction network of genes shared by two diseases and the similarity of drugs. <i>Bioinformatics</i> , 2013, 9, 89-93.	0.2	27
19571	Protein interaction network for Alzheimer's disease using computational approach. <i>Bioinformatics</i> , 2013, 9, 968-972.	0.2	15
19572	Insilico identification of protein-protein interactions in Silkworm, <i>Bombyx mori</i> . <i>Bioinformatics</i> , 2014, 10, 56-62.	0.2	5
19573	Computational study of 'HUB' microRNA in human cardiac diseases. <i>Bioinformatics</i> , 2017, 13, 17-20.	0.2	4



#	ARTICLE	IF	CITATIONS
19574	Analysis of MAP kinase MPK4/MEKK1/MKK genes of <i>Carica papaya</i> L. comparative to other plant homologues. <i>Bioinformatics</i> , 2017, 13, 31-41.	0.2	2
19575	Non-canonical interactions of the $\hat{1}^2$ subunit of the translation elongation complex eEF1B and analysis of their possible functional role. <i>Biopolymers and Cell</i> , 2016, 32, 347-358.	0.1	6
19576	Protein partners of the eEF1B $\hat{1}^2$ subunit of the translation elongation complex eEF1B in the nuclear fraction of human lung carcinoma cells. <i>Biopolymers and Cell</i> , 2017, 33, 243-255.	0.1	5
19577	Mass-spectrometric and bioinformatic analysis of eEF1B $\hat{1}^3$ interactome in the cytoplasmic fraction of A549 cells. <i>Biopolymers and Cell</i> , 2018, 34, 292-302.	0.1	4
19578	Analysis of eEF1B $\hat{1}^3$ interactome in the nuclear fraction of A549 human lung adenocarcinoma cells. <i>Biopolymers and Cell</i> , 2019, 35, 268-287.	0.1	2
19579	A manually curated network of the PML nuclear body interactome reveals an important role for PML-NBs in SUMOylation dynamics. <i>International Journal of Biological Sciences</i> , 2010, 6, 51-67.	2.6	175
19580	Interactive Extraction of Metabolic Subnets – the Netsplitter software implementation. <i>Journal of Molecular Engineering and Systems Biology</i> , 2012, 1, 2.	1.0	2
19581	Characterizing protein domain associations by Small-molecule ligand binding. <i>Journal of Proteome Science and Computational Biology</i> , 2012, 1, 6.	1.0	5
19582	Annotation of glycoside hydrolases in <i>Sorghum bicolor</i> using proteins interaction approach. <i>Journal of Proteome Science and Computational Biology</i> , 2013, 2, 2.	1.0	6
19584	Transcriptome Network Analysis Reveals Potential Candidate Genes for Esophageal Squamous Cell Carcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 767-773.	0.5	4
19585	Bioinformatics Analysis Reveals Connection of Squamous Cell Carcinoma and Adenocarcinoma of the Lung. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 1477-1482.	0.5	7
19586	Transcription Regulation Network Analysis of MCF7 Breast Cancer Cells Exposed to Estradiol. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 3681-3685.	0.5	5
19587	Meta-analysis of Gene Expression Data Identifies Causal Genes for Prostate Cancer. <i>Asian Pacific Journal of Cancer Prevention</i> , 2013, 14, 457-461.	0.5	11
19588	Partial Least Squares Based Gene Expression Analysis in EBV-Positive and EBV-Negative Posttransplant Lymphoproliferative Disorders. <i>Asian Pacific Journal of Cancer Prevention</i> , 2013, 14, 6347-6350.	0.5	3
19589	Association of miR-193b Down-regulation and miR-196a up-Regulation with Clinicopathological Features and Prognosis in Gastric Cancer. <i>Asian Pacific Journal of Cancer Prevention</i> , 2014, 15, 8893-8900.	0.5	34
19590	Pathway and Network Analysis in Glioma with the Partial Least Squares Method. <i>Asian Pacific Journal of Cancer Prevention</i> , 2014, 15, 3145-3149.	0.5	2
19591	Expanding the olfactory code by in silico decoding of odor-receptor chemical space. <i>ELife</i> , 2013, 2, e01120.	2.8	59
19592	Coordinated genomic control of ciliogenesis and cell movement by RFX2. <i>ELife</i> , 2014, 3, e01439.	2.8	121

#	ARTICLE	IF	CITATIONS
19593	Proteomic analysis of the response to cell cycle arrests in human myeloid leukemia cells. <i>ELife</i> , 2015, 4, .	2.8	46
19594	Inhibitory activities of short linear motifs underlie Hox interactome specificity in vivo. <i>ELife</i> , 2015, 4, .	2.8	43
19595	Anatomy of BioJS, an open source community for the life sciences. <i>ELife</i> , 2015, 4, .	2.8	29
19596	Activation of PTHrP-cAMP-CREB1 signaling following p53 loss is essential for osteosarcoma initiation and maintenance. <i>ELife</i> , 2016, 5, .	2.8	38
19597	An integrative transcriptomic atlas of organogenesis in human embryos. <i>ELife</i> , 2016, 5, .	2.8	61
19598	Evidence for evolutionary divergence of activity-dependent gene expression in developing neurons. <i>ELife</i> , 2016, 5, .	2.8	42
19599	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. <i>ELife</i> , 2017, 6, .	2.8	51
19600	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. <i>ELife</i> , 2017, 6, .	2.8	33
19601	The interactome of the copper transporter ATP7A belongs to a network of neurodevelopmental and neurodegeneration factors. <i>ELife</i> , 2017, 6, .	2.8	61
19602	TFAP2 transcription factors are regulators of lipid droplet biogenesis. <i>ELife</i> , 2018, 7, .	2.8	34
19603	A resource for the <i>Drosophila</i> antennal lobe provided by the connectome of glomerulus VA1v. <i>ELife</i> , 2018, 7, .	2.8	42
19604	Temporal profiling of redox-dependent heterogeneity in single cells. <i>ELife</i> , 2018, 7, .	2.8	27
19605	Transition between fermentation and respiration determines history-dependent behavior in fluctuating carbon sources. <i>ELife</i> , 2018, 7, .	2.8	44
19606	Metabolic network percolation quantifies biosynthetic capabilities across the human oral microbiome. <i>ELife</i> , 2019, 8, .	2.8	24
19607	Emergence of trait variability through the lens of nitrogen assimilation in <i>Prochlorococcus</i> . <i>ELife</i> , 2019, 8, .	2.8	57
19608	Functional proteomic atlas of HIV infection in primary human CD4+ T cells. <i>ELife</i> , 2019, 8, .	2.8	34
19609	Genome-wide interrogation of extracellular vesicle biology using barcoded miRNAs. <i>ELife</i> , 2018, 7, .	2.8	27
19610	Plant necrotroph co-transcriptome networks illuminate a metabolic battlefield. <i>ELife</i> , 2019, 8, .	2.8	46

#	ARTICLE	IF	CITATIONS
19611	Identification of compounds that rescue otic and myelination defects in the zebrafish <i>adgrg6</i> ( <i>gpr126</i> ) mutant. <i>ELife</i> , 2019, 8, .	2.8	19
19612	Bacterial contribution to genesis of the novel germ line determinant <i>oskar</i> . <i>ELife</i> , 2020, 9, .	2.8	21
19613	Noroviruses subvert the core stress granule component G3BP1 to promote viral VPg-dependent translation. <i>ELife</i> , 2019, 8, .	2.8	48
19614	Genetic interactions of G-quadruplexes in humans. <i>ELife</i> , 2019, 8, .	2.8	91
19615	Evolution of neuronal anatomy and circuitry in two highly divergent nematode species. <i>ELife</i> , 2019, 8, .	2.8	53
19616	Elevating acetyl-CoA levels reduces aspects of brain aging. <i>ELife</i> , 2019, 8, .	2.8	94
19617	A regulatory microRNA network controls endothelial cell phenotypic switch during sprouting angiogenesis. <i>ELife</i> , 2020, 9, .	2.8	35
19618	Discovery proteomics in aging human skeletal muscle finds change in spliceosome, immunity, proteostasis and mitochondria. <i>ELife</i> , 2019, 8, .	2.8	132
19619	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. <i>ELife</i> , 2019, 8, .	2.8	84
19620	Cardiac mitochondrial function depends on BUD23 mediated ribosome programming. <i>ELife</i> , 2020, 9, .	2.8	10
19621	Systematic detection of horizontal gene transfer across genera among multidrug-resistant bacteria in a single hospital. <i>ELife</i> , 2020, 9, .	2.8	85
19622	Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases. <i>ELife</i> , 2020, 9, .	2.8	53
19623	A quantitative inventory of yeast P body proteins reveals principles of composition and specificity. <i>ELife</i> , 2020, 9, .	2.8	90
19624	Dithranol targets keratinocytes, their crosstalk with neutrophils and inhibits the IL-36 inflammatory loop in psoriasis. <i>ELife</i> , 2020, 9, .	2.8	24
19625	Biochemical basis for the regulation of biosynthesis of antiparasitics by bacterial hormones. <i>ELife</i> , 2020, 9, .	2.8	3
19626	16p11.2 microdeletion imparts transcriptional alterations in human iPSC-derived models of early neural development. <i>ELife</i> , 2020, 9, .	2.8	30
19627	An essential role for MEF2C in the cortical response to loss of sleep in mice. <i>ELife</i> , 2020, 9, .	2.8	25
19628	The effect of hybridization on transposable element accumulation in an undomesticated fungal species. <i>ELife</i> , 2020, 9, .	2.8	29

#	ARTICLE	IF	CITATIONS
19629	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. <i>ELife</i> , 2020, 9, .	2.8	44
19630	A large accessory protein interactome is rewired across environments. <i>ELife</i> , 2020, 9, .	2.8	24
19631	GRNsight: a web application and service for visualizing models of small- to medium-scale gene regulatory networks. <i>PeerJ Computer Science</i> , 0, 2, e85.	2.7	2
19632	Integrated network pharmacology and molecular docking approaches to reveal the synergistic mechanism of multiple components in <i>Venenum Bufonis</i> for ameliorating heart failure. <i>PeerJ</i> , 2020, 8, e10107.	0.9	5
19633	Constitution of a comprehensive phytochemical profile and network pharmacology based investigation to decipher molecular mechanisms of <i>Teucrium polium</i> L. in the treatment of type 2 diabetes mellitus. <i>PeerJ</i> , 2020, 8, e10111.	0.9	6
19634	Identification of key genes and pathways in endometriosis by integrated expression profiles analysis. <i>PeerJ</i> , 2020, 8, e10171.	0.9	8
19635	Integrated analysis of lncRNA and mRNA reveals novel insights into cashmere fineness in Tibetan cashmere goats. <i>PeerJ</i> , 2020, 8, e10217.	0.9	17
19636	Identification of significant genes signatures and prognostic biomarkers in cervical squamous carcinoma via bioinformatic data. <i>PeerJ</i> , 2020, 8, e10386.	0.9	10
19637	Identifying <i>MMP14</i> and <i>COL12A1</i> as a potential combination of prognostic biomarkers in pancreatic ductal adenocarcinoma using integrated bioinformatics analysis. <i>PeerJ</i> , 2020, 8, e10419.	0.9	17
19638	Identification and characterization of critical genes associated with tamoxifen resistance in breast cancer. <i>PeerJ</i> , 2020, 8, e10468.	0.9	11
19639	Identification of biomarkers associated with clinical severity of chronic obstructive pulmonary disease. <i>PeerJ</i> , 2020, 8, e10513.	0.9	3
19640	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . <i>PeerJ</i> , 2015, 3, e1435.	0.9	42
19641	Characterization of microbial associations with methanotrophic archaea and sulfate-reducing bacteria through statistical comparison of nested Magneto-FISH enrichments. <i>PeerJ</i> , 2016, 4, e1913.	0.9	43
19642	Different RNA splicing mechanisms contribute to diverse infective outcome of classical swine fever viruses of differing virulence: insights from the deep sequencing data in swine umbilical vein endothelial cells. <i>PeerJ</i> , 2016, 4, e2113.	0.9	4
19643	Formal modeling and analysis of the hexosamine biosynthetic pathway: role of O-linked N-acetylglucosamine transferase in oncogenesis and cancer progression. <i>PeerJ</i> , 2016, 4, e2348.	0.9	16
19644	Network-based analysis of differentially expressed genes in cerebrospinal fluid (CSF) and blood reveals new candidate genes for multiple sclerosis. <i>PeerJ</i> , 2016, 4, e2775.	0.9	52
19645	Determining virus-host interactions and glycerol metabolism profiles in geographically diverse solar salterns with metagenomics. <i>PeerJ</i> , 2017, 5, e2844.	0.9	6
19646	<i>LoTo</i> : a graphlet based method for the comparison of local topology between gene regulatory networks. <i>PeerJ</i> , 2017, 5, e3052.	0.9	10

#	ARTICLE	IF	CITATIONS
19647	Identification of dysregulated genes in rheumatoid arthritis based on bioinformatics analysis. PeerJ, 2017, 5, e3078.	0.9	12
19648	Putative archaeal viruses from the mesopelagic ocean. PeerJ, 2017, 5, e3428.	0.9	46
19649	PrePhyloPro: phylogenetic profile-based prediction of whole proteome linkages. PeerJ, 2017, 5, e3712.	0.9	15
19650	Allele specific expression analysis identifies regulatory variation associated with stress-related genes in the Mexican highland maize landrace Palomero Toluqueño. PeerJ, 2017, 5, e3737.	0.9	32
19651	Constructing a comprehensive gene co-expression based interactome in <i>Bos taurus</i> . PeerJ, 2017, 5, e4107.	0.9	9
19652	Proteomic identification of galectin-11 and 14 ligands from <i>Haemonchus contortus</i> . PeerJ, 2018, 6, e4510.	0.9	7
19653	Breast cancer identification via modeling of peripherally circulating miRNAs. PeerJ, 2018, 6, e4551.	0.9	22
19654	Increased chemical acetylation of peptides and proteins in rats after daily ingestion of diacetyl analyzed by Nano-LC-MS/MS. PeerJ, 2018, 6, e4688.	0.9	4
19655	Sexually dimorphic venom proteins in long-jawed orb-weaving spiders ( <i>Tetragnatha</i> ) comprise novel gene families. PeerJ, 2018, 6, e4691.	0.9	21
19656	Identification of potential crucial genes and pathways associated with vein graft restenosis based on gene expression analysis in experimental rabbits. PeerJ, 2018, 6, e4704.	0.9	2
19657	Genome-wide characterization and expression analysis of GRAS gene family in pepper ( <i>Capsicum</i> ) Tj ETQq0 0 0 rBT /Overlock 10 Tf	0.9	45
19658	Finding novel relationships with integrated gene-gene association network analysis of <i>Synechocystis</i> sp. PCC 6803 using species-independent text-mining. PeerJ, 2018, 6, e4806.	0.9	4
19659	Specalyzer—an interactive online tool to analyze spectral reflectance measurements. PeerJ, 2018, 6, e5031.	0.9	2
19660	Differential expression of NF- $\kappa$ B heterodimer RelA/p50 in human urothelial carcinoma. PeerJ, 2018, 6, e5563.	0.9	3
19661	Effects of rheumatoid arthritis associated transcriptional changes on osteoclast differentiation network in the synovium. PeerJ, 2018, 6, e5743.	0.9	6
19662	A candidate multimodal functional genetic network for thermal adaptation. PeerJ, 2014, 2, e578.	0.9	24
19663	Genome-wide identification and analysis of the <i>CNGC</i> gene family in maize. PeerJ, 2018, 6, e5816.	0.9	20
19664	RIP-MD: a tool to study residue interaction networks in protein molecular dynamics. PeerJ, 2018, 6, e5998.	0.9	44

#	ARTICLE	IF	CITATIONS
19665	Screening of prognostic biomarkers for endometrial carcinoma based on a ceRNA network. PeerJ, 2018, 6, e6091.	0.9	10
19666	Construction and comparison of gene co-expression networks shows complex plant immune responses. PeerJ, 2014, 2, e610.	0.9	28
19667	Genome-wide analysis of circular RNAs in goat skin fibroblast cells in response to Orf virus infection. PeerJ, 2019, 7, e6267.	0.9	26
19668	Integrated bioinformatics analysis of As, Au, Cd, Pb and Cu heavy metal responsive marker genes through <i>Arabidopsis thaliana</i> GEO datasets. PeerJ, 2019, 7, e6495.	0.9	14
19669	Identification of four hub genes associated with adrenocortical carcinoma progression by WGCNA. PeerJ, 2019, 7, e6555.	0.9	36
19670	Music-performance regulates microRNAs in professional musicians. PeerJ, 2019, 7, e6660.	0.9	13
19671	Integrative analysis of common genes and driver mutations implicated in hormone stimulation for four cancers in women. PeerJ, 2019, 7, e6872.	0.9	12
19672	Comprehensive analysis of an lncRNA-miRNA-mRNA competing endogenous RNA network in pulpitis. PeerJ, 2019, 7, e7135.	0.9	34
19673	Identification of diagnostic markers for major depressive disorder by cross-validation of data from whole blood samples. PeerJ, 2019, 7, e7171.	0.9	10
19674	Association network analysis identifies enzymatic components of gut microbiota that significantly differ between colorectal cancer patients and healthy controls. PeerJ, 2019, 7, e7315.	0.9	10
19675	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
19676	Identification of significant gene and pathways involved in HBV-related hepatocellular carcinoma by bioinformatics analysis. PeerJ, 2019, 7, e7408.	0.9	64
19677	Identification of crucial genes based on expression profiles of hepatocellular carcinomas by bioinformatics analysis. PeerJ, 2019, 7, e7436.	0.9	48
19678	Identification of pivotal lncRNAs in papillary thyroid cancer using lncRNA-mRNA-miRNA ceRNA network analysis. PeerJ, 2019, 7, e7441.	0.9	18
19679	Metabolic alterations in pea leaves during arbuscular mycorrhiza development. PeerJ, 2019, 7, e7495.	0.9	27
19680	Comparative transcriptomics reveals the difference in early endosperm development between maize with different amylose contents. PeerJ, 2019, 7, e7528.	0.9	8
19681	Identification of hub genes and molecular mechanisms in infant acute lymphoblastic leukemia with <i>MLL</i> gene rearrangement. PeerJ, 2019, 7, e7628.	0.9	5
19682	Tandem mass tag-based quantitative proteomic analysis of lycorine treatment in highly pathogenic avian influenza H5N1 virus infection. PeerJ, 2019, 7, e7697.	0.9	24



#	ARTICLE	IF	CITATIONS
19683	Ecological networks reveal contrasting patterns of bacterial and fungal communities in glacier-fed streams in Central Asia. PeerJ, 2019, 7, e7715.	0.9	17
19684	<i>CD36</i> identified by weighted gene co-expression network analysis as a hub candidate gene in lupus nephritis. PeerJ, 2019, 7, e7722.	0.9	14
19685	Bark tissue transcriptome analyses of inverted <i>Populus yunnanensis</i> cuttings reveal the crucial role of plant hormones in response to inversion. PeerJ, 2019, 7, e7740.	0.9	5
19686	Computational analysis of the LRRK2 interactome. PeerJ, 2015, 3, e778.	0.9	48
19687	Identification of hub genes and small-molecule compounds related to intracerebral hemorrhage with bioinformatics analysis. PeerJ, 2019, 7, e7782.	0.9	22
19688	Identification of key genes and multiple molecular pathways of metastatic process in prostate cancer. PeerJ, 2019, 7, e7899.	0.9	12
19689	Identification of key genes and long non-coding RNA associated ceRNA networks in hepatocellular carcinoma. PeerJ, 2019, 7, e8021.	0.9	20
19690	Analysis of miRNA expression profiles in the liver of <i>Clock<sup>fl<sup>+</sup>/19</sup></i> mutant mice. PeerJ, 2019, 7, e8119.	0.9	5
19691	Genetic links between endometriosis and cancers in women. PeerJ, 2019, 7, e8135.	0.9	14
19692	Identification of key genes in non-small cell lung cancer by bioinformatics analysis. PeerJ, 2019, 7, e8215.	0.9	17
19693	Identification and validation of a three-gene signature as a candidate prognostic biomarker for lower grade glioma. PeerJ, 2020, 8, e8312.	0.9	32
19694	Genome-wide analysis of lncRNAs, miRNAs, and mRNAs forming a prognostic scoring system in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e8368.	0.9	13
19695	Co-expression network analysis reveals the pivotal role of mitochondrial dysfunction and interferon signature in juvenile dermatomyositis. PeerJ, 2020, 8, e8611.	0.9	7
19696	Molecular docking and network connections of active compounds from the classical herbal formula Ding Chuan Tang. PeerJ, 2020, 8, e8685.	0.9	11
19697	Alternative dietary protein and water temperature influence the skin and gut microbial communities of yellowtail kingfish ( <i>Seriola lalandi</i> ). PeerJ, 2020, 8, e8705.	0.9	21
19698	Comparative proteogenomics profiling of non-small and small lung carcinoma cell lines using mass spectrometry. PeerJ, 2020, 8, e8779.	0.9	7
19699	Weighted gene correlation network analysis reveals novel biomarkers associated with mesenchymal stromal cell differentiation in early phase. PeerJ, 2020, 8, e8907.	0.9	10
19700	Identification of key miRNAs in the progression of hepatocellular carcinoma using an integrated bioinformatics approach. PeerJ, 2020, 8, e9000.	0.9	3

#	ARTICLE	IF	CITATIONS
19701	Identification of exosomal miRNAs associated with the anthracycline-induced liver injury in postoperative breast cancer patients by small RNA sequencing. PeerJ, 2020, 8, e9021.	0.9	14
19702	Comparative study of gut microbiota in Tibetan wild asses ( <i>Equus kiang</i> ) and domestic donkeys ( <i>Equus asinus</i> ) on the Qinghai-Tibet plateau. PeerJ, 2020, 8, e9032.	0.9	20
19703	High expression of stromal signatures correlated with macrophage infiltration, angiogenesis and poor prognosis in glioma microenvironment. PeerJ, 2020, 8, e9038.	0.9	29
19704	Aberrant expression of two miRNAs promotes proliferation, hepatitis B virus amplification, migration and invasion of hepatocellular carcinoma cells: evidence from bioinformatic analysis and experimental validation. PeerJ, 2020, 8, e9100.	0.9	5
19705	VIRdb: a comprehensive database for interactive analysis of genes/proteins involved in the pathogenesis of vitiligo. PeerJ, 2020, 8, e9119.	0.9	3
19706	Identification of prognostic risk factors for pancreatic cancer using bioinformatics analysis. PeerJ, 2020, 8, e9301.	0.9	9
19707	Host transcriptome-guided drug repurposing for COVID-19 treatment: a meta-analysis based approach. PeerJ, 2020, 8, e9357.	0.9	44
19708	Microenvironment-related gene TNFSF13B predicts poor prognosis in kidney renal clear cell carcinoma. PeerJ, 2020, 8, e9453.	0.9	7
19709	Identification and validation of prognostic signature for breast cancer based on genes potentially involved in autophagy. PeerJ, 2020, 8, e9621.	0.9	11
19710	Genome-wide identification of CpG island methylator phenotype related gene signature as a novel prognostic biomarker of gastric cancer. PeerJ, 2020, 8, e9624.	0.9	11
19711	Mining of prognosis-related genes in cervical squamous cell carcinoma immune microenvironment. PeerJ, 2020, 8, e9627.	0.9	5
19712	Multi-omics analysis to examine microbiota, host gene expression and metabolites in the intestine of black tiger shrimp ( <i>Penaeus monodon</i> ) with different growth performance. PeerJ, 2020, 8, e9646.	0.9	22
19713	Predictive models for stage and risk classification in head and neck squamous cell carcinoma (HNSCC). PeerJ, 2020, 8, e9656.	0.9	10
19714	The nine ADAMs family members serve as potential biomarkers for immune infiltration in pancreatic adenocarcinoma. PeerJ, 2020, 8, e9736.	0.9	9
19715	Characterization of the transcriptional response of <i>Candida parapsilosis</i> to the antifungal peptide MAF-1A. PeerJ, 2020, 8, e9767.	0.9	4
19716	Transcriptome analysis reveals potential immune function-related regulatory genes/pathways of female Lubo goat submandibular glands at different developmental stages. PeerJ, 2020, 8, e9947.	0.9	8
19717	Phylogenetic characteristics of bacterial populations and isolation of aromatic compounds utilizing bacteria from humus layer of oak forest. Korean Journal of Microbiology, 2016, 52, 175-182.	0.2	1
19718	Up-regulation of MELK by E2F1 promotes the proliferation in cervical cancer cells. International Journal of Biological Sciences, 2021, 17, 3875-3888.	2.6	15

#	ARTICLE	IF	CITATIONS
19719	Global Prediction of Candidate R-Loop Binding and R-Loop Regulatory Proteins. SSRN Electronic Journal, 0, , .	0.4	0
19720	Identification of Conserved Pappalysin 1-Derived Circular RNA-Mediated Competing Endogenous RNA in Osteosarcoma. Evolutionary Bioinformatics, 2021, 17, 117693432110413.	0.6	0
19721	Long non-coding RNA SNHG3 promotes the progression of clear cell renal cell carcinoma via regulating BIRC5 expression. Translational Cancer Research, 2021, 10, 4502-4513.	0.4	7
19722	<i>Chrysanthemi Flos</i> extract alleviated acetaminophen-induced rat liver injury via inhibiting oxidative stress and apoptosis based on network pharmacology analysis. Pharmaceutical Biology, 2021, 59, 1376-1385.	1.3	14
19723	Proximity-dependent biotin identification (BioID) reveals a dynamic LSD1â€CoREST interactome during embryonic stem cell differentiation. Molecular Omics, 2022, 18, 31-44.	1.4	11
19724	R-loopBase: a knowledgebase for genome-wide R-loop formation and regulation. Nucleic Acids Research, 2022, 50, D303-D315.	6.5	19
19725	Protein profiling reveals potential isomiR-associated cross-talks among RNAs in cholangiocarcinoma. Computational and Structural Biotechnology Journal, 2021, 19, 5722-5734.	1.9	3
19726	Genetic and Immune Profile Discrepancies between Early-Stage Single Primary Lung Cancer and Synchronous Multiple Primary Lung Cancer. SSRN Electronic Journal, 0, , .	0.4	0
19727	Complex Portal 2022: new curation frontiers. Nucleic Acids Research, 2022, 50, D578-D586.	6.5	27
19728	Network pharmacology-based exploration of the mechanism of guanxinning tablet for the treatment of stable coronary artery disease. World Journal of Traditional Chinese Medicine, 2021, 7, 456.	0.9	10
19729	Genomic and Epigenomic Evaluation of Electrically Induced Exercise in People with Spinal Cord Injury: Application to Precision Rehabilitation. Physical Therapy, 2021, , .	1.1	10
19730	Identification of potential biomarkers with colorectal cancer based on bioinformatics analysis and machine learning. Mathematical Biosciences and Engineering, 2021, 18, 8997-9015.	1.0	11
19731	Identification of a prognostic chemoresistance-related gene signature associated with immune microenvironment in breast cancer. Bioengineered, 2021, 12, 8419-8434.	1.4	5
19732	An integrated comparative physiology and molecular approach pinpoints mediators of breath-hold capacity in dolphins. Evolution, Medicine and Public Health, 2021, 9, 420-430.	1.1	5
19733	A new prognostic risk model based on autophagy-related genes in kidney renal clear cell carcinoma. Bioengineered, 2021, 12, 7805-7819.	1.4	9
19734	SCANCell reveals diverse inter-cluster interaction patterns in systemic lupus erythematosus across the disease spectrum. Bioinformatics, 2022, 38, 1361-1368.	1.8	1
19735	POU class 2 homeobox associating factor 1 (POU2AF1) participates in abdominal aortic aneurysm enlargement based on integrated bioinformatics analysis. Bioengineered, 2021, 12, 8980-8993.	1.4	3
19736	Graphical Modeling of Multiple Biological Pathways in Genomic Studies. Emerging Topics in Statistics and Biostatistics, 2021, , 431-459.	0.1	0

#	ARTICLE	IF	CITATIONS
19737	Advancements in capturing and mining mass spectrometry data are transforming natural products research. <i>Natural Product Reports</i> , 2021, 38, 2066-2082.	5.2	38
19738	A seven-gene signature and the C motif chemokine receptor family genes are the sarcoma-related immune genes. <i>Bioengineered</i> , 2021, 12, 7616-7630.	1.4	1
19739	Iduronate-2-Sulfatase Interactome: Validation by Yeast Two-Hybrid Assay. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
19740	Early 2 factor (E2F) transcription factors contribute to malignant progression and have clinical prognostic value in lower-grade glioma. <i>Bioengineered</i> , 2021, 12, 7765-7779.	1.4	3
19742	Discovery of Native Protein Complexes by Liquid Chromatography Followed by Quantitative Mass Spectrometry. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1336, 105-128.	0.8	0
19743	Consensus-Building on Citations in Peer-to-Peer Systems. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
19744	Five genes involved in circular RNA-associated competitive endogenous RNA network correlates with metastasis in papillary thyroid carcinoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 9016-9032.	1.0	3
19745	A Genome-Wide Association Study Reveals New Genes in a Molecular Network Associated with Alcohol Dependence and Related Clinical Measures. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
19746	High expression of transmembrane P24 trafficking protein 9 predicts poor prognosis in breast carcinoma. <i>Bioengineered</i> , 2021, 12, 8965-8979.	1.4	8
19747	Exploration the potential mechanism of the SIRT1 and its target gene FOXO1/PPARGC1A in uteropelvic junction obstruction. <i>Translational Andrology and Urology</i> , 2021, 10, 4192-4205.	0.6	0
19748	Bioinformatics screening of biomarkers related to liver cancer. <i>BMC Bioinformatics</i> , 2021, 22, 521.	1.2	10
19749	The network analysis of international relations: Overview of an emergent methodology. <i>Journal of International Studies</i> , 2021, 14, 155-171.	0.7	1
19750	FPX-G: First Person Exploration for Graph. , 2021, , .		0
19751	Multispecies probiotics alter fecal short-chain fatty acids and lactate levels in weaned pigs by modulating gut microbiota. <i>Journal of Animal Science and Technology</i> , 2021, 63, 1142-1158.	0.8	35
19752	Investigation of the active components and mechanism of Sanao Decoction in treating chronic cough by network pharmacology and molecular docking. <i>Digital Chinese Medicine</i> , 2021, 4, 191-201.	0.5	0
19753	Neurogenomic divergence during speciation by reinforcement of mating behaviors in chorus frogs ( <i>Pseudacris</i> ). <i>BMC Genomics</i> , 2021, 22, 711.	1.2	3
19754	Comparative genome-wide analysis of WRKY, MADS-box and MYB transcription factor families in <i>Arabidopsis</i> and rice. <i>Scientific Reports</i> , 2021, 11, 19678.	1.6	38
19755	Exploring the Molecular Mechanism of <i>Astragali Radix-Curcumae Rhizoma</i> against Gastric Intraepithelial Neoplasia by Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-11.	0.5	2

#	ARTICLE	IF	CITATIONS
19756	Integrated Proteotranscriptomics of Human Myometrium in Labor Landscape Reveals the Increased Molecular Associated With Inflammation Under Hypoxia Stress. <i>Frontiers in Immunology</i> , 2021, 12, 722816.	2.2	14
19757	Interaction Between Chronic Endometritis Caused Endometrial Microbiota Disorder and Endometrial Immune Environment Change in Recurrent Implantation Failure. <i>Frontiers in Immunology</i> , 2021, 12, 748447.	2.2	39
19758	Systematic Construction and Validation of a Prognostic Model for Hepatocellular Carcinoma Based on Immune-Related Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 700553.	1.8	6
19760	An Interactive View of Glycosylation. <i>Methods in Molecular Biology</i> , 2022, 2370, 41-65.	0.4	0
19761	CTHRC1 expression is a novel shared diagnostic and prognostic biomarker of survival in six different human cancer subtypes. <i>Scientific Reports</i> , 2021, 11, 19873.	1.6	14
19762	Genome-wide association of the metabolic shifts underpinning dark-induced senescence in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2022, 34, 557-578.	3.1	29
19765	System biology analysis of endosulfan biodegradation in bacteria and its effect in other living systems: modeling and simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 13171-13183.	2.0	9
19766	Mechanisms Underlying the Effects of Lianhua Qingwen on Sepsis-Induced Acute Lung Injury: A Network Pharmacology Approach. <i>Frontiers in Pharmacology</i> , 2021, 12, 717652.	1.6	16
19770	Spatially confined sub-tumor microenvironments in pancreatic cancer. <i>Cell</i> , 2021, 184, 5577-5592.e18.	13.5	182
19773	Integrated Analysis of Metabolome and Transcriptome Reveals Insights for Cold Tolerance in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 721681.	1.7	61
19774	Genome-wide investigation and expression profiling of polyphenol oxidase (PPO) family genes uncover likely functions in organ development and stress responses in <i>Populus trichocarpa</i> . <i>BMC Genomics</i> , 2021, 22, 731.	1.2	26
19776	Isobaric tags for relative and absolute quantification (iTRAQ)-based quantitative analysis of the salivary proteome during healthy pregnancy and pregnancy gingivitis. <i>Journal of Clinical Periodontology</i> , 2021, 48, 1559-1569.	2.3	4
19777	Identification of Novel Biomarkers Related to Lung Squamous Cell Carcinoma Using Integrated Bioinformatics Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-18.	0.7	4
19778	Integrated omics networks reveal the temporal signaling events of brassinosteroid response in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2021, 12, 5858.	5.8	54
19779	Genome-wide dynamic network analysis reveals the potential genes for MeJA-induced growth-to-defense transition. <i>BMC Plant Biology</i> , 2021, 21, 450.	1.6	9
19780	Effect of the skincare product on facial skin microbial structure and biophysical parameters: A pilot study. <i>MicrobiologyOpen</i> , 2021, 10, e1236.	1.2	6
19781	Dissection of the potential anti-diabetes mechanism of salvianolic acid B by metabolite profiling and network pharmacology. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, e9205.	0.7	5
19782	Recognition of DNA Methylation Molecular Features for Diagnosis and Prognosis in Gastric Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 758926.	1.1	6

#	ARTICLE	IF	CITATIONS
19783	The central role of the glutamate metabolism in long-term antiretroviral treated HIV-infected individuals with metabolic syndrome. <i>Aging</i> , 2021, 13, 22732-22751.	1.4	14
19784	Comparison of PCR versus PCR-Free DNA Library Preparation for Characterising the Human Faecal Virome. <i>Viruses</i> , 2021, 13, 2093.	1.5	9
19785	StemBond hydrogels control the mechanical microenvironment for pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 6132.	5.8	22
19786	A novel multi-biomarker combination predicting relapse from long-term remission after discontinuation of biological drugs in rheumatoid arthritis. <i>Scientific Reports</i> , 2021, 11, 20771.	1.6	6
19787	Analysis of micropollutants in a marine outfall using network analysis and decision tree. <i>Science of the Total Environment</i> , 2022, 806, 150938.	3.9	5
19788	Intelligent host engineering for metabolic flux optimisation in biotechnology. <i>Biochemical Journal</i> , 2021, 478, 3685-3721.	1.7	8
19789	Prolonged epigenomic and synaptic plasticity alterations following single exposure to a psychedelic in mice. <i>Cell Reports</i> , 2021, 37, 109836.	2.9	82
19790	Virtual screening of functional foods and dissecting their roles in modulating gene functions to support post COVID-19 complications. <i>Journal of Food Biochemistry</i> , 2021, 45, e13961.	1.2	11
19791	Combination of Pseudo-LC-NMR and HRMS/MS-Based Molecular Networking for the Rapid Identification of Antimicrobial Metabolites From <i>Fusarium petrophilum</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 725691.	1.6	4
19792	Systematic analysis of potential targets of the curcumin analog pentagamavunon-1 (PGV-1) in overcoming resistance of glioblastoma cells to bevacizumab. <i>Saudi Pharmaceutical Journal</i> , 2021, 29, 1289-1302.	1.2	3
19793	Patterns of Carbon-Bound Exogenous Compounds in Patients with Lung Cancer and Association with Disease Pathophysiology. <i>Cancer Research</i> , 2021, 81, 5862-5875.	0.4	12
19794	Extracellular calcium alters calcium-sensing receptor network integrating intracellular calcium-signaling and related key pathway. <i>Scientific Reports</i> , 2021, 11, 20576.	1.6	8
19795	Mining Fiskeby III and Mandarin (Ottawa) Expression Profiles to Understand Iron Stress Tolerant Responses in Soybean. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11032.	1.8	3
19796	Identifying Complex lncRNA/Pseudogene-miRNA-mRNA Crosstalk in Hormone-Dependent Cancers. <i>Biology</i> , 2021, 10, 1014.	1.3	5
19797	Whole-Transcriptome Sequence of Degenerative Meniscus Cells Unveiling Diagnostic Markers and Therapeutic Targets for Osteoarthritis. <i>Frontiers in Genetics</i> , 2021, 12, 754421.	1.1	10
19798	Tissue and Temperature-Specific RNA-Seq Analysis Reveals Genomic Versatility and Adaptive Potential in Wild Sea Turtle Hatchlings ( <i>Caretta caretta</i> ). <i>Animals</i> , 2021, 11, 3013.	1.0	3
19800	Magnolol Attenuates Right Ventricular Hypertrophy and Fibrosis in Hypoxia-Induced Pulmonary Arterial Hypertensive Rats Through Inhibition of the JAK2/STAT3 Signaling Pathway. <i>Frontiers in Pharmacology</i> , 2021, 12, 755077.	1.6	10
19801	Exploring the Potential Mechanism of Xiaokui Jiedu Decoction for Ulcerative Colitis Based on Network Pharmacology and Molecular Docking. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	9



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19802	Comparison of CRISPR-Cas Immune Systems in Healthcare-Related Pathogens. <i>Frontiers in Microbiology</i> , 2021, 12, 758782.	1.5	16
19803	Identification and Validation of IFI44 as Key Biomarker in Lupus Nephritis. <i>Frontiers in Medicine</i> , 2021, 8, 762848.	1.2	18
19804	The GH19 Engineering Database: Sequence diversity, substrate scope, and evolution in glycoside hydrolase family 19. <i>PLoS ONE</i> , 2021, 16, e0256817.	1.1	14
19805	Exploring biological basis of Syndrome differentiation in coronary heart disease patients with two distinct Syndromes by integrated multi-omics and network pharmacology strategy. <i>Chinese Medicine</i> , 2021, 16, 109.	1.6	18
19806	A unique population of neutrophils generated by air pollutant-induced lung damage exacerbates airway inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 1253-1269.e8.	1.5	13
19807	LncRNA FOXP4-AS1 Promotes Progression of Ewing Sarcoma and Is Associated With Immune Infiltrates. <i>Frontiers in Oncology</i> , 2021, 11, 718876.	1.3	10
19808	Grass pea natural variation reveals oligogenic resistance to <i>Fusarium oxysporum</i> f. sp. <i>pisi</i> . <i>Plant Genome</i> , 2021, 14, e20154.	1.6	5
19809	Modulation of Global Gene Expression by Aneuploidy and CNV of Dosage Sensitive Regulatory Genes. <i>Genes</i> , 2021, 12, 1606.	1.0	5
19810	Prognostic Gene Signature for Squamous Cell Carcinoma with a Higher Risk for Treatment Failure and Accelerated MEK-ERK Pathway Activity. <i>Cancers</i> , 2021, 13, 5182.	1.7	5
19811	Metabolic Molecule PLA2G2D Is a Potential Prognostic Biomarker Correlating With Immune Cell Infiltration and the Expression of Immune Checkpoint Genes in Cervical Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 755668.	1.3	11
19812	The Honey Bee Gene Bee Antiviral Protein-1 Is a Taxonomically Restricted Antiviral Immune Gene. <i>Frontiers in Insect Science</i> , 2021, 1, .	0.9	3
19813	Genome-wide analysis of valine-glutamine motif-containing proteins related to abiotic stress response in cucumber ( <i>Cucumis sativus</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 492.	1.6	8
19814	Expression Profile and Potential Function of Circular RNAs in Peripheral Blood Mononuclear Cells in Male Patients With Primary Gout. <i>Frontiers in Genetics</i> , 2021, 12, 728091.	1.1	4
19815	Cellular Proteo-Transcriptomic Changes in the Immediate Early-Phase of Lentiviral Transduction. <i>Microorganisms</i> , 2021, 9, 2207.	1.6	4
19816	Functional genomics of abiotic environmental adaptation in lacertid lizards and other vertebrates. <i>Journal of Animal Ecology</i> , 2022, 91, 1163-1179.	1.3	4
19817	Sequential Defects in Cardiac Lineage Commitment and Maturation Cause Hypoplastic Left Heart Syndrome. <i>Circulation</i> , 2021, 144, 1409-1428.	1.6	29
19818	Temporal metabolite responsiveness of microbiota in the tea plant phyllosphere promotes continuous suppression of fungal pathogens. <i>Journal of Advanced Research</i> , 2022, 39, 49-60.	4.4	24
19819	MoNET: an R package for multi-omic network analysis. <i>Bioinformatics</i> , 2021, , .	1.8	2

#	ARTICLE	IF	CITATIONS
19820	Lamellipodin-RICTOR Signaling Mediates Glioblastoma Cell Invasion and Radiosensitivity Downstream of EGFR. <i>Cancers</i> , 2021, 13, 5337.	1.7	1
19821	A k-mer based approach for classifying viruses without taxonomy identifies viral associations in human autism and plant microbiomes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5911-5919.	1.9	10
19822	The human hepatocyte TXG-MAPr: gene co-expression network modules to support mechanism-based risk assessment. <i>Archives of Toxicology</i> , 2021, 95, 3745-3775.	1.9	16
19823	Component of oligomeric Golgi complex 1 deficiency leads to hypoglycemia: a case report and literature review. <i>BMC Pediatrics</i> , 2021, 21, 442.	0.7	1
19824	Complementary Transcriptomic and Proteomic Analysis in the Substantia Nigra of Parkinson's Disease. <i>Disease Markers</i> , 2021, 2021, 1-10.	0.6	4
19825	Network Pharmacology-Based and Molecular Docking-Based Analysis of Suanzaoren Decoction for the Treatment of Parkinson's Disease with Sleep Disorder. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	21
19826	Radiation-induced dysfunction of energy metabolism in the heart results in the fibrosis of cardiac tissues. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	19
19827	Multiomic Profiling of Central Nervous System Leukemia Identifies mRNA Translation as a Therapeutic Target. <i>Blood Cancer Discovery</i> , 2022, 3, 16-31.	2.6	4
19828	The Analysis of Herpes Simplex Virus Type 1 (HSV-1)-Encoded MicroRNAs Targets: A Likely Relationship of Alzheimer's Disease and HSV-1 Infection. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 2849-2861.	1.7	4
19829	A construction and comprehensive analysis of ceRNA networks and infiltrating immune cells in papillary renal cell carcinoma. <i>Cancer Medicine</i> , 2021, 10, 8192-8209.	1.3	7
19830	In Silico Analysis of the Gene Expression Patterns between Aldosterone-Producing Adenoma and Nonfunctional Adrenocortical Adenoma. <i>Genetical Research</i> , 2021, 2021, 1-15.	0.3	0
19831	Interaction of Male Specific Lethal complex and genomic imbalance on global gene expression in <i>Drosophila</i> . <i>Scientific Reports</i> , 2021, 11, 19679.	1.6	5
19832	Humans and machines in biomedical knowledge curation: hypertrophic cardiomyopathy molecular mechanisms representation. <i>BioData Mining</i> , 2021, 14, 45.	2.2	7
19833	Comparative analysis of integrative and conjugative mobile genetic elements in the genus <i>Mesorhizobium</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
19834	Comparative Analyses of Sperm DNA Methylomes Among Three Commercial Pig Breeds Reveal Vital Hypomethylated Regions Associated With Spermatogenesis and Embryonic Development. <i>Frontiers in Genetics</i> , 2021, 12, 740036.	1.1	7
19835	A Potential Three-Gene-Based Diagnostic Signature for Hypertension in Pregnancy. <i>International Journal of General Medicine</i> , 2021, Volume 14, 6847-6856.	0.8	3
19836	Parkinson's Disease Phenotypes in Patient Neuronal Cultures and Brain Organoids Improved by Hydroxypropyl-β-Cyclodextrin Treatment. <i>Movement Disorders</i> , 2022, 37, 80-94.	2.2	37
19837	Differential bacterial endophytophite in Foc-resistant banana cultivar displays enhanced antagonistic activity against <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> ( <i>Foc</i> ). <i>Environmental Microbiology</i> , 2022, 24, 2701-2715.	1.8	12

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19838	Network Pharmacology to Explore the Molecular Mechanisms of <i>Prunella vulgaris</i> for Treating Hashimoto's Thyroiditis. <i>Frontiers in Pharmacology</i> , 2021, 12, 700896.	1.6	19
19839	Microscopic and Transcriptomic Analyses of Dalbergoid Legume Peanut Reveal a Divergent Evolution Leading to Nod-Factor-Dependent Epidermal Crack-Entry and Terminal Bacteroid Differentiation. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 131-145.	1.4	11
19840	Natural Compounds from Hatikana Extract Potentiate Antidiabetic Actions as Displayed by In Vivo Assays and Verified by Network Pharmacological Tools. <i>BioMed Research International</i> , 2021, 2021, 1-17.	0.9	3
19841	Patient Heterogeneity in Acute Myeloid Leukemia: Leukemic Cell Communication by Release of Soluble Mediators and Its Effects on Mesenchymal Stem Cells. <i>Diseases (Basel, Switzerland)</i> , 2021, 9, 74.	1.0	4
19842	Distinctive Network Topology of Phase-Separated Proteins in Human Interactome. <i>Journal of Molecular Biology</i> , 2022, 434, 167292.	2.0	3
19843	Early Pro-Inflammatory Signal and T-Cell Activation Associate With Vaccine-Induced Anti-Vaccinia Protective Neutralizing Antibodies. <i>Frontiers in Immunology</i> , 2021, 12, 737487.	2.2	2
19844	Prognostic Significance of Dysregulated Epigenomic and Chromatin Modifiers in Cervical Cancer. <i>Cells</i> , 2021, 10, 2665.	1.8	4
19845	Identification of Three Core Secretome Genes Associated with Immune Infiltration in High Tumor Mutation Burden Across 14 Major Solid Tumors. <i>International Journal of General Medicine</i> , 2021, Volume 14, 6755-6767.	0.8	2
19847	A global screening identifies chromatin-enriched RNA-binding proteins and the transcriptional regulatory activity of QKI5 during monocytic differentiation. <i>Genome Biology</i> , 2021, 22, 290.	3.8	13
19848	The Hitchhiker's Guide to Untargeted Lipidomics Analysis: Practical Guidelines. <i>Metabolites</i> , 2021, 11, 713.	1.3	9
19849	Transcriptome dynamics during metamorphosis of imaginal discs into wings and thoracic dorsum in <i>Apis mellifera</i> castes. <i>BMC Genomics</i> , 2021, 22, 756.	1.2	7
19850	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. <i>Environmental Research</i> , 2022, 207, 112183.	3.7	7
19851	Assessment of CircRNA Expression Profiles and Potential Functions in Brown Adipogenesis. <i>Frontiers in Genetics</i> , 2021, 12, 769690.	1.1	8
19852	A Transcriptome Analysis Revealing the New Insight of Green Light on Tomato Plant Growth and Drought Stress Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 649283.	1.7	8
19855	Circadian miR-449c-5p regulates uterine Ca <sup>2+</sup> transport during eggshell calcification in chickens. <i>BMC Genomics</i> , 2021, 22, 764.	1.2	7
19856	Integrated multi-omics reveals common properties underlying stress granule and P-body formation. <i>RNA Biology</i> , 2021, 18, 655-673.	1.5	10
19857	Bromodomain Containing Protein 4 (BRD4) Regulates Expression of its Interacting Coactivators in the Innate Response to Respiratory Syncytial Virus. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 728661.	1.6	12
19858	Student biocuration projects as a learning environment. <i>F1000Research</i> , 2021, 10, 1023.	0.8	0

#	ARTICLE	IF	CITATIONS
19859	Regulated splicing of large exons is linked to phase separation of vertebrate transcription factors. <i>EMBO Journal</i> , 2021, 40, e107485.	3.5	8
19860	Three Unusual Sesquiterpenes with Distinctive Ring Skeletons from <i>Daphne penicillata</i> Uncovered by Molecular Networking Strategies. <i>Journal of Organic Chemistry</i> , 2021, 86, 15298-15306.	1.7	44
19861	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab090.	1.5	10
19862	CENPA promotes clear cell renal cell carcinoma progression and metastasis via Wnt/ $\beta$ -catenin signaling pathway. <i>Journal of Translational Medicine</i> , 2021, 19, 417.	1.8	28
19863	Mir-21 Suppression Promotes Mouse Hepatocarcinogenesis. <i>Cancers</i> , 2021, 13, 4983.	1.7	17
19865	How dam construction affects the activity of alkaline phosphatases in reservoir sediments: A study of two highly regulated rivers. <i>Environmental Research</i> , 2022, 207, 112236.	3.7	6
19866	Transcriptome-based identification of novel endotypes in adult atopic dermatitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 1486-1498.	2.7	8
19867	Comparative Transcriptome Analysis of Male Sterile Anthers Induced by High Temperature in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 727966.	1.7	5
19868	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	4.9	33
19869	Whole transcriptome analysis of RNA expression profiles reveals the potential regulating action of long noncoding RNA in lactating cows fed a high concentrate diet. <i>Animal Nutrition</i> , 2021, 7, 1315-1328.	2.1	2
19870	Topological Dissection of Proteomic Changes Linked to the Limbic Stage of Alzheimer's Disease. <i>Frontiers in Immunology</i> , 2021, 12, 750665.	2.2	5
19872	High-confidence structural annotation of metabolites absent from spectral libraries. <i>Nature Biotechnology</i> , 2022, 40, 411-421.	9.4	100
19873	Analysis of Shared Genetic Regulatory Networks for Alzheimer's Disease and Epilepsy. <i>BioMed Research International</i> , 2021, 2021, 1-8.	0.9	4
19874	International Prognostic Index-Based Immune Prognostic Model for Diffuse Large B-Cell Lymphoma. <i>Frontiers in Immunology</i> , 2021, 12, 732006.	2.2	10
19875	Proteomics of ZIKV infected amniotic fluids of microcephalic fetuses reveals extracellular matrix and immune system dysregulation. <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100041.	0.8	5
19876	Mechanistic Insight Into the Regulation of Immune-Related Genes Expression in Autism Spectrum Disorder. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 754296.	1.6	8
19877	A network pharmacological approach to reveal the multidrug resistance reversal and associated mechanisms of acetogenins against colorectal cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 13527-13546.	2.0	2
19878	Huanglianjiedu Decoction as an effective treatment for oral squamous cell carcinoma based on network pharmacology and experimental validation. <i>Cancer Cell International</i> , 2021, 21, 553.	1.8	3

#	ARTICLE	IF	CITATIONS
19879	Drought Sensitivity of Sugarcane Cultivars Shapes Rhizosphere Bacterial Community Patterns in Response to Water Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 732989.	1.5	8
19880	Chromatin Accessibility and Transcriptomic Alterations in Murine Ovarian Granulosa Cells upon Deoxynivalenol Exposure. <i>Cells</i> , 2021, 10, 2818.	1.8	4
19881	Unraveling Protein Interactions between the Temperate Virus Bam35 and Its Bacillus Host Using an Integrative Yeast Two Hybridâ€“High Throughput Sequencing Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11105.	1.8	0
19882	Fate of antibiotic resistance genes in abandoned swine feedlots in China: seasonal variation. <i>Environmental Sciences Europe</i> , 2021, 33, .	2.6	1
19883	Integrated computational analyses reveal novel insights into the stromal microenvironment of SHH-subtype medulloblastoma. <i>Scientific Reports</i> , 2021, 11, 20694.	1.6	2
19884	Proteogenomics Reveals Perturbed Signaling Networks in Malignant Melanoma Cells Resistant to BRAF Inhibition. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100163.	2.5	7
19885	Drug repurposing improves disease targeting 11-fold and can be augmented by network module targeting, applied to COVID-19. <i>Scientific Reports</i> , 2021, 11, 20687.	1.6	5
19886	Ion transporters and their exploration for conferring abiotic stress tolerance in plants. <i>Plant Growth Regulation</i> , 2022, 96, 1-23.	1.8	6
19888	Transcriptome profiling of pepper leaves by RNA-Seq during an incompatible and a compatible pepper-tobamovirus interaction. <i>Scientific Reports</i> , 2021, 11, 20680.	1.6	10
19890	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPSC cell-derived neural progenitor cells. <i>iScience</i> , 2021, 24, 103321.	1.9	2
19891	Natural products for infectious microbes and diseases: an overview of sources, compounds, and chemical diversities. <i>Science China Life Sciences</i> , 2022, 65, 1123-1145.	2.3	19
19892	Mechanistic insights into COVID-19 by global analysis of the SARS-CoV-2 3CLpro substrate degradome. <i>Cell Reports</i> , 2021, 37, 109892.	2.9	60
19893	Gene Ontology curation of the bloodâ€“brain barrier to improve the analysis of Alzheimerâ€™s and other neurological diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	6
19894	IRAK1-dependent Regnase-1-14-3-3 complex formation controls Regnase-1-mediated mRNA decay. <i>ELife</i> , 2021, 10, .	2.8	12
19895	Functional drugâ€“targetâ€“disease network analysis of geneâ€“phenotype connectivity for curcumin in hepatocellular carcinoma. <i>PeerJ</i> , 2021, 9, e12339.	0.9	2
19897	Differential Association of Free, Conjugated, and Bound Forms of Polyamines and Transcript Abundance of Their Biosynthetic and Catabolic Genes During Drought/Salinity Stress in Tomato ( <i>Solanum lycopersicum</i> L.) Leaves. <i>Frontiers in Plant Science</i> , 2021, 12, 743568.	1.7	8
19898	Integrative Analysis to Identify Genes Associated with Stemness and Immune Infiltration in Glioblastoma. <i>Cells</i> , 2021, 10, 2765.	1.8	6
19899	The proliferation role of LH on porcine primordial germ cellâ€“like cells (pPGCLCs) through ceRNA network construction. <i>Clinical and Translational Medicine</i> , 2021, 11, e560.	1.7	5

#	ARTICLE	IF	CITATIONS
19900	Dementia subtype prediction models constructed by penalized regression methods for multiclass classification using serum microRNA expression data. <i>Scientific Reports</i> , 2021, 11, 20947.	1.6	5
19901	Andrographolide ameliorates aortic valve calcification by regulation of lipid biosynthesis and glycerolipid metabolism targeting MGLL expression in vitro and in vivo. <i>Cell Calcium</i> , 2021, 100, 102495.	1.1	18
19902	Study on the mechanism of treating COVID-19 with Shenqi Wan based on network pharmacology. <i>Drug Development and Industrial Pharmacy</i> , 2021, , 1-11.	0.9	8
19903	Comparative epigenetic analysis of tumour initiating cells and syngeneic EPSC-derived neural stem cells in glioblastoma. <i>Nature Communications</i> , 2021, 12, 6130.	5.8	14
19905	NTRK1/TrkA Signaling in Neuroblastoma Cells Induces Nuclear Reorganization and Intra-Nuclear Aggregation of Lamin A/C. <i>Cancers</i> , 2021, 13, 5293.	1.7	7
19906	A ten-genes-based diagnostic signature for atherosclerosis. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 513.	0.7	9
19907	WikiNetworks: translating manually created biological pathways for topological analysis. <i>Bioinformatics</i> , 2022, 38, 869-871.	1.8	7
19908	The Single-Cell Transcriptomic Analysis of Prefrontal Pyramidal Cells and Interneurons Reveals the Neuronal Expression of Genes Encoding Antimicrobial Peptides and Immune Proteins. <i>Frontiers in Immunology</i> , 2021, 12, 749433.	2.2	1
19909	Transcriptomic Analysis Reveals Candidate Genes Responding Maize Gray Leaf Spot Caused by <i>Cercospora zeina</i> . <i>Plants</i> , 2021, 10, 2257.	1.6	9
19910	Cell type-specific potential pathogenic genes and functional pathways in Alzheimer's Disease. <i>BMC Neurology</i> , 2021, 21, 381.	0.8	21
19911	Genome-Wide Identification and Expression Analysis of AP2/ERF Transcription Factor Related to Drought Stress in Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 750761.	1.1	21
19912	A network pharmacology-based approach to explore the active ingredients and molecular mechanism of Lei-gong-gen formula granule on a spontaneously hypertensive rat model. <i>Chinese Medicine</i> , 2021, 16, 99.	1.6	14
19913	Integrative Systems Biology Analysis Elucidates Mastitis Disease Underlying Functional Modules in Dairy Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 712306.	1.1	18
19916	Alterations in HLA Class I-Presented Immunopeptidome and Class II-Interactome upon Osimertinib Resistance in EGFR Mutant Lung Adenocarcinoma. <i>Cancers</i> , 2021, 13, 4977.	1.7	5
19917	Identification of Significant Genes in Lung Cancer of Nonsmoking Women via Bioinformatics Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	2
19918	Western and non-western gut microbiomes reveal new roles of <i>Prevotella</i> in carbohydrate metabolism and mouth-gut axis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 77.	2.9	28
19919	Genetic Elucidation of Quorum Sensing and Cobamide Biosynthesis in Divergent Bacterial-Fungal Associations Across the Soil-Mangrove Root Interface. <i>Frontiers in Microbiology</i> , 2021, 12, 698385.	1.5	0
19920	Comprehensive analysis of the MIR4435-2HG/miR-1-3p/MMP9/miR-29-3p/DUXAP8 ceRNA network axis in hepatocellular carcinoma. <i>Discover Oncology</i> , 2021, 12, 38.	0.8	7



#	ARTICLE	IF	CITATIONS
19922	A Network Pharmacology Analysis of the Systems-Perspective Anticancer Mechanisms of the Herbal Drug FDY2004 for Breast Cancer. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110491.	0.2	0
19923	CD4 <sup>+</sup> T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. <i>Epigenetics</i> , 2022, 17, 1040-1055.	1.3	4
19924	KrasG12D induces changes in chromatin territories that differentially impact early nuclear reprogramming in pancreatic cells. <i>Genome Biology</i> , 2021, 22, 289.	3.8	6
19925	Heritability and genetic correlations of plasma metabolites of pigs with production, resilience and carcass traits under natural polymicrobial disease challenge. <i>Scientific Reports</i> , 2021, 11, 20628.	1.6	6
19927	Genomic and transcriptomic dissection of Theionarchaea in marine ecosystem. <i>Science China Life Sciences</i> , 2021, , 1.	2.3	2
19928	Novel implications of a strictly monomorphic (GCC) repeat in the human PRKACB gene. <i>Scientific Reports</i> , 2021, 11, 20629.	1.6	13
19929	CircRNA expression profiling of PBMCs from patients with hepatocellular carcinoma by RNA-seq. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1467.	0.8	3
19930	Indole-3-Propionic Acid, a Gut-Derived Tryptophan Metabolite, Associates with Hepatic Fibrosis. <i>Nutrients</i> , 2021, 13, 3509.	1.7	25
19931	Alkyl-Quinolones derivatives as potential biomarkers for <i>Pseudomonas aeruginosa</i> infection chronicity in Cystic Fibrosis. <i>Scientific Reports</i> , 2021, 11, 20722.	1.6	3
19933	Protistan-Bacterial Microbiota Exhibit Stronger Species Sorting and Greater Network Connectivity Offshore than Nearshore across a Coast-to-Basin Continuum. <i>MSystems</i> , 2021, 6, e0010021.	1.7	5
19934	Similar heterotrophic communities but distinct interactions supported by red and green snow algae in the Antarctic Peninsula. <i>New Phytologist</i> , 2022, 233, 1358-1368.	3.5	7
19935	Deciphering the link between Diabetes mellitus and SARS-CoV-2 infection through differential targeting of microRNAs in the human pancreas. <i>Journal of Endocrinological Investigation</i> , 2022, 45, 537-550.	1.8	12
19936	Identification of MYH6 as the potential gene for human ischaemic cardiomyopathy. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 10736-10746.	1.6	15
19937	Network Analysis of Symptoms Co-Occurrence in Chronic Fatigue Syndrome. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 10736.	1.2	7
19938	Ecological Dynamics and Co-occurrences Among Prokaryotes and Microeukaryotes in a Diatom Bloom Process in Xiangshan Bay, China. <i>Microbial Ecology</i> , 2021, , 1.	1.4	4
19939	Analysis of Prognostic Alternative Splicing Reveals the Landscape of Immune Microenvironment in Thyroid Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 763886.	1.3	1
19941	Predictive regulatory and metabolic network models for systems analysis of <i>Clostridioides difficile</i> . <i>Cell Host and Microbe</i> , 2021, 29, 1709-1723.e5.	5.1	12
19942	Proteomic and phosphoproteomic analyses identify liver-related signaling in retinal pigment epithelial cells during EMT. <i>Cell Reports</i> , 2021, 37, 109866.	2.9	3

#	ARTICLE	IF	CITATIONS
19943	Protein Cargo of Salivary Small Extracellular Vesicles as Potential Functional Signature of Oral Squamous Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11160.	1.8	14
19944	Telomerase (hTERT) Overexpression Reveals a Promising Prognostic Biomarker and Therapeutical Target in Different Clinical Subtypes of Pediatric Acute Lymphoblastic Leukaemia. <i>Genes</i> , 2021, 12, 1632.	1.0	3
19945	Identification of Novel Drug Candidate for Epithelial Ovarian Cancer via In Silico Investigation and In Vitro Validation. <i>Frontiers in Oncology</i> , 2021, 11, 745590.	1.3	4
19946	Identification of Apocarotenoids as Chemical Markers of In Vitro Anti-Inflammatory Activity for Spirulina Supplements. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 12674-12685.	2.4	3
19947	<i>Mycoplasma genitalium</i> and <i>M. pneumoniae</i> Regulate a Distinct Set of Protein-Coding Genes in Epithelial Cells. <i>Frontiers in Immunology</i> , 2021, 12, 738431.	2.2	8
19948	SWATH-MS based quantitative proteomics reveal regulatory metabolism and networks of androdioecy breeding system in <i>Osmanthus fragrans</i> . <i>BMC Plant Biology</i> , 2021, 21, 468.	1.6	1
19949	Changing and stable chromatin accessibility supports transcriptional overhaul during neural stem cell activation and is altered with age. <i>Aging Cell</i> , 2021, 20, e13499.	3.0	13
19950	Delineating infection strategies of <i>Leishmania donovani</i> secretory proteins in Human through host-pathogen protein Interactome prediction. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	2
19952	Knock-Down of Heterogeneous Nuclear Ribonucleoprotein A1 Results in Neurite Damage, Altered Stress Granule Biology, and Cellular Toxicity in Differentiated Neuronal Cells. <i>ENeuro</i> , 2021, 8, ENEURO.0350-21.2021.	0.9	9
19953	Functional analysis of co-expression networks of zebrafish <i>ace2</i> reveals enrichment of pathways associated with development and disease.. <i>Genome</i> , 2021, , 1-18.	0.9	0
19954	Network Pharmacology-Based Study of the Underlying Mechanisms of Huangqi Sijunzi Decoction for Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	5
19958	Network Pharmacology-Based Strategy to Investigate Pharmacological Mechanisms of the Drug Pair <i>Astragalus-Angelica</i> for Treatment of Male Infertility. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	2
19959	Effects and Components of Herb Pair <i>Huanglian-Banxia</i> on Diabetic Gastroparesis by Network Pharmacology. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	7
19960	Prediction of Cancer-Related piRNAs Based on Network-Based Stratification Analysis. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2022, 36, .	0.7	1
19961	Identification of N6-Methyladenosine-Related LncRNAs for Predicting Overall Survival and Clustering of a Potentially Novel Molecular Subtype of Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 742944.	1.3	7
19962	Transcriptomic and Coexpression Network Analyses Revealed Pine Chalcone Synthase Genes Associated with Pine Wood Nematode Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11195.	1.8	11
19963	Screening and predicted value of potential biomarkers for breast cancer using bioinformatics analysis. <i>Scientific Reports</i> , 2021, 11, 20799.	1.6	29
19965	Epididymal mRNA and miRNA transcriptome analyses reveal important genes and miRNAs related to sperm motility in roosters. <i>Poultry Science</i> , 2022, 101, 101558.	1.5	8

#	ARTICLE	IF	CITATIONS
19966	Hypomethylation and downregulation of miR-23b-3p are associated with upregulated PLAU: a diagnostic and prognostic biomarker in head and neck squamous cell carcinoma. <i>Cancer Cell International</i> , 2021, 21, 564.	1.8	4
19967	Identification of immune-related genes and susceptible population of pulmonary tuberculosis by constructing TF-miRNA-mRNA regulatory network. <i>Tuberculosis</i> , 2021, 131, 102139.	0.8	3
19968	Spatiotemporal dynamics of the resistome and virulome of riverine microbiomes disturbed by a mining mud tsunami. <i>Science of the Total Environment</i> , 2022, 806, 150936.	3.9	6
19969	Resiniferatoxin Hampers the Nocifensive Response of <i>Caenorhabditis elegans</i> to Noxious Heat, and Pathway Analysis Revealed that the Wnt Signaling Pathway is Involved. <i>Neurochemical Research</i> , 2022, 47, 622-633.	1.6	4
19970	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
19971	Population genomics and evidence of clonal replacement of <i>Plasmodium falciparum</i> in the Peruvian Amazon. <i>Scientific Reports</i> , 2021, 11, 21212.	1.6	8
19972	Insights into molecular pathways and fatty acid membrane composition during the temperature stress response in the murine C2C12 cell model. <i>Science of the Total Environment</i> , 2021, 807, 151019.	3.9	2
19973	Butyrophilin-like 9 expression is associated with outcome in lung adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 1096.	1.1	10
19974	Dysregulated lncRNA and mRNA may promote the progression of ischemic stroke via immune and inflammatory pathways: results from RNA sequencing and bioinformatics analysis. <i>Genes and Genomics</i> , 2022, 44, 97-108.	0.5	6
19975	Identification of SUMO Targets Associated With the Pluripotent State in Human Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100164.	2.5	8
19976	Gene correlation network analysis to identify regulatory factors in sciatic nerve injury. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 622.	0.9	5
19977	The Omic Insights on Unfolding Saga of COVID-19. <i>Frontiers in Immunology</i> , 2021, 12, 724914.	2.2	3
19978	Disentangling the Effects of Physicochemical, Genetic, and Microbial Properties on Phase-Driven Resistome Dynamics during Multiple Manure Composting Processes. <i>Environmental Science &amp; Technology</i> , 2021, 55, 14732-14745.	4.6	16
19979	Tlr2/4 Double Knockout Attenuates the Degeneration of Primary Auditory Neurons: Potential Mechanisms From Transcriptomic Perspectives. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 750271.	1.8	1
19980	Impact of Proinflammatory Cytokines on Alternative Splicing Patterns in Human Islets. <i>Diabetes</i> , 2022, 71, 116-127.	0.3	4
19981	Interleukin-22 Deficiency Contributes to Dextran Sulfate Sodium-Induced Inflammation in Japanese Medaka, <i>Oryzias latipes</i> . <i>Frontiers in Immunology</i> , 2021, 12, 688036.	2.2	11
19982	Screening of Biomarkers Involved in Idiopathic Pulmonary Fibrosis and Regulation of Upstream miRNAs. <i>American Journal of the Medical Sciences</i> , 2022, 363, 55-63.	0.4	3
19983	Sinensetin attenuates oxygen-glucose deprivation/reperfusion-induced neurotoxicity by MAPK pathway in human cerebral microvascular endothelial cells. <i>Journal of Applied Toxicology</i> , 2022, 42, 683-693.	1.4	6

#	ARTICLE	IF	CITATIONS
19984	Genetics Responses to Hypoxia and Reoxygenation Stress in <i>Larimichthys crocea</i> Revealed via Transcriptome Analysis and Weighted Gene Co-Expression Network. <i>Animals</i> , 2021, 11, 3021.	1.0	3
19985	Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. <i>Communications Biology</i> , 2021, 4, 1217.	2.0	14
19986	An antibody-based proximity labeling map reveals mechanisms of SARS-CoV-2 inhibition of antiviral immunity. <i>Cell Chemical Biology</i> , 2022, 29, 5-18.e6.	2.5	26
19987	Nkx3-1 and Fech genes might be switch genes involved in pituitary non-functioning adenoma invasiveness. <i>Scientific Reports</i> , 2021, 11, 20943.	1.6	3
19988	Multi-Omics-Based Identification and Functional Characterization of Gh_A06G1257 Proves Its Potential Role in Drought Stress Tolerance in <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 746771.	1.7	13
19989	Dynamic transcriptional reprogramming leads to immunotherapeutic vulnerabilities in myeloma. <i>Nature Cell Biology</i> , 2021, 23, 1199-1211.	4.6	22
19990	Experiment level curation of transcriptional regulatory interactions in neurodevelopment. <i>PLoS Computational Biology</i> , 2021, 17, e1009484.	1.5	4
19991	A three-organelle complex made by wrappER contacts with peroxisomes and mitochondria responds to liver lipid flux changes. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	20
19992	Identification and Validation of <i>TREM2</i> in Intracranial Aneurysms. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 646-653.	0.3	3
19993	Decrypting molecular mechanism insight of <i>Phyllanthus emblica</i> L. fruit in the treatment of type 2 diabetes mellitus by network pharmacology. <i>Phytomedicine Plus</i> , 2021, 1, 100144.	0.9	6
19994	Identifying disease-gene associations using a convolutional neural network-based model by embedding a biological knowledge graph with entity descriptions. <i>PLoS ONE</i> , 2021, 16, e0258626.	1.1	20
19995	Cathepsin C Is Involved in Macrophage M1 Polarization via p38/MAPK Pathway in Sudden Cardiac Death. <i>Cardiovascular Therapeutics</i> , 2021, 2021, 1-12.	1.1	7
19997	Impact of human papillomavirus on the tumor microenvironment in oropharyngeal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2022, 150, 521-531.	2.3	6
19998	Machine Learning for Prediction of Drug Targets in Microbe Associated Cardiovascular Diseases by Incorporating Host-Pathogen Interaction Network Parameters. <i>Molecular Informatics</i> , 2022, 41, e2100115.	1.4	7
19999	Identification S100A9 as a potential biomarker in neuroblastoma. <i>Molecular Biology Reports</i> , 2021, 48, 7743-7753.	1.0	3
20000	Quantitative analysis of phosphoproteome in necroptosis reveals a role of TRIM28 phosphorylation in promoting necroptosis-induced cytokine production. <i>Cell Death and Disease</i> , 2021, 12, 994.	2.7	7
20001	Pathophysiological pathways in patients with heart failure and atrial fibrillation. <i>Cardiovascular Research</i> , 2022, 118, 2478-2487.	1.8	5
20002	Network propagation-based prioritization of long tail genes in 17 cancer types. <i>Genome Biology</i> , 2021, 22, 287.	3.8	7

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20003	Novel lncRNA-miRNA-mRNA Competing Endogenous RNA Triple Networks Associated Programmed Cell Death in Heart Failure. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 747449.	1.1	18
20004	miR profile in pagetic osteoclasts: from large-scale sequencing to gene expression study. <i>Journal of Molecular Medicine</i> , 2021, 99, 1771-1781.	1.7	4
20005	INfrastructure for a PHAge REference Database: Identification of Large-Scale Biases in the Current Collection of Cultured Phage Genomes. <i>Phage</i> , 2021, 2, 214-223.	0.8	121
20006	Spatial metabolomics identifies localized chemical changes in heart tissue during chronic cardiac Chagas Disease. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009819.	1.3	18
20007	STAT1: a novel candidate biomarker and potential therapeutic target of the recurrent aphthous stomatitis. <i>BMC Oral Health</i> , 2021, 21, 524.	0.8	1
20008	New Prognostic Biomarkers and Drug Targets for Skin Cutaneous Melanoma via Comprehensive Bioinformatic Analysis and Validation. <i>Frontiers in Oncology</i> , 2021, 11, 745384.	1.3	1
20009	miR-542-3p Attenuates Bone Loss and Marrow Adiposity Following Methotrexate Treatment by Targeting sFRP-1 and Smurf2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10988.	1.8	5
20010	A phosphate starvation response-centered network regulates mycorrhizal symbiosis. <i>Cell</i> , 2021, 184, 5527-5540.e18.	13.5	151
20011	Metabolomics atlas of oral 13C-glucose tolerance test in mice. <i>Cell Reports</i> , 2021, 37, 109833.	2.9	20
20013	Identification of ferroptosis-associated genes exhibiting altered expression in response to cardiopulmonary bypass during corrective surgery for pediatric tetralogy of fallot. <i>Science Progress</i> , 2021, 104, 003685042110502.	1.0	6
20014	Fluid flow exposure promotes epithelial-to-mesenchymal transition and adhesion of breast cancer cells to endothelial cells. <i>Breast Cancer Research</i> , 2021, 23, 97.	2.2	8
20016	CD4+ T-Cell Activation Prompts Suppressive Function by Extracellular Vesicle-Associated MicroRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 753884.	1.8	3
20017	MicroRNAs May Play an Important Role in Sexual Reversal Process of Chinese Soft-Shelled Turtle, <i>Pelodiscus sinensis</i> . <i>Genes</i> , 2021, 12, 1696.	1.0	7
20019	The role of PDGFRA as a therapeutic target in young colorectal cancer patients. <i>Journal of Translational Medicine</i> , 2021, 19, 446.	1.8	11
20020	Tonsillar Cancer with High CD8+ T-Cell Infiltration Features Increased Levels of Dendritic Cells and Transcriptional Regulation Associated with an Inflamed Tumor Microenvironment. <i>Cancers</i> , 2021, 13, 5341.	1.7	7
20021	Attention to time-of-day variability improves the reproducibility of gene expression patterns in multiple sclerosis. <i>iScience</i> , 2021, 24, 103247.	1.9	2
20022	Verapamil ameliorates proximal tubular epithelial cells apoptosis and fibrosis in diabetic kidney. <i>European Journal of Pharmacology</i> , 2021, 911, 174552.	1.7	0
20023	Microbiome associated with the tetrodotoxin-bearing anuran <i>Brachycephalus pitanga</i> . <i>Toxicon</i> , 2021, 203, 139-146.	0.8	2

#	ARTICLE	IF	CITATIONS
20024	Identification of a lncRNA/circRNA-miRNA-mRNA network to explore the effects of ricin toxin-induced inflammation in RAW264.7 cells. <i>Toxicol</i> , 2021, 203, 129-138.	0.8	4
20025	MINCR: A long non-coding RNA shared between cancer and neurodegeneration. <i>Genomics</i> , 2021, 113, 4039-4051.	1.3	14
20026	A network pharmacology approach to investigate the anticancer mechanism of cinobufagin against hepatocellular carcinoma via downregulation of EGFR-CDK2 signaling. <i>Toxicology and Applied Pharmacology</i> , 2021, 431, 115739.	1.3	15
20027	Interdependence of neural network dysfunction and microglial alterations in Alzheimer's disease-related models. <i>iScience</i> , 2021, 24, 103245.	1.9	11
20028	From innate to adaptive immunity: Abomasal transcriptomic responses of merino sheep to <i>Haemonchus contortus</i> infection. <i>Molecular and Biochemical Parasitology</i> , 2021, 246, 111424.	0.5	4
20029	Systems analysis of steroid induced osteonecrosis shows role for heme and vitamin D in pathogenesis. <i>Gene Reports</i> , 2021, 25, 101383.	0.4	4
20030	Metabolic variation in Caribbean giant barrel sponges: Influence of age and sea-depth. <i>Marine Environmental Research</i> , 2021, 172, 105503.	1.1	1
20031	Caffeate may play an important role in the somatic embryogenesis of oil palm ( <i>Elaeis guineensis</i> Jacq.). <i>Industrial Crops and Products</i> , 2021, 174, 114143.	2.5	9
20032	Searchable database of frequent R-groups in medicinal chemistry and their preferred replacements. <i>Data in Brief</i> , 2021, 39, 107456.	0.5	0
20033	Unravelling the role of hub genes associated with cardio renal syndrome through an integrated bioinformatics approach. <i>Gene Reports</i> , 2021, 25, 101382.	0.4	2
20034	Dynamic flow enables long-term maintenance of 3D vascularized human skin models. <i>Applied Materials Today</i> , 2021, 25, 101213.	2.3	10
20035	Dynamic transcriptome and co-expression analysis suggest the potential roles of small secreted peptides from Tartary buckwheat ( <i>Fagopyrum tataricum</i> ) in low nitrogen stress response. <i>Plant Science</i> , 2021, 313, 111091.	1.7	4
20036	Systems biology analysis of pyrethroid biodegradation in bacteria and its effect on the cellular environment of pests and humans. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 106582.	3.3	22
20037	The effects of different coculture patterns with salt-tolerant yeast strains on the microbial community and metabolites of soy sauce moromi. <i>Food Research International</i> , 2021, 150, 110747.	2.9	13
20039	Adenylate kinase 2 deficiency limits survival and regulates various genes during larval stages of <i>Drosophila melanogaster</i> . <i>Journal of Medical Investigation</i> , 2000, 40, 137-150.	0.2	0
20040	Microarray Analysis of Gene Expression Changes in Aging. , 2005, , 295-333.		0
20041	A Computer Visualization Model for the De Novo Sphingolipid Biosynthetic Pathway. , 2006, , 493-508.		0
20042	SPDBS: An SBML-Based Biochemical Pathway Database System. <i>Lecture Notes in Computer Science</i> , 2006, , 543-550.	1.0	1



#	ARTICLE	IF	CITATIONS
20043	HSPPIP: An Online Tool for Prediction of Protein-Protein Interactions in Humans. Lecture Notes in Computer Science, 2006, , 603-611.	1.0	0
20044	Assessing Significance of Connectivity and Conservation in Protein Interaction Networks. Lecture Notes in Computer Science, 2006, , 45-59.	1.0	3
20045	Aggregation of Bioinformatics Data Using Semantic Web Technology. SSRN Electronic Journal, 0, , .	0.4	1
20048	<b>explorase</b>: Multivariate Exploratory Analysis and Visualization for Systems Biology. Journal of Statistical Software, 2008, 25, .	1.8	1
20049	Topology of Plant Metabolic Networks. , 2009, , 173-209.		0
20051	GT-Miner: a graph-theoretic data miner, viewer, and model processor. Bioinformatics, 2008, 3, 235-237.	0.2	1
20052	Scientific Databases. , 2009, , 2502-2506.		0
20053	Reaction Centric Layout for Metabolic Networks. Lecture Notes in Computer Science, 2009, , 81-91.	1.0	1
20054	Dynamics of Protein-Protein Interaction Network in Plasmodium Falciparum. , 2009, , 257-284.		0
20055	Detecting and Characterizing the Modular Structure of the Yeast Transcription Network. Studies in Computational Intelligence, 2009, , 35-46.	0.7	0
20056	Visualization of Gene Regulatory Networks. Lecture Notes in Computer Science, 2009, , 909-918.	1.0	0
20057	Gene Regulatory Network Reconstruction of P38 MAPK Pathway Using Ordinary Differential Equation with Linear Regression Analysis. Advances in Intelligent and Soft Computing, 2009, , 299-308.	0.2	2
20058	Graphical Analysis and Visualization Tools for Protein Interaction Networks. , 2009, , 286-311.		0
20059	Biological Data Integration and Model Building. , 2009, , 511-524.		0
20060	The Bioverse API and Web Application. Methods in Molecular Biology, 2009, 541, 511-534.	0.4	2
20061	Linking Life Sciences Data Using Graph-Based Mapping. Lecture Notes in Computer Science, 2009, , 16-30.	1.0	2
20062	Graph-based Exploratory Analysis of Biological Interaction Networks. , 0, , .		0
20064	Visualizing Gene Co-expression as Google Maps. Lecture Notes in Computer Science, 2010, , 494-503.	1.0	0

#	ARTICLE	IF	CITATIONS
20065	Graph visualization with latent variable models. , 2010, , .		3
20066	ProteoLens: A Database-Driven Visual Data Mining Tool for Network Biology. Systems Biology, 2010, , 857-875.	0.1	0
20067	PNmerger: a Cytoscape Plugin to Merge Biological Pathways and Protein Interaction Networks*. Progress in Biochemistry and Biophysics, 2010, 2009, 1613-1616.	0.3	0
20068	Systems-Level Analyses of the Mammalian Innate Immune Response. Systems Biology, 2010, , 531-560.	0.1	1
20069	FERN “ Stochastic Simulation and Evaluation of Reaction Networks. Systems Biology, 2010, , 751-775.	0.1	1
20070	Data Visualization and Network Languages Applied to Heterogeneous Data in Bioinformatics. International Journal of Computer Applications, 2010, 1, 37-45.	0.2	0
20073	Bioinformatics of High-Throughput Insertional Mutagenesis. , 2011, , 167-188.		0
20075	Protein Function Prediction Using Protein“Protein Interaction Networks. , 2011, , 243-270.		0
20076	Systems Biology: A Promising Tool to Study Abiotic Stress Responses. , 2011, , 163-172.		6
20077	Modules in Biological Networks. , 2011, , 248-274.		0
20078	Stable Isotopic Labeling for Proteomics. , 2011, , 549-573.		2
20080	Network-Driven Analysis Methods and their Application to Drug Discovery. , 2011, , 294-315.		0
20081	Data Management and Application on CPSE-Bio. Lecture Notes in Electrical Engineering, 2011, , 591-599.	0.3	0
20082	Systematic and Integrative Analysis of Proteomic Data using Bioinformatics Tools. International Journal of Advanced Computer Science and Applications, 2011, 2, .	0.5	1
20083	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 2011, , 225-247.		0
20084	Filtering and Interpreting Large-Scale Experimental Protein“Protein Interaction Data. Methods in Molecular Biology, 2011, 781, 295-309.	0.4	0
20085	ldBean: a Java GUI application for conversion of biological identifiers. BMB Reports, 2011, 44, 107-112.	1.1	1
20086	Building Network Visualization Tools to Facilitate Metacognition in Complex Analysis. Leonardo, 2011, 44, 248-249.	0.2	0

#	ARTICLE	IF	CITATIONS
20089	On-Chip Living-Cell Microarrays for Network Biology. , 0, , .		0
20090	Identifying genes related with non-small cell lung cancer via transcription factors-target genes relationship. International Journal of Physical Sciences, 2011, 6, .	0.1	0
20091	System-Scale Network Modeling of Cancer Using EPoC. Advances in Experimental Medicine and Biology, 2012, 736, 617-643.	0.8	1
20092	Network Analysis in Translational Research. Translational Bioinformatics, 2012, , 265-285.	0.0	0
20093	Modelling a Biological System: Network Creation by Triplet Extraction from Biological Literature. Lecture Notes in Computer Science, 2012, , 427-437.	1.0	1
20094	Network-Based Methods for Computational Diagnostics by Means of R. , 2012, , 185-197.		2
20095	HINT-KB: The Human Interactome Knowledge Base. International Federation for Information Processing, 2012, , 612-621.	0.4	1
20097	Visualization of Protein Interaction Networks. , 0, , 125-139.		1
20099	Application of Bioinformatics Tools in Gel-Based Proteomics. , 0, , .		0
20100	Transcription factors and target genes relationship based method reveals potential thermal injury related genes. African Journal of Pharmacy and Pharmacology, 2012, 6, .	0.2	0
20101	A regulatory network for human adenocarcinoma. African Journal of Biotechnology, 2012, 11, .	0.3	0
20102	Scalable, Integrative Analysis and Visualization of Protein Interactions. , 0, , .		1
20103	Study on transcription regulation network in rheumatoid arthritis via bioinformatics analysis. African Journal of Pharmacy and Pharmacology, 2012, 6, .	0.2	1
20104	Dis2PPI. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 67-85.	0.8	1
20105	Analyses of Complex Genome-Scale Biological Networks. SpringerBriefs in Systems Biology, 2013, , 43-55.	0.1	0
20106	Concurrent Dynamic Visualizations With Expressive Petri Net Representations to Enrich the Understanding of Biological and Pathological Processes: an Application to Signaling Pathways. Journal of Applied Research and Technology, 2012, 10, .	0.6	0
20107	Prioritizing Disease Genes and Understanding Disease Pathways. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 31-49.	0.8	0
20108	Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30.	0.8	0

#	ARTICLE	IF	CITATIONS
20109	Modeling CAS. SpringerBriefs in Cognitive Computation, 2013, , 33-53.	0.1	0
20110	Information Transfer in Biological and Bio-Inspired Systems. Springer Theses, 2013, , 177-202.	0.0	0
20112	On Different Aspects of Network Analysis in Systems Biology. , 2013, , 181-207.		3
20113	Networks of Financial Contagion. Studies in Computational Intelligence, 2013, , 31-48.	0.7	2
20114	Inferring Gene Networks from Gene Expression Data Using Dynamic Bayesian Network with Different Scoring Metric Approaches. Studies in Computational Intelligence, 2013, , 77-86.	0.7	1
20115	Quantitative Characterization of Protein Networks of the Oral Cavity. Advances in Intelligent Systems and Computing, 2013, , 61-68.	0.5	0
20116	Application of Next-Generation Sequencing to Analysis of TGF $\beta$ 2/SMAD4 Targets in Ovarian Cancer. , 2013, , 119-135.		0
20117	Biological Data Integration and Model Building. , 2013, , 1-19.		0
20118	Network Visualization Tools to Enhance Metabolic Engineering Platforms. Advances in Intelligent Systems and Computing, 2013, , 137-144.	0.5	1
20119	Computational Tools and Resources for Integrative Modeling in Systems Biology. , 2013, , 399-428.		0
20120	Role of Protein Aggregation and Interactions between $\alpha$ -Synuclein and Calbindin in Parkinson's Disease. Lecture Notes in Computer Science, 2013, , 677-684.	1.0	0
20122	Modulation of the Hepatic Lipidome and Transcriptome of Apoe <sup>-/-</sup> Mice in Response to Smoking Cessation. Journal of Liver, 2013, 02, .	0.3	1
20123	Biologia de Sistemas de Pectinases do Fungo Moniliophthora perniciosa. Diálogos & Ciência, 2013, 11, 27-30.	0.1	0
20125	C-element: A New Clustering Algorithm to Find High Quality Functional Modules in PPI Networks. PLoS ONE, 2013, 8, e72366.	1.1	1
20126	ANGDelMut " a web-based tool for predicting and analyzing functional loss mechanisms of deleterious angiogenin mutations causing amyotrophic lateral sclerosis. F1000Research, 2013, 2, 227.	0.8	3
20127	Abstract C213: Protein interaction analysis of mll-aff4 and mll-fel oncogenic fusion proteins using data mining approach.. , 2013, , .		0
20129	A Web-oriented Framework for Graph Simplification and Interactive Visualization. Journal of Computers, 2013, 8, .	0.4	1
20130	Network Topology and Functional Analysis of Genes in Ocular Disorders. Journal of Applied Bioinformatics & Computational Biology, 2014, 3, .	0.2	0

#	ARTICLE	IF	CITATIONS
20131	Bioinformatics for Proteomics: Opportunities at the Interface Between the Scientists, Their Experiments, and the Community. <i>Methods in Molecular Biology</i> , 2014, 1156, 239-248.	0.4	0
20132	Visualization in Biology and Medicine. <i>Mathematics and Visualization</i> , 2014, , 247-263.	0.4	0
20134	Friends and Circles—A Design Study for Contact Management in Egocentric Online Social Networks. <i>Lecture Notes in Social Networks</i> , 2014, , 129-161.	0.8	2
20135	Modeling Structural Protein Interaction Networks for Betweenness Analysis. , 2014, , 367-376.		1
20136	3DProlN: Protein-Protein Interaction Networks and Structure Visualization. <i>American Journal of Bioinformatics and Computational Biology</i> , 2014, 2, 32-37.	0.0	0
20137	VOSD: A General-Purpose Virtual Observatory over Semantic Databases. <i>Acta Cybernetica</i> , 2014, 21, 353-366.	0.5	1
20138	Network Biomarker Construction for Molecular Investigation and Diagnosis of Lung Cancer via Microarray Data. , 2014, , 3-29.		0
20139	OMICS for Tumor Biomarker Research. , 2014, , 1-22.		0
20140	Analysis of pathways and networks influencing the differential expression of genes in coronary artery disease. <i>Archives of Biological Sciences</i> , 2014, 66, 983-988.	0.2	1
20141	Scientific Collaboration Networks Using Biomedical Text. <i>Methods in Molecular Biology</i> , 2014, 1159, 147-157.	0.4	1
20142	Visualization and Clustering of High-Dimensional Transcriptome Data Using GATE. <i>Methods in Molecular Biology</i> , 2014, 1150, 131-139.	0.4	0
20143	In Silico Investigation of Cancer Using Publicly Available Data. , 2014, , 327-351.		0
20144	Measuring the evolution of a revised document. <i>Journal of Writing Research</i> , 2014, 6, 1-28.	0.6	3
20145	Analysis of microRNA Regulated Seed Biology Networks in Arabidopsis. <i>International Journal of Knowledge Discovery in Bioinformatics</i> , 2014, 4, 11-20.	0.8	0
20146	Cyrface: An interface from Cytoscape to R that provides a user interface to R packages. <i>F1000Research</i> , 2013, 2, 192.	0.8	2
20147	Construction of a Protein-Protein Interaction Network for Chronic Myelocytic Leukemia and Pathway Prediction of Molecular Complexes. <i>Asian Pacific Journal of Cancer Prevention</i> , 2014, 15, 5325-5330.	0.5	2
20148	SCREENING OF BIOACTIVE COMPOUNDS AGAINST NONRECEPTOR FYN KINASE: VIRTUAL SCREENING AND NETWORK APPROACH. <i>International Journal for Computational Biology</i> , 2014, 3, 10.	0.1	0
20149	Subspace Clustering of DNA Microarray Data. <i>International Journal of Computational Models and Algorithms in Medicine</i> , 2014, 4, 1-52.	0.4	1

#	ARTICLE	IF	CITATIONS
20150	Network based meta-analysis prediction of microenvironmental relays involved in stemness of human embryonic stem cells. PeerJ, 2014, 2, e618.	0.9	2
20151	Selecting relevant nodes and structures in biological networks. BiNAT: a new plugin for Cytoscape. F1000Research, 0, 3, 287.	0.8	0
20154	Systems Approaches to Study Infectious Diseases. , 2015, , 151-172.		0
20155	Large-Scale Regulatory Network Analysis from Microarray Data. Advances in Bioinformatics and Biomedical Engineering Book Series, 2015, , 60-85.	0.2	1
20157	A Graph Community Approach for Constructing microRNA Networks. Lecture Notes in Computer Science, 2015, , 283-293.	1.0	0
20158	Construction of a gene-gene interaction network with a combined score across multiple approaches. Genetics and Molecular Research, 2015, 14, 7018-7030.	0.3	3
20159	On Evaluation of Rankings in Analysis of NGS Data. Journal of Next Generation Sequencing & Applications, 2015, 01, .	0.3	0
20160	Chapter 11: Systems biology " applications in intestinal health. , 2015, , 253-272.		0
20161	Cloud Computing for Cytopathologists. , 2015, , 1312-1332.		2
20162	Toxicological Assessment Via Gene Network Analysis. Methods in Pharmacology and Toxicology, 2015, , 161-180.	0.1	0
20164	Computational Data Integration in Toxicogenomics. Methods in Pharmacology and Toxicology, 2015, , 371-392.	0.1	0
20165	Growth and evolution of category fluency network graphs. Journal of Systems and Integrative Neuroscience, 2015, 1, 6-13.	0.6	3
20166	Systematic network analysis of herb formula in Traditional East Asian Medicine discloses synergistic operation of medicinal herb pairs with statistical significance. Tang [humanitas Medicine], 2015, 5, 11.1-11.5.	0.2	0
20167	A Relational Database Model for Science Mapping Analysis. Acta Polytechnica Hungarica, 2015, 12, .	2.5	7
20169	Epitope specificity and protein signaling interactions driving epidemic occurrences of Ebola disease. F1000Research, 0, 4, 166.	0.8	2
20170	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	8
20172	Social Network: a Cytoscape app for visualizing co-publication networks. F1000Research, 2015, 4, 481.	0.8	6
20177	Protein disorder reduced in Saccharomyces cerevisiae to survive heat shock. F1000Research, 2015, 4, 1222.	0.8	2



#	ARTICLE	IF	CITATIONS
20180	Computational Methods for Prediction of Protein-Protein Interactions. Advances in Bioinformatics and Biomedical Engineering Book Series, 2016, , 184-215.	0.2	0
20181	Inferring Disease-Related Domain Using Network-Based Method. Lecture Notes in Computer Science, 2016, , 775-783.	1.0	0
20182	Agent Perspective Social Networks: Distributed Second Degree Estimation. , 2016, , 1-12.		2
20183	The SDREM Method for Reconstructing Signaling and Regulatory Response Networks: Applications for Studying Disease Progression. Methods in Molecular Biology, 2016, 1303, 493-506.	0.4	4
20184	Obesity-Related Genes and Oral Cancer: A Bioinformatics Approach and Systematic Review. Journal of Applied Bioinformatics & Computational Biology, 2016, 05, .	0.2	0
20185	Design, Principles, Network Architecture and Their Analysis Strategies as Applied to Biological Systems. , 2016, , 21-31.		0
20186	Visual Methods and Tools for Social Network Analysis. , 2016, , 1-17.		0
20188	Innovation Cartography and Patentomics: Past, Present and Future. , 2016, , 225-242.		0
20189	Building the SeqChromMM Markov property atlas of the human genome by analyzing the 200-bp units of the 15 different chromatin regions of ENCODE. Genetics and Molecular Research, 2016, 15, .	0.3	0
20190	An Interactive Visualization System for Large Hierarchical Graphs and Its Application to Web Media Analysis. Journal of the Visualization Society of Japan, 2016, 36, 9-13.	0.0	0
20191	Visualizing Next-Generation Sequencing Cancer Data Sets with Cloud Computing. Lecture Notes in Computer Science, 2016, , 50-62.	1.0	1
20192	Estudio de proteÃnas reductoras de cromo en Escherichia coli. , 0, , .		0
20193	AnÃlisis de la estructura de una red de conocimiento en MÃ©xico. Revista De Ciencias Sociales, 2016, 21, .	0.1	0
20197	Integrated Bioinformatics Approach Reveals Crosstalk Between Tumor Stroma and Peripheral Blood Mononuclear Cells in Breast Cancer. Asian Pacific Journal of Cancer Prevention, 2016, 17, 1003-1008.	0.5	1
20204	webANIMO: Improving the accessibility of ANIMO. F1000Research, 0, 5, 1714.	0.8	1
20211	Bioinformatics analysis for drug repositioning. The Korean Journal of Public Health, 2016, 53, 19-27.	0.2	0
20212	Identification of multiple key genes involved in pathogen defense and multi-stress tolerance using microarray and network analysis. Journal of Plant Biotechnology, 2016, 43, 347-358.	0.1	4
20216	The complexity of genome integration process in human lentivirus. Revista De La Academia Colombiana De Ciencias Exactas, Físicas Y Naturales, 2016, 40, 382.	0.0	0

#	ARTICLE	IF	CITATIONS
20229	Scientific Databases. , 2017, , 1-6.		0
20230	2DIs: A SBML Compliant Web Platform for the Design and Modeling of Immune System Interactions. Lecture Notes in Computer Science, 2017, , 145-154.	1.0	0
20232	A Flexible Approach for Finding Optimal Paths with Minimal Conflicts. Lecture Notes in Computer Science, 2017, , 209-225.	1.0	2
20234	Genome and Transcriptome-Wide Research of Brain Evolution. Diversity and Commonality in Animals, 2017, , 187-212.	0.7	0
20237	Network Pharmacology of JinChaiKangBingDu Capsule Against Influenza A (H1N1) Virus Infection. , 2017, , ,		0
20238	Plug-and-Play Macroscopes: Network Workbench (NWB), Science of Science Tool (Sci2), and Epidemiology Tool (EpiC). , 2017, , 1-11.		0
20239	Computational Methods for Prediction of Protein-Protein Interactions. , 2017, , 309-340.		0
20240	Improvement of Generic Skills by Working in Diverse Groups and Establishment of Students's Evaluation Approaches. Journal of Jsee, 2017, 65, 1_58-1_65.	0.0	0
20241	A Semi-automatic Approach for Tech Mining and Interactive Taxonomy Visualization. Lecture Notes in Computer Science, 2017, , 102-115.	1.0	0
20242	Tutorial on Protein Ontology Resources. Methods in Molecular Biology, 2017, 1558, 57-78.	0.4	2
20255	Interinstitutional collaboration for end-user bioinformatics training: Cytoscape as a case study. Journal of the Medical Library Association: JMLA, 2017, 105, 179-184.	0.6	7
20266	An indicator cell assay for blood-based diagnostics. PLoS ONE, 2017, 12, e0178608.	1.1	0
20282	Interactome Analysis of 11-Dehydrosinulariolide-Treated Oral Carcinoma Cell Lines Such as Ca9-22 and CAL-27 and Melanoma Cell Line. International Journal of Cancer Management, 2017, 10, .	0.2	2
20284	dot-app: a Graphviz-Cytoscape conversion plug-in. F1000Research, 2016, 5, 2543.	0.8	2
20298	Identification of novel Ack1-interacting proteins and Ack1 phosphorylated sites in mouse brain by mass spectrometry. Oncotarget, 2017, 8, 101146-101157.	0.8	3
20301	Pathway Crosstalk Network Analysis Provides Insight Into Novel Pathways in Breast Cancer. Iranian Red Crescent Medical Journal, 2017, 19, .	0.5	0
20305	Maize phyllosphere microbial community niche development across stages of host leaf growth. F1000Research, 2017, 6, 1698.	0.8	5
20320	A Proposed Pharmacogenetic Solution for IT-Based Health Care. Lecture Notes in Networks and Systems, 2018, , 113-121.	0.5	0

#	ARTICLE	IF	CITATIONS
20323	Multi-Omics Insights into Functional Alterations of the Liver in Insulin-Deficient Diabetes Mellitus. SSRN Electronic Journal, 0, , .	0.4	0
20325	BioBroker: Knowledge Discovery Framework for Heterogeneous Biomedical Ontologies and Data. Journal of Intelligent Learning Systems and Applications, 2018, 10, 1-20.	0.4	5
20326	Bone Cancer: Dysregulation of Signaling Cascades by microRNAs. , 2018, , 119-128.		0
20327	Transcriptome Reveals That Genic SNPs Contributes to Heterosis in Cattle. , 2018, , .		1
20328	Emerging Technologies Serving Cytopathology. Advances in Medical Diagnosis, Treatment, and Care, 2018, , 114-152.	0.1	0
20329	Visual Methods and Tools for Social Network Analysis. , 2018, , 3298-3314.		0
20331	Scientific Databases. , 2018, , 3314-3319.		0
20332	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. SSRN Electronic Journal, 0, , .	0.4	0
20339	A National Initiative in Data Science for Health: An Evaluation of the UK Farr Institute. SSRN Electronic Journal, 0, , .	0.4	0
20340	Agent Perspective Social Networks: Distributed Second Degree Estimation. , 2018, , 29-40.		0
20341	Policy Directions to Induce Collaborative Research among Korean Domestic Biotechnology Researchers by Applying Co-author Network Analysis. Journal of Social Science, 2018, 29, 85-109.	0.0	0
20342	Plug-and-Play Macroscopes: Network Workbench (NWB), Science of Science Tool (Sci2), and Epidemiology Tool (EpiC). , 2018, , 1790-1800.		0
20343	Tulip 5. , 2018, , 3185-3212.		4
20350	FindPrimaryPairs: An efficient algorithm for predicting element-transferring reactant/product pairs in metabolic networks. PLoS ONE, 2018, 13, e0192891.	1.1	0
20365	An Exploratory Study of Radiation Dermatitis in Breast Cancer Patients. Anticancer Research, 2018, 38, 1615-1622.	0.5	4
20367	Meta-Analysis Of Brain And Central Nervous System Microarray Datasets. International Journal for Computational Biology, 2018, 7, 3.	0.1	0
20372	Transcriptome profiling of the interconnection of pathways involved in malignant transformation and response to hypoxia. Oncotarget, 2018, 9, 19730-19744.	0.8	1
20380	Automation of ReactomeFIViz via CyREST API. F1000Research, 2018, 7, 531.	0.8	0

#	ARTICLE	IF	CITATIONS
20384	Automation of ReactomeFIViz via CyREST API. F1000Research, 2018, 7, 531.	0.8	1
20385	Evaluating Academic Research Networks. Canadian Journal of Program Evaluation, 2018, 33, 69-89.	0.1	3
20387	ANIMA: Association network integration for multiscale analysis. Wellcome Open Research, 2018, 3, 27.	0.9	5
20391	Screening hub genes in coronary artery disease based on integrated analysis. Cardiology Journal, 2018, 25, 403-411.	0.5	6
20394	Analysis of Protein-Protein Interaction Network of Laminopathy Based on Topological Properties. Biomedical and Pharmacology Journal, 2018, 11, 1091-1103.	0.2	2
20403	Identifier Mapping in Cytoscape: idmapper. F1000Research, 2018, 7, 725.	0.8	5
20416	Co-expression network of secondary cell wall biogenesis genes in Eucalyptus tereticornis. Silvae Genetica, 2018, 67, 72-78.	0.4	3
20418	A Network Biology Approach for Assessing the Role of Pathologic Adipose Tissues in Insulin Resistance Using Meta-analysis of Microarray Datasets. Current Genomics, 2018, 19, 630-636.	0.7	3
20422	Network Analysis Tools. SpringerBriefs in Applied Sciences and Technology, 2019, , 1-4.	0.2	0
20432	Human Prolactinoma: A View of Protein-Protein Interaction Pattern. International Journal of Endocrinology and Metabolism, 2018, In Press, e67332.	0.3	8
20436	Specific Gene Expression and Small-Molecule Drug Investigation in Ankylosing Spondylitis under Interferon- $\beta$ Stimulation. International Journal of Pharmacology, 2018, 14, 1020-1028.	0.1	0
20445	Providing gene-to-variant and variant-to-gene database identifier mappings to use with BridgeDb mapping services.. F1000Research, 0, 7, 1390.	0.8	1
20455	A unified GenomeSpace recipe to identify essential genes and associated subnetworks from Genome-Scale CRISPR-Cas9 knockout screens. F1000Research, 0, 7, 1636.	0.8	0
20479	Celastrol Binds to HSP90 Trigger Functional Protein Interaction Network Against Pancreatic Cancer. Advances in Intelligent Systems and Computing, 2019, , 413-419.	0.5	0
20497	Mikrobak $\pi$ z $\pi$ ss $\pi$ gek metabolikus aktivit $\pi$ sa $\pi$ s 16S rRNS g $\pi$ n alap $\pi$ e filogenetikai diverzit $\pi$ sa kukorica monokult $\pi$ ra rizoszf $\pi$ ra-talajban. Agrokemia Es Talajtan, 2018, 67, 227-244.	0.1	0
20498	Robustness Through Regime Flips in Collapsing Ecological Networks. Studies in Computational Intelligence, 2019, , 841-853.	0.7	0
20500	Applications of Computational Systems Biology in Cancer Signaling Pathways. , 2019, , 513-537.		0
20501	Status and Prospects of Systems Biology in Grapevine Research. Compendium of Plant Genomes, 2019, , 137-166.	0.3	2

#	ARTICLE	IF	CITATIONS
20502	[Special Issue for Honor Award dedicating to Prof Kimito Funatsu]Prediction of Metabolite Activities by Repetitive Clustering of the Structural Similarity Based Networks. Journal of Computer Aided Chemistry, 2019, 20, 76-83.	0.3	0
20503	A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development. SSRN Electronic Journal, 0, , .	0.4	5
20507	Genes Associated with Disease-Free Survival Prognosis of Renal Cancers. , 2019, , 221-234.		0
20510	Plantâ€™Microbe Interaction: Gene-to-Metabolite Network. , 2019, , 75-100.		4
20514	Ultrahigh-Density Screens for Genome-Wide Yeast EMAPs in a Single Plate. Methods in Molecular Biology, 2019, 2049, 73-85.	0.4	0
20515	Inefficient Secretion of Anti-Sigma Factor FlgM Inhibits Bacterial Motility at High Temperature. SSRN Electronic Journal, 0, , .	0.4	0
20516	ggenealogy: An R Package for Visualizing Genealogical Data. Journal of Statistical Software, 2019, 89, .	1.8	3
20517	Landscape of the &lt;i>Plasmodium</i> Interactome. SSRN Electronic Journal, 0, , .	0.4	1
20518	Three-Dimensional Cell Culture and Tissue Restoration of Neural Stem Cells Under Microgravity. Research for Development, 2019, , 235-279.	0.2	1
20519	Systems biology in inflammatory bowel diseases: on the way to precision medicine. Annals of Gastroenterology, 2019, 32, 233-246.	0.4	7
20520	Analysing Cancer Signalling Pathways: A Structural Bioinformatics Approach. , 2019, , 271-293.		1
20521	A Novel Curriculum Visualization Method Using a Combination of Competencies, Cosine Similarity, Multidimensional Scaling Methods, and Scatter Plotting. Information Engineering Express, 2019, 5, 127-143.	0.2	2
20523	Enhancing gene set enrichment using networks. F1000Research, 2019, 8, 129.	0.8	4
20524	The Circadian Protein Nocturnin Regulates Metabolic Adaptation in Brown Adipose Tissue. SSRN Electronic Journal, 0, , .	0.4	0
20526	Transcriptional Signatures of Progressive Neuropathology in Transgenic Models of Tau and Amyloid Pathology. SSRN Electronic Journal, 0, , .	0.4	0
20528	NAMPT Antagonizes Tegument Protein Incorporation to Restrict Herpesvirus Lytic Replication. SSRN Electronic Journal, 0, , .	0.4	0
20529	Identification of Candidate Biomarkers and Pathways Associated with Liver Cancer by Bioinformatics Analysis. Lecture Notes in Computer Science, 2019, , 547-557.	1.0	0
20530	Gene Regulatory Networks: Current Updates and Applications in Plant Biology. Energy, Environment, and Sustainability, 2019, , 395-417.	0.6	2

#	ARTICLE	IF	CITATIONS
20531	Can Greenbergian universals be induced from language networks?. , 2019, , .		2
20532	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
20533	Role and Applications of Bioinformatics in Improvement of Nutritional Quality and Yield of Crops. Concepts and Strategies in Plant Sciences, 2019, , 485-498.	0.6	0
20534	The analysis of a time-course transcriptome profile by systems biology approaches reveals key molecular processes in acute kidney injury. Journal of Research in Medical Sciences, 2019, 24, 3.	0.4	2
20535	Bioinformatics Analysis of Key Genes and Pathways for Medulloblastoma as a Therapeutic Target. Asian Pacific Journal of Cancer Prevention, 2019, 20, 221-227.	0.5	4
20536	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0
20537	Corporate governance, CSR and financial performances: What types of relationships exist between these dimensions?. , 2019, , .		1
20538	Rapid, Progressive Sub-Graph Explorations for Interactive Visual Analytics over Large-Scale Graph Datasets. , 2019, , .		0
20539	Formal model of the interplay between TGF- $\beta$ 1 and MMP-9 and their dynamics in hepatocellular carcinoma. Mathematical Biosciences and Engineering, 2019, 16, 3285-3310.	1.0	6
20540	Mobile Health Applications and Cloud Computing in Cytopathology. Advances in Healthcare Information Systems and Administration Book Series, 2019, , 165-202.	0.2	3
20543	High-Resolution Streaming Functionality in SAGE2 Screen Sharing. Lecture Notes in Networks and Systems, 2020, , 384-399.	0.5	1
20564	Y $\ddot{a}$ rksek $\ddot{a}$ retim Program $\ddot{a}$ Tercihlerinin $\ddot{a}$ ncelenmesinde Karma $\ddot{a}$ k A $\ddot{y}$ Analizi Yakla $\ddot{a}$ m $\ddot{a}$ . Bitlis Eren $\ddot{a}$ eniversitesi Fen Bilimleri Dergisi, 2019, 8, 176-186.	0.1	0
20566	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. F1000Research, 2018, 7, 1906.	0.8	3
20568	MSF: Modulated Sub-graph Finder. F1000Research, 0, 7, 1346.	0.8	1
20572	Targeting Negative Regulators of TRIF-dependent TLR Signaling Pathway as a Novel Therapeutic Strategy. Current Signal Transduction Therapy, 2019, 14, 49-54.	0.3	0
20575	Identification of CDKN3 and UBE2C mRNAs as Prognostic Biomarkers in Early-Stage Lung Adenocarcinoma Using Bioinformatics Strategy. Iranian Red Crescent Medical Journal, 2019, In Press, .	0.5	0
20577	Complejidad de la expresi $\ddot{a}$ n de genes asociados a obesidad en el tejido adiposo humano. Revista Med, 2019, 26, 14-25.	0.1	1
20579	Positively Selected Orthologous Genes Identified in Sesame ( <i>Sesamum indicum</i> ) by Deep Resequencing. Plant Breeding and Biotechnology, 2019, 7, 24-33.	0.3	0



#	ARTICLE	IF	CITATIONS
20589	MSF: Modulated Sub-graph Finder. F1000Research, 2018, 7, 1346.	0.8	1
20591	Microarray-based differential expression profiling of long noncoding RNAs and messenger RNAs in formalin-fixed paraffin-embedded human papillary thyroid carcinoma samples. Translational Cancer Research, 2019, 8, 439-451.	0.4	2
20593	Transkriptom Verisi ve Omik Arařlar Kullarıarak Otoimmün Hastalar ile İnsan Baırsak Mikrobiyotası Arasındaki İlişkinin Analizi. Journal of Natural and Applied Sciences, 0, , 20-29.	0.1	0
20596	Using <i>Ipomoea aquatic</i> as an environmental-friendly alternative to <i>Elodea nuttallii</i> for the aquaculture of Chinese mitten crab. PeerJ, 2019, 7, e6785.	0.9	6
20600	The Combination of the CIGB-300 Anticancer Peptide and Cisplatin Modulates Proteins Related to Cell Survival, DNA Repair and Metastasis in a Lung Cancer Cell Line Model. Current Proteomics, 2019, 16, 338-349.	0.1	0
20611	Computational Methods to Identify Transcription Factor Binding Sites Using CAGE Information. , 2019, , 137-152.		0
20613	Protein-Protein interaction network analyses of human WNT proteins involved in neural development. Bioinformatics, 2019, 15, 307-314.	0.2	11
20614	Integrating species and interactions into similarity metrics: a graph theory-based approach to understanding community similarity. PeerJ, 2019, 7, e7013.	0.9	4
20647	High-throughput Exploration of the Network Dependent on AKT1 in Mouse Ovarian Granulosa Cells. Molecular and Cellular Proteomics, 2019, 18, 1307-1319.	2.5	8
20651	Graphical Animations of the Suzuki-Kasami Distributed Mutual Exclusion Protocol. , 2019, , .		0
20652	Interpreting and integrating big data in non-coding RNA research. Emerging Topics in Life Sciences, 2019, 3, 343-355.	1.1	2
20653	On Quantitative Comparison of Chemical Reaction Network Models. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 296, 14-27.	0.8	1
20668	Transcriptome and Network Dissection of Microsatellite Stable and Highly Instable Colorectal Cancer. Asian Pacific Journal of Cancer Prevention, 2019, 20, 2445-2454.	0.5	1
20669	Competitive endogenous RNA network identifies four long non-coding RNA signature as a candidate prognostic biomarker for lung adenocarcinoma. Translational Cancer Research, 2019, 8, 1046-1064.	0.4	6
20673	Breast Cancer Interaction Network Concept from Mostly Related Components. , 2019, 8, 1298.		4
20675	Survival-based bioinformatics analysis to identify hub genes and key pathways in non-small cell lung cancer. Translational Cancer Research, 2019, 8, 1188-1198.	0.4	2
20676	A 4-miRNA signature act as a novel prognostic biomarker in patients with Sarcoma. Translational Cancer Research, 2019, 8, 1412-1422.	0.4	2
20686	Evaluation of the target genes of arsenic trioxide in pancreatic cancer by bioinformatics analysis. Oncology Letters, 2019, 18, 5163-5172.	0.8	4

#	ARTICLE	IF	CITATIONS
20688	GizMO -- A Customizable Representation Model for Graph-Based Visualizations of Ontologies. , 2019, , .		1
20689	RC-Network and Comm-Network for Improvement of Research Collaboration and Communication Among Delhi University Teachers. <i>Asset Analytics</i> , 2020, , 227-236.	0.4	0
20696	Identification of prognostic biomarkers for malignant melanoma using microarray datasets. <i>Oncology Letters</i> , 2019, 18, 5243-5254.	0.8	3
20697	Network-based Observability and Controllability Analysis of Dynamical Systems: the NOCAD toolbox. <i>F1000Research</i> , 2019, 8, 646.	0.8	0
20699	Construction of a model to predict the prognosis of patients with cholangiocarcinoma using alternative splicing events. <i>Oncology Letters</i> , 2019, 18, 4677-4690.	0.8	3
20713	Investigating Therapeutic Effects of Retinoic Acid on Thyroid Cancer via Protein-Protein Interaction Network Analysis. <i>International Journal of Cancer Management</i> , 2019, 12, .	0.2	0
20718	De Novo Pathway Enrichment with KeyPathwayMiner. <i>Methods in Molecular Biology</i> , 2020, 2074, 181-199.	0.4	3
20731	Predicting Synthetic Lethal Genetic Interactions in Breast Cancer using Decision Tree. , 2019, , .		1
20732	Sistemas de innovaci3n y resiliencia regional: un an3lisis de redes. <i>Revista Espanola De Sociologia</i> , 2019, 28, 35-52.	0.1	3
20733	In-silico Gene Annotation Prediction Using the Co-expression Network Structure. <i>Studies in Computational Intelligence</i> , 2020, , 802-812.	0.7	5
20736	Networks of Function and Shared Ancestry Provide Insights into Diversification of Histone Fold Domain in the Plant Kingdom. <i>Studies in Computational Intelligence</i> , 2020, , 789-801.	0.7	0
20746	Using Transcriptional Signatures to Find Cancer Drivers with LURE. , 2019, , .		3
20748	miR7705p modulates resistance to methotrexate in human colorectal adenocarcinoma cells by downregulating HIPK1. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 339-346.	0.8	10
20752	Transcriptional Differences of Coding and Non-Coding Genes Related to the Absence of Melanocyte in Skins of Bama Pig. <i>Genes</i> , 2020, 11, 47.	1.0	4
20754	Identification of key candidate tumor biomarkers in non-small cell lung cancer by in silico analysis. <i>Oncology Letters</i> , 2020, 19, 1008-1016.	0.8	4
20765	Integrated Analysis Revealed Prognostic Factors for Prostate Cancer Patients. <i>Medical Science Monitor</i> , 2019, 25, 9991-10007.	0.5	1
20768	Token-Curated Registry with Citation Graph. <i>Ledger</i> , 0, 4, .	0.0	2
20772	In silico identification of EP400 and TIA1 as critical transcription factors involved in human hepatocellular carcinoma relapse. <i>Oncology Letters</i> , 2020, 19, 952-964.	0.8	6

#	ARTICLE	IF	CITATIONS
20774	Jarvis: A Multimodal Visualization Tool for Bioinformatic Data. <i>Lecture Notes in Computer Science</i> , 2020, , 104-116.	1.0	1
20776	PLAG1 silencing promotes cell chemosensitivity in ovarian cancer via the IGF2 signaling pathway. <i>International Journal of Molecular Medicine</i> , 2020, 45, 703-714.	1.8	5
20784	Empty SV40 capsids increase survival of septic rats by eliciting numerous host signaling networks that participate in a number of systemic functions. <i>Oncotarget</i> , 2020, 11, 574-588.	0.8	0
20787	Exosomal proteome from the serum, bone marrow, and palm and toe pustular skin tissues of a single patient with SAPHO syndrome. <i>Journal of Proteomics</i> , 2020, 216, 103673.	1.2	1
20792	Deciphering the expression dynamics of ANGPTL8 associated regulatory network in insulin resistance using formal modelling approaches. <i>IET Systems Biology</i> , 2020, 14, 47-58.	0.8	1
20795	Two cases of type-a <i>Haemophilus influenzae</i> meningitis within the same week in the same hospital are phylogenetically unrelated but recently exchanged capsule genes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3
20796	STAT1 is a modulator of the expression of frequently rearranged in advanced Tâ€cell lymphomas; ½1 expression in U251 cells. <i>Oncology Letters</i> , 2020, 20, 248-256.	0.8	0
20806	Open-source Software Sustainability Models: Initial White Paper From the Informatics Technology for Cancer Research Sustainability and Industry Partnership Working Group. <i>Journal of Medical Internet Research</i> , 2021, 23, e20028.	2.1	2
20810	Proteomics analysis of important molecules in serum from meningitic piglets caused by <i>Streptococcus suis</i> serotype 2. <i>Journal of Infection in Developing Countries</i> , 2020, 14, 502-510.	0.5	3
20813	Bioinformatics analysis of the network of histone H3 lysine 9 trimethylation in acute myeloid leukaemia. <i>Oncology Reports</i> , 2020, 44, 543-554.	1.2	4
20824	Identification of lncRNA and mRNA Biomarkers in Osteoarthritic Degenerative Meniscus by Weighted Gene Coexpression Network and Competing Endogenous RNA Network Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	5
20828	Structure and Reaction Mechanism of YcjR, an Epimerase That Facilitates the Interconversion of d-Gulosides to d-Glucosides in <i>Escherichia coli</i> . <i>Biochemistry</i> , 2020, 59, 2069-2077.	1.2	0
20829	Comprehensive analysis of the differential expression profile of microRNAs in rats with spinal cord injury treated by electroacupuncture. <i>Molecular Medicine Reports</i> , 2020, 22, 751-762.	1.1	7
20839	Upregulated expression of MMP family genes is associated with poor survival in patients with esophageal squamous cell carcinoma via regulation of proliferation and epithelialâ€mesenchymal transition. <i>Oncology Reports</i> , 2020, 44, 29-42.	1.2	2
20849	Identification of Target Genes and Transcription Factors in Mice with LMNA-Related Dilated Cardiomyopathy by Integrated Bioinformatic Analyses. <i>Medical Science Monitor</i> , 2020, 26, e924576.	0.5	1
20859	Identification of SPRR3 as a novel diagnostic/prognostic biomarker for oral squamous cell carcinoma via RNA sequencing and bioinformatic analyses. <i>PeerJ</i> , 2020, 8, e9393.	0.9	11
20860	Integrative analysis of competitive endogenous RNA network reveals the regulatory role of non-coding RNAs in high-glucose-induced human retinal endothelial cells. <i>PeerJ</i> , 2020, 8, e9452.	0.9	6
20862	Risk gene identification and support vector machine learning to construct an early diagnosis model of myocardial infarction. <i>Molecular Medicine Reports</i> , 2020, 22, 1775-1782.	1.1	4

#	ARTICLE	IF	CITATIONS
20863	Chestnut polysaccharides benefit spermatogenesis through improvement in the expression of important genes. <i>Aging</i> , 2020, 12, 11431-11445.	1.4	13
20868	Stress response in periodontal ligament stem cells may contribute to bisphosphonate-associated osteonecrosis of the jaw: A gene expression array analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 2043-2051.	1.1	2
20871	Current Update on the Risk Factor Modification and Exercise Following Coronary Artery Disease. <i>Biomolecular and Health Science Journal</i> , 2020, 3, 56.	0.1	1
20872	Hepatoprotective effects of <i>Hovenia dulcis</i> seeds against alcoholic liver injury and related mechanisms investigated via network pharmacology. <i>World Journal of Gastroenterology</i> , 2020, 26, 3432-3446.	1.4	7
20874	Comprehensive multi-factors reveal the pathogenesis of degenerative intervertebral disc. <i>Cellular and Molecular Biology</i> , 2020, 66, 65-71.	0.3	1
20877	Identification of glioblastoma-specific prognostic biomarkers via an integrative analysis of DNA methylation and gene expression. <i>Oncology Letters</i> , 2020, 20, 1619-1628.	0.8	4
20879	Assessment of the Microbiome Role in Skin Protection Against UV Irradiation Via Network Analysis. <i>Journal of Lasers in Medical Sciences</i> , 2020, 11, 238-242.	0.4	6
20882	Expression profiling of small intestinal neuroendocrine tumors identified pathways and gene networks linked to tumorigenesis and metastasis. <i>Bioscience Reports</i> , 2020, 40, .	1.1	6
20883	Wide-ranging analysis of survival-related alternative splicing events in invasive breast carcinoma. <i>Oncology Letters</i> , 2020, 20, 1866-1878.	0.8	1
20889	Identification of Target Genes Related to Sulfasalazine in Triple-Negative Breast Cancer Through Network Pharmacology. <i>Medical Science Monitor</i> , 2020, 26, e926550.	0.5	5
20891	Bioinformatic screening and identification of downregulated hub genes in adrenocortical carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 2730-2742.	0.8	2
20893	Identifying the Medical Lethality of Suicide Attempts Using Network Analysis and Deep Learning: Nationwide Study. <i>JMIR Medical Informatics</i> , 2020, 8, e14500.	1.3	4
20895	Thyrotropin receptor signaling deficiency impairs spatial learning and memory in mice. <i>Journal of Endocrinology</i> , 2020, 246, 41-55.	1.2	13
20900	iNOA. , 2020, , .		0
20903	Changes in the Microbial Community of the Mottled Skate ( <i>Beringraja pulchra</i> ) During Alkaline Fermentation. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 1195-1206.	0.9	4
20909	Identification of key pathways and genes shared between Crohn's disease and breast cancer using bioinformatics analysis. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	7
20915	COL3A1, COL6A3, and SERPINH1 Are Related to Glucocorticoid-Induced Osteoporosis Occurrence According to Integrated Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2020, 26, e925474.	0.5	3
20916	Dysregulation of microRNA in cholangiocarcinoma identified through a meta-analysis of microRNA profiling. <i>World Journal of Gastroenterology</i> , 2020, 26, 4356-4371.	1.4	6

#	ARTICLE	IF	CITATIONS
20921	VIRdb 2.0: Interactive analysis of comorbidity conditions associated with vitiligo pathogenesis using co-expression network-based approach. <i>F1000Research</i> , 2020, 9, 1055.	0.8	1
20932	A Systematic Review on Complex Networks and its Performance Evaluation Metrics. <i>International Journal of Computer Applications</i> , 2020, 175, 27-37.	0.2	0
20933	Expression and regulatory network of miRNAs in head and neck squamous cell carcinoma. <i>Translational Cancer Research</i> , 2020, 9, 4607-4617.	0.4	1
20934	<i>Cuscuta</i> sect. <i>Californicae</i> (Convolvulaceae) Revisited: Cryptic Speciation and Host Range Differentiation. <i>Systematic Botany</i> , 2020, 45, 638-651.	0.2	5
20937	Using bioinformatics and metabolomics to identify altered granulosa cells in patients with diminished ovarian reserve. <i>PeerJ</i> , 2020, 8, e9812.	0.9	9
20940	Investigating the correlation between DNA methylation and immune-associated genes of lung adenocarcinoma based on a competing endogenous RNA network. <i>Molecular Medicine Reports</i> , 2020, 22, 3173-3182.	1.1	3
20942	Genome-Wide Imaging-Based Phenomic Screening Using Yeast ( <i>Saccharomyces cerevisiae</i> ) Strain Collections. <i>Methods in Molecular Biology</i> , 2021, 2196, 85-95.	0.4	0
20944	Comparative transcriptome analysis of gynoeious and monoecious inflorescences reveals regulators involved in male flower development in the woody perennial plant <i>Jatropha curcas</i> . <i>Plant Reproduction</i> , 2020, 33, 191-204.	1.3	5
20947	Cell spinpods are a simple inexpensive suspension culture device to deliver fluid shear stress to renal proximal tubular cells. <i>Scientific Reports</i> , 2021, 11, 21296.	1.6	2
20948	TP53 Mutation Is a Prognostic Factor in Lower Grade Glioma and May Influence Chemotherapy Efficacy. <i>Cancers</i> , 2021, 13, 5362.	1.7	13
20949	Identification of Potential Novel Prognosis-Related Genes Through Transcriptome Sequencing, Bioinformatics Analysis, and Clinical Validation in Acute Myeloid Leukemia. <i>Frontiers in Genetics</i> , 2021, 12, 723001.	1.1	4
20950	Identification of sheep lncRNAs related to the immune response to vaccines and aluminium adjuvants. <i>BMC Genomics</i> , 2021, 22, 770.	1.2	1
20951	Dysbiosis and structural disruption of the respiratory microbiota in COVID-19 patients with severe and fatal outcomes. <i>Scientific Reports</i> , 2021, 11, 21297.	1.6	48
20953	Screening of characteristic genes in ulcerative colitis by integrating gene expression profiles. <i>BMC Gastroenterology</i> , 2021, 21, 415.	0.8	2
20954	Quantitative proteomic analysis of hepatic tissue in allotetraploid hybridized from red crucian carp and common carp identified crucial proteins and pathways associated with metabolism and growth rate. <i>Proteomics</i> , 2022, 22, e2100115.	1.3	3
20956	Biogeography of Bacterial Communities and Specialized Metabolism in Human Aerodigestive Tract Microbiomes. <i>Microbiology Spectrum</i> , 2021, 9, e0166921.	1.2	3
20957	A five-gene methylation signature predicts overall survival of patients with clear cell renal cell carcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24031.	0.9	2
20958	Disrupted PGR-B and ESR1 signaling underlies defective decidualization linked to severe preeclampsia. <i>ELife</i> , 2021, 10, .	2.8	15

#	ARTICLE	IF	CITATIONS
20959	Proteo-transcriptomics meta-analysis identifies SUMO2 as a promising target in glioblastoma multiforme therapeutics. <i>Cancer Cell International</i> , 2021, 21, 575.	1.8	1
20960	Anticipate, Target and Characterize: MS <sup>2</sup> -anticipated C-glycosylflavones from <i>Erythrococca anomala</i> . <i>Planta Medica International Open</i> , 2021, 8, e131-e142.	0.3	1
20961	RNA Sequencing Reveals Phenylpropanoid Biosynthesis Genes and Transcription Factors for <i>Hevea brasiliensis</i> Reaction Wood Formation. <i>Frontiers in Genetics</i> , 2021, 12, 763841.	1.1	9
20962	Multi-Omics Approach to Elucidate Cerebrospinal Fluid Changes in Dogs with Intervertebral Disc Herniation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11678.	1.8	3
20963	Long non-coding RNA profiles in plasma exosomes of patients with gastric high-grade intraepithelial neoplasia. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 1.	0.8	10
20965	Network Pharmacological Dissection of the Mechanisms of <i>Eucommiae Cortex-Achyranthis Radix</i> Combination for Intervertebral Disc Herniation Treatment. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110550.	0.2	0
20966	Analysis of multiple gene co-expression networks to discover interactions favoring CFTR biogenesis and F508-CFTR rescue. <i>BMC Medical Genomics</i> , 2021, 14, 258.	0.7	2
20967	Transcriptome and metabolome analyses of response of <i>Synechocystis</i> sp. PCC 6803 to methyl viologen. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8377-8392.	1.7	2
20969	Identifying miRNA-mRNA Networks Associated With COPD Phenotypes. <i>Frontiers in Genetics</i> , 2021, 12, 748356.	1.1	12
20970	Oncogene-mediated metabolic gene signature predicts breast cancer outcome. <i>Npj Breast Cancer</i> , 2021, 7, 141.	2.3	20
20971	A miR-129-5P/ARID3A Negative Feedback Loop Modulates Diffuse Large B Cell Lymphoma Progression and Immune Evasion Through Regulating the PD-1/PD-L1 Checkpoint. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 735855.	1.8	4
20972	Profiling and Characterization of microRNAs Responding to Sodium Butyrate Treatment in Gastric Cancer Cells. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 1875-1888.	0.6	2
20974	Genome-wide identification, classification, and expression analysis of the JmjC domain-containing histone demethylase gene family in birch. <i>BMC Genomics</i> , 2021, 22, 772.	1.2	10
20975	Identification of Novel Kinase-Transcription Factor-mRNA-miRNA Regulatory Network in Nasopharyngeal Carcinoma by Bioinformatics Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7453-7469.	0.8	2
20977	Dynamic light- and acetate-dependent regulation of the proteome and lysine acetylome of <i>Chlamydomonas</i> . <i>Plant Journal</i> , 2022, 109, 261-277.	2.8	10
20978	SARS-CoV-2-host proteome interactions for antiviral drug discovery. <i>Molecular Systems Biology</i> , 2021, 17, e10396.	3.2	53
20980	Importance-Penalized Joint Graphical Lasso (IPJGL): differential network inference via GGMs. <i>Bioinformatics</i> , 2022, 38, 770-777.	1.8	2
20981	The impact of Hfq-mediated sRNA-mRNA interactome on the virulence of enteropathogenic <i>Escherichia coli</i> . <i>Science Advances</i> , 2021, 7, eabi8228.	4.7	22



#	ARTICLE	IF	CITATIONS
20982	ANAT 3.0: a framework for elucidating functional protein subnetworks using graph-theoretic and machine learning approaches. <i>BMC Bioinformatics</i> , 2021, 22, 526.	1.2	3
20984	A Multidisciplinary Approach to Unraveling the Natural Product Biosynthetic Potential of a <i>Streptomyces</i> Strain Collection Isolated from Leaf-Cutting Ants. <i>Microorganisms</i> , 2021, 9, 2225.	1.6	7
20985	Study on the Mechanism of Liuwei Dihuang Pills in Treating Parkinson's Disease Based on Network Pharmacology. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	6
20986	Ral GEF with the PH Domain and SH3 Binding Motif 1 Regulated by Splicing Factor Junction Plakoglobin and Pyrimidine Metabolism Are Prognostic in Uterine Carcinosarcoma. <i>Disease Markers</i> , 2021, 2021, 1-17.	0.6	1
20987	Automated Exploration of Prebiotic Chemical Reaction Space: Progress and Perspectives. <i>Life</i> , 2021, 11, 1140.	1.1	6
20988	QNBC Is Associated with High Genomic Instability Characterized by Copy Number Alterations and miRNA Deregulation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11548.	1.8	10
20989	Centrality of drug targets in protein networks. <i>BMC Bioinformatics</i> , 2021, 22, 527.	1.2	7
20991	Apolipoprotein D as a Potential Biomarker and Construction of a Transcriptional Regulatory-Immune Network Associated with Osteoarthritis by Weighted Gene Coexpression Network Analysis. <i>Cartilage</i> , 2021, 13, 1702S-1717S.	1.4	9
20992	Clinical values and potential pathways of miR-183-5p in gastric cancer: a study based on integrational bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 2123-2131.	0.6	2
20993	Resistin forms a network with inflammatory cytokines and is associated with prognosis in major burns. <i>Burns</i> , 2022, 48, 1680-1689.	1.1	4
20994	Selecting Hub Genes and Predicting Target Genes of microRNAs in Tuberculosis via the Bioinformatics Analysis. <i>Genetical Research</i> , 2021, 2021, 1-11.	0.3	3
20996	Screening and cellular validation of prognostic genes regulated by super enhancers in oral squamous cell carcinoma. <i>Bioengineered</i> , 2021, 12, 10073-10088.	1.4	4
20997	Independent transcriptomic and proteomic networks reveal common differentially expressed chaperone and interactor genes during tomato cv. Micro-Tom fruit ripening. <i>Plant Gene</i> , 2021, 28, 100346.	1.4	4
20998	Multiple pathways are responsible to the inhibitory effect of butorphanol on OGD/R-induced apoptosis in AC16 cardiomyocytes. <i>Journal of Applied Toxicology</i> , 2021, , .	1.4	2
21001	COMPUTATIONAL APPROACHES FOR DRUG DISCOVERY FROM MEDICINAL PLANTS IN THE ERA OF DATA DRIVEN RESEARCH. <i>Indian Drugs</i> , 2021, 58, 7-23.	0.1	0
21002	Changes in Porcine Corpus Luteum Proteome Associated with Development, Maintenance, Regression, and Rescue during Estrous Cycle and Early Pregnancy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11740.	1.8	5
21003	A sugarcane smut fungus effector simulates the host endogenous elicitor peptide to suppress plant immunity. <i>New Phytologist</i> , 2022, 233, 919-933.	3.5	21
21004	Structure and diversity of fungal communities in long-term copper-contaminated agricultural soil. <i>Science of the Total Environment</i> , 2022, 806, 151302.	3.9	20

#	ARTICLE	IF	CITATIONS
21005	Integrated bioinformatics analysis of the anti-atherosclerotic mechanisms of the polysaccharide CM1 from <i>Cordyceps militaris</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 193, 1274-1285.	3.6	8
21006	Complex Network Analysis in Microbial Systems: Theory and Examples. <i>Methods in Molecular Biology</i> , 2022, 2349, 167-191.	0.4	1
21007	Overlapping haplotype blocks indicate shared genomic regions between a composite beef cattle breed and its founder breeds. <i>Livestock Science</i> , 2021, 254, 104747.	0.6	0
21008	Screening of potential hub genes in pulmonary thromboembolism. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 18.	0.8	1
21009	Fecal Microbiota Transplantation Commonly Failed in Children With Co-Morbidities. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2022, 74, 227-235.	0.9	4
21010	Identification of biomarkers and ceRNA network in glioblastoma through bioinformatic analysis and evaluation of potential prognostic values. <i>Annals of Translational Medicine</i> , 2021, 9, 1561-1561.	0.7	3
21011	Statin-mediated disruption of Rho GTPase prenylation and activity inhibits respiratory syncytial virus infection. <i>Communications Biology</i> , 2021, 4, 1239.	2.0	5
21012	Individualized Proteogenomics Reveals the Mutational Landscape of Melanoma Patients in Response to Immunotherapy. <i>Cancers</i> , 2021, 13, 5411.	1.7	1
21013	Inhibition of Soluble Epoxide Hydrolase Is Protective against the Multiomic Effects of a High Glycemic Diet on Brain Microvascular Inflammation and Cognitive Dysfunction. <i>Nutrients</i> , 2021, 13, 3913.	1.7	14
21014	High-quality reference genome and annotation aids understanding of berry development for evergreen blueberry ( <i>Vaccinium darrowii</i> ). <i>Horticulture Research</i> , 2021, 8, 228.	2.9	17
21015	Multidimensional Mutational Profiling of the Indian HNSCC Sub-Population Provides IRAK1, a Novel Driver Gene and Potential Druggable Target. <i>Frontiers in Oncology</i> , 2021, 11, 723162.	1.3	7
21016	Cytotoxic and Antifungal Amides Derived from Ferulic Acid: Molecular Docking and Mechanism of Action. <i>BioMed Research International</i> , 2021, 2021, 1-18.	0.9	6
21017	Salinity Drives Functional and Taxonomic Diversities in Global Water Metagenomes. <i>Frontiers in Microbiology</i> , 2021, 12, 719725.	1.5	6
21018	Low Expression of SLC7A11 Confers Drug Resistance and Worse Survival in Ovarian Cancer via Inhibition of Cell Autophagy as a Competing Endogenous RNA. <i>Frontiers in Oncology</i> , 2021, 11, 744940.	1.3	9
21019	Identification of Cross-Pathway Connections via Protein-Protein Interactions Linked to Altered States of Metabolic Enzymes in Cervical Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 736495.	1.2	3
21020	ANXA1 (Annexin A1) regulated by MYC (MYC proto-oncogene) promotes the growth of papillary thyroid carcinoma. <i>Bioengineered</i> , 2021, 12, 9251-9265.	1.4	10
21021	Identification of hub genes associated with cognition in the hippocampus of Alzheimer's Disease. <i>Bioengineered</i> , 2021, 12, 9598-9609.	1.4	12
21022	Metabolomic profiling of <i>Burkholderia cenocepacia</i> in synthetic cystic fibrosis sputum medium reveals nutrient environment-specific production of virulence factors. <i>Scientific Reports</i> , 2021, 11, 21419.	1.6	9

#	ARTICLE	IF	CITATIONS
21023	Transcriptome and Exome Analyses of Hepatocellular Carcinoma Reveal Patterns to Predict Cancer Recurrence in Liver Transplant Patients. <i>Hepatology Communications</i> , 2022, 6, 710-727.	2.0	9
21024	Gene regulation by morpholines and piperidines in the cardiac embryonic stem cell test. <i>Toxicology and Applied Pharmacology</i> , 2021, 433, 115781.	1.3	1
21025	Sub-chronic low-dose arsenic in rice exposure induces gut microbiome perturbations in mice. <i>Ecotoxicology and Environmental Safety</i> , 2021, 227, 112934.	2.9	19
21026	Identification of modules based on integrative analysis for drug prediction in colorectal cancer. <i>Gene Reports</i> , 2021, 25, 101403.	0.4	0
21027	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	0
21031	Integrative analysis of an lncRNA-associated competing endogenous RNA network in human trabecular meshwork cells under oxidative stress. <i>Molecular Medicine Reports</i> , 2020, 21, 1606-1614.	1.1	10
21033	Stochastic Mechanisms of Information Flow in Phosphate Economy of <i>Escherichia coli</i> . <i>Lecture Notes in Computer Science</i> , 2020, , 131-145.	1.0	0
21035	Inferring Communities and Key Genes of Triple Negative Breast Cancer Based on Robust Principal Component Analysis and Network Analysis. <i>Communications in Computer and Information Science</i> , 2020, , 137-151.	0.4	0
21037	Genes Associated with Calcium Signaling are Involved in Alcohol-Induced Breast Cancer Growth. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 79-91.	1.4	0
21039	Analysis of differential expression of long non-coding RNAs in exosomes derived from mature and immature dendritic cells. <i>Molecular Medicine Reports</i> , 2020, 23, .	1.1	5
21047	Genomics- and Metabolomics-Based Investigation of the Deep-Sea Sediment-Derived Yeast, <i>Rhodotorula mucilaginosa</i> 50-3-19/20B. <i>Marine Drugs</i> , 2021, 19, 14.	2.2	15
21048	Identification of adriamycin resistance genes in breast cancer based on microarray data analysis. <i>Translational Cancer Research</i> , 2020, 9, 7486-7494.	0.4	1
21051	In Silico Repurposing of J147 for Neonatal Encephalopathy Treatment: Exploring Molecular Mechanisms of Mutant Mitochondrial ATP Synthase. <i>Current Pharmaceutical Biotechnology</i> , 2020, 21, 1551-1566.	0.9	5
21052	Novel therapeutic compounds for prostate adenocarcinoma treatment. <i>Medicine (United States)</i> , 2020, 99, e23768.	0.4	2
21053	ADAM10 promotes the proliferation of ligamentum flavum cells by activating the PI3K/AKT pathway. <i>International Journal of Molecular Medicine</i> , 2020, 47, 688-698.	1.8	7
21054	The Identification and Verification of Key Long Noncoding RNAs in Ischemic Stroke. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	7
21055	Network analysis of MicroRNA transcripts revealed relevant MicroRNAs and gene candidates for angiogenesis in gastric cancer. <i>Gene Reports</i> , 2020, 21, 100903.	0.4	0
21056	Gene Copy Number Variation Does Not Reflect Structure or Environmental Selection in Two Recently Diverged California Populations of <i>Suillus brevipes</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4591-4597.	0.8	2

#	ARTICLE	IF	CITATIONS
21062	Comprehensive assessment of PD-L1 and PD-L2 dysregulation in gastrointestinal cancers. <i>Epigenomics</i> , 2020, 12, 2155-2171.	1.0	4
21065	Screening of <i>Plectranthus amboinicus</i> against COVID-19 " in silico approach. <i>Journal of Applied Pharmaceutical Science</i> , 0, , .	0.7	0
21067	Feature Selection for Topological Proximity Prediction of Single-Cell Transcriptomic Profiles in <i>Drosophila</i> Embryo Using Genetic Algorithm. <i>Genes</i> , 2021, 12, 28.	1.0	3
21068	Mapping protein networks in yeast mitochondria using proximity-dependent biotin identification coupled to proteomics. <i>STAR Protocols</i> , 2020, 1, 100219.	0.5	1
21071	Effect of a Traditional Chinese Medicine Formula (CoTOL) on Serum Uric Acid and Intestinal Flora in Obese Hyperuricemic Mice Inoculated with Intestinal Bacteria. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-10.	0.5	10
21074	Bioinformatics analysis of microenvironment-related genes associated with radioresistance in glioblastoma. <i>Translational Cancer Research</i> , 2020, 9, 7495-7504.	0.4	3
21075	Bioinformatics analysis identifies potential diagnostic signatures for coronary artery disease. <i>Journal of International Medical Research</i> , 2020, 48, 030006052097985.	0.4	2
21080	MNBDR: A Module Network Based Method for Drug Repositioning. <i>Genes</i> , 2021, 12, 25.	1.0	6
21083	Classification and phylogeny for the annotation of novel eukaryotic GNAT acetyltransferases. <i>PLoS Computational Biology</i> , 2020, 16, e1007988.	1.5	7
21085	Jie-Du-Hua-Yu Granules Promote Liver Regeneration in Rat Models of Acute Liver Failure: miRNA-mRNA Expression Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-11.	0.5	2
21087	Identification of the diagnostic signature of sepsis based on bioinformatic analysis of gene expression and machine learning. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, .	0.6	2
21088	Microbial community composition in the rhizosphere of <i>Larix decidua</i> under different light regimes with additional focus on methane cycling microorganisms. <i>Scientific Reports</i> , 2020, 10, 22324.	1.6	20
21090	Characterisation of gene and pathway expression in stabilised blood from children with coeliac disease. <i>BMJ Open Gastroenterology</i> , 2020, 7, e000536.	1.1	2
21091	Network Pharmacology Approach to Uncover the Mechanism Governing the Effect of Simiao Powder on Knee Osteoarthritis. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	22
21096	Identification of potential microRNAs in glioblastoma using bioinformatic analysis and prognostic evaluation. <i>Translational Cancer Research</i> , 2020, 9, 7432-7439.	0.4	0
21097	Knowledge Graph Visualization: Challenges, Framework, and Implementation. , 2020, , .		6
21098	Stiffness estimate of information propagation in biological systems modelled as spring networks. , 2020, , .		1
21099	Active Anaerobic Archaeal Methanotrophs in Recently Emerged Cold Seeps of Northern South China Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 612135.	1.5	10

#	ARTICLE	IF	CITATIONS
21103	Prognostic Hub Genes in the Immune Microenvironment of Lung Adenocarcinoma by Estimation. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 25, 77-89.	0.6	0
21104	Differential alternative splicing between hepatocellular carcinoma with normal and elevated serum alpha-fetoprotein. <i>BMC Medical Genomics</i> , 2020, 13, 194.	0.7	5
21106	Liver-Brain Axis in Sporadic Alzheimer's Disease: Role of Ten Signature Genes in a Mouse Model. <i>CNS and Neurological Disorders - Drug Targets</i> , 2021, 20, 871-885.	0.8	4
21107	A Workflow-Based Methodological Framework for Hybrid Human-AI Enabled Scientometrics. , 2020, , .		3
21108	Integrated transcriptomic and metabolomic analyses reveal regulation of terpene biosynthesis in the stems of <i>Sindora glabra</i> . <i>Tree Physiology</i> , 2021, 41, 1087-1102.	1.4	14
21109	Integrated Analysis of Key Pathways and Drug Targets Associated With Vogt-Koyanagi-Harada Disease. <i>Frontiers in Immunology</i> , 2020, 11, 587443.	2.2	11
21110	Biological Processes underlying the Reinforcing Primary Qi Delivered by Ginseng. , 2020, , .		0
21111	Quantitative Proteomic Profiling of Small Molecule Treated Mesenchymal Stem Cells Using Chemical Probes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 160.	1.8	2
21112	Mechanism of <i>Salviae Miltiorrhizae Radix et Rhizoma</i> in the Treatment of Knee Osteoarthritis Based on Network Pharmacology. <i>Natural Product Communications</i> , 2020, 15, 1934578X2098313.	0.2	0
21114	Analysis of pharmacological mechanisms of Yinyanghuo as treatment of erectile dysfunction with network pharmacology-based strategy. <i>Andrologia</i> , 2021, 53, e13943.	1.0	3
21115	Identification of a disease-specific gene expression profile of children with acute asthma by weighted gene co-expression network analysis. <i>Genes and Genetic Systems</i> , 2020, 95, 315-321.	0.2	1
21117	Transcriptional profiles of human islet and exocrine endothelial cells in subjects with or without impaired glucose metabolism. <i>Scientific Reports</i> , 2020, 10, 22315.	1.6	3
21121	An Analysis of Gene Regulatory Network Topology Using Results of DNA Microchip Experiments. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 130-144.	0.5	0
21124	Clibenzamide, ATP and metformin increases the expression of human bile salt export pump ABCB11. <i>F1000Research</i> , 2020, 9, 1497.	0.8	6
21127	Re-Exploring Biomarkers and Therapeutic Targets in Primary Melanoma Patients: Insights from Network-Based Analysis of Microarray Data. <i>Chinese Journal of Plastic and Reconstructive Surgery</i> , 2020, 2, 228-240.	0.1	0
21129	Drug compound prediction-based analysis of cigarette smoking to Pancreatic Cancer patients: A Bioinformatics study. , 2020, , .		1
21130	TMEM158 May Serve as a Diagnostic Biomarker for Anaplastic Thyroid Carcinoma: An Integrated Bioinformatic Analysis. <i>Current Medical Science</i> , 2020, 40, 1137-1147.	0.7	3
21132	Construction of competitive endogenous RNA network related to circular RNA and prognostic nomogram model in lung adenocarcinoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 9806-9821.	1.0	0

#	ARTICLE	IF	CITATIONS
21133	Age-Associated Induction of Senescent Transcriptional Programs in Human Glial Progenitor Cells. SSRN Electronic Journal, 0, , .	0.4	0
21134	Carbonic Anhydrase IX Interactome and the Regulation of Cancer Progression. Progress in Drug Research Fortschritte Der Arzneimittelforschung Progres Des Recherches Pharmaceutiques, 2021, , 179-204.	0.6	0
21135	Diverse single-stranded DNA viruses identified in New Zealand (Aotearoa) South Island robin (Petroica) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	13
21136	Global Lysine Acetylome Analysis of Flower bud Development in Catalpa bungei. Phyton, 2022, 91, 507-524.	0.4	1
21137	High ORAI3 expression correlates with good prognosis in human muscle-invasive bladder cancer. Gene, 2022, 808, 145994.	1.0	4
21138	Integrative analysis of transcriptome-wide association study and mRNA expression profile identified candidate genes and pathways associated with aortic aneurysm and dissection. Gene, 2022, 808, 145993.	1.0	4
21139	Microbes drive changes in arsenic species distribution during the landfill process. Environmental Pollution, 2022, 292, 118322.	3.7	11
21140	Phosphorus enrichment affects trait network topologies and the growth of submerged macrophytes. Environmental Pollution, 2022, 292, 118331.	3.7	15
21141	A systems biology approach to understand the role of TDP-43 in amyotrophic lateral sclerosis. , 2022, , 135-151.		0
21142	Genes from oxidative phosphorylation complexes II-V and two dual-function subunits of complex I are transcribed in Viscum album despite absence of the entire mitochondrial holo-complex I. Mitochondrion, 2022, 62, 1-12.	1.6	7
21143	Integrating SNPs-based genetic risk factor with blood epigenomic response of differentially arsenic-exposed rural subjects reveals disease-associated signaling pathways. Environmental Pollution, 2022, 292, 118279.	3.7	8
21144	MicroRNAs based regulation of cytokine regulating immune expressed genes and their transcription factors in COVID-19. Meta Gene, 2022, 31, 100990.	0.3	17
21145	Short-term cellulose addition decreases microbial diversity and network complexity in an Ultisol following 32-year fertilization. Agriculture, Ecosystems and Environment, 2022, 325, 107744.	2.5	20
21146	New insights to the difference in microbial composition and interspecies interactions between fouling layer and mixed liquor in a membrane bioreactor. Journal of Membrane Science, 2022, 643, 120034.	4.1	8
21147	Invention of Artificial Rice Field Soil: A Tool to Study the Effect of Soil Components on the Activity and Community of Microorganisms Involved in Anaerobic Organic Matter Decomposition. Microbes and Environments, 2020, 35, n/a.	0.7	1
21148	Bacterial RF3 Senses Chaperone Function in Co-Translational Folding. SSRN Electronic Journal, 0, , .	0.4	0
21149	Construction of a prognosis-associated long noncoding RNA-mRNA network for multiple myeloma based on microarray and bioinformatics analysis. Molecular Medicine Reports, 2020, 21, 999-1010.	1.1	9
21151	Network pharmacology and experimental investigation of <i>Rhizoma polygonati</i> extract targeted kinase with herbzyme activity for potent drug delivery. Drug Delivery, 2021, 28, 2187-2197.	2.5	49



#	ARTICLE	IF	CITATIONS
21152	İnsan Protein Etkileşim Ağı Kullanarak Tiroid Karsinomu ile İlgili Moleküller Hedef ve Biyoyararlı Adayların Belirlenmesi. International Journal of Advances in Engineering and Pure Sciences, 0, , .	0.2	0
21153	UPLC-MS/MS-based metabolomic characterization and comparison of pancreatic adenocarcinoma tissues using formalin-fixed, paraffin-embedded and optimal cutting temperature-embedded materials. International Journal of Oncology, 2019, 55, 1249-1260.	1.4	2
21157	Evaluation of consumption behavior during mealtime using network analysis. Japanese Journal of Sensory Evaluation, 2019, 23, 109-116.	0.1	0
21159	Muscle Recovery Is Highlighted by IR Laser Therapy. Journal of Lasers in Medical Sciences, 2019, 10, S49-S53.	0.4	3
21161	Protein Interaction Networks: Functional and Statistical Approaches. Methods in Molecular Biology, 2020, 2139, 21-56.	0.4	7
21162	Dysregulated circulating SOCS3 and HP expression associated with stable CAD and acute coronary syndrome: an integrated study based on bioinformatics analysis and case control validation. Anatolian Journal of Cardiology, 2020, 24, 160-174.	0.5	6
21168	Bioinformatics Excavation of Potential Genes for Intracranial Aneurysm Rupture. Advances in Clinical Medicine, 2020, 10, 1840-1846.	0.0	0
21169	Single-Cell RNA-Seq Reveals Dynamic Change in Tumor Microenvironment During Pancreatic Ductal Adenocarcinoma Malignant Progression. SSRN Electronic Journal, 0, , .	0.4	0
21170	Identification and Validation of SNP-Containing Genes with Prognostic Value in Gastric Cancer via Integrated Bioinformatics Analysis. Advances in Clinical Medicine, 2020, 10, 2832-2847.	0.0	0
21172	Changes of pro-inflammatory and anti-inflammatory macrophages after peripheral nerve injury. RSC Advances, 2020, 10, 38767-38773.	1.7	14
21173	Comparing Community Detection Methods in Brain Functional Connectivity Networks. Communications in Computer and Information Science, 2020, , 3-17.	0.4	1
21175	Identification of Potential Key Genes Involved in Progression of Gastric Cancer Using Bioinformatics Analysis. Diagnostics and Therapeutic Advances in GI Malignancies, 2020, , 101-114.	0.2	0
21176	Modelling Oxidative Stress Pathways. Computational Biology, 2020, , 277-300.	0.1	0
21177	cyTRON and cyTRON/JS: Two Cytoscape-Based Applications for the Inference of Cancer Evolution Models. Lecture Notes in Computer Science, 2020, , 13-18.	1.0	0
21178	Characterizing Relationship of Microbial Community in <i>Xiaoqu</i> and Volatiles of Light-aroma-type <i>Xiaoqu</i> Baijiu. Food Science and Technology Research, 2020, 26, 749-758.	0.3	7
21180	Biomarker Identification in Colorectal Cancer Using Subnetwork Analysis with Feature Selection. Advances in Intelligent Systems and Computing, 2020, , 119-127.	0.5	0
21181	WebShapes: Network Visualization with 3D Shapes. , 2020, , .		1
21182	Modelling and Simulating Complex Systems in Biology. , 2020, , 898-929.		0

#	ARTICLE	IF	CITATIONS
21185	The Pharmacogenomics "Side-effect" of TP53/EGFR in Non-small Cell Lung Cancer Accompanied with Atorvastatin Therapy: A Functional Network Analysis. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2020, 19, 2060-2071.	0.9	1
21186	Overexpression of rice F-box protein OsFBX322 confers increased sensitivity to gamma irradiation in <i>Arabidopsis</i> . <i>Genetics and Molecular Biology</i> , 2020, 43, e20180273.	0.6	2
21187	Identification of Molecular Signatures in Mild Intrinsic Atopic Dermatitis by Bioinformatics Analysis. <i>Annals of Dermatology</i> , 2020, 32, 130.	0.3	5
21188	Identification and Analysis of Genes Involved in Stages of Colon Cancer. <i>Lecture Notes in Computer Science</i> , 2020, , 161-172.	1.0	1
21189	Structure-Function Relationships in Assembly of the Radical-Initiating Cofactors of Class Ia "e Ribonucleotide Reductases. , 2020, , 415-441.		0
21191	Comprehensive Genomic Characterization Analysis of lncRNAs in Cells With Porcine Delta Coronavirus Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 3036.	1.5	7
21192	&lt;b&gt;Lrrc34&nbsp; Is Highly Expressed in SSC and Is Necessary for SSCs Expansion &i&gt;In Vitro&i&gt;. <i>Chinese Medical Sciences Journal</i> , 2020, 35, 1.	0.2	1
21193	Small Nucleolar RNA Host Gene 1 (SNHG1) and Chromosome 2 Open Reading Frame 48 (C2orf48) as Potential Prognostic Signatures for Liver Cancer by Constructing Regulatory Networks. <i>Medical Science Monitor</i> , 2020, 26, e920482.	0.5	3
21194	Nuclear Isoform of FGF13 Regulates Postnatal Neurogenesis in Hippocampus Through Epigenetic Mechanism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21196	The NOCAD MATLAB/Octave Toolbox Developed for the Analysis of Dynamical Systems. <i>SpringerBriefs in Computer Science</i> , 2020, , 71-81.	0.2	0
21197	A Dashboard Component for Pathway Visualization. <i>Journal of the Visualization Society of Japan</i> , 2020, 40, 8-13.	0.0	0
21198	A Systems Biology Driven Approach to Map the EP300 Interactors Using Comprehensive Protein Interaction Network. <i>Lecture Notes in Computer Science</i> , 2020, , 204-214.	1.0	0
21199	Topological Analysis of Cancer Protein Subnetwork in Deubiquitinase (DUB) Interactome. <i>Lecture Notes in Computer Science</i> , 2020, , 249-260.	1.0	0
21202	Screening and identification of genes associated with cell proliferation in cholangiocarcinoma. <i>Aging</i> , 2020, 12, 2626-2646.	1.4	1
21213	A Network Pharmacology Study on the Mechanisms of the Herbal Extract, Christina Loosestrife, for the Treatment of Nephrolithiasis. <i>Medical Science Monitor</i> , 2020, 26, e919360.	0.5	6
21216	Introducing Serine as Cardiovascular Disease Biomarker Candidate via Pathway Analysis. , 2020, 9, 1696.		3
21219	Abnormal Bile Acid Metabolism is an Important Feature of Gut Microbiota and Fecal Metabolites in Patients with Slow Transit Constipation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21220	The effects and the mechanisms of naringenin from <i>Artemisia ordosica</i> Krasch on allergic rhinitis based on mast cell degranulation model and network pharmacology. <i>Journal of Pharmacy and Pharmacology</i> , 2022, 74, 397-408.	1.2	2

#	ARTICLE	IF	CITATIONS
21228	Potential therapies for residual hepatoblastoma following incomplete ablation treatment in a nude mouse subcutaneous xenograft model based on lncRNA and mRNA expression profiles. <i>Oncology Reports</i> , 2020, 43, 1915-1927.	1.2	2
21230	Structural insights into the mechanism of oxidative activation of heme-free H-NOX from <i>Vibrio cholerae</i> . <i>Biochemical Journal</i> , 2020, 477, 1123-1136.	1.7	3
21232	Identification of differentially expressed genes and biological pathways in para-carcinoma tissues of HCC with different metastatic potentials. <i>Oncology Letters</i> , 2020, 19, 3799-3814.	0.8	0
21233	Identification of lapatinib sensitivity-related genes by integrative functional module analysis. <i>Translational Cancer Research</i> , 2020, 9, 1351-1360.	0.4	1
21237	Regionalización de las migraciones residenciales interurbanas en Chile en el período 1997-2002. <i>Confins</i> , 2020, , .	0.0	0
21238	Identification of hub driving genes and regulators of lung adenocarcinoma based on the gene Co-expression network. <i>Bioscience Reports</i> , 2020, 40, .	1.1	4
21258	YRDC is upregulated in non-small cell lung cancer and promotes cell proliferation by decreasing cell apoptosis. <i>Oncology Letters</i> , 2020, 20, 43-52.	0.8	1
21267	Integrative genomics analysis of eQTL and GWAS summary data identifies <i>PPP1CB</i> as a novel bone mineral density risk genes. <i>Bioscience Reports</i> , 2020, 40, .	1.1	0
21269	Deciphering mouse uterine receptivity for embryo implantation at single-cell resolution. <i>Cell Proliferation</i> , 2021, 54, e13128.	2.4	19
21270	Gene Signatures Detect Damaged Liver Sinusoidal Endothelial Cells in Chronic Liver Diseases. <i>Frontiers in Medicine</i> , 2021, 8, 750044.	1.2	9
21271	Integrated Single-Cell Bioinformatics Analysis Reveals Intrinsic and Extrinsic Biological Characteristics of Hematopoietic Stem Cell Aging. <i>Frontiers in Genetics</i> , 2021, 12, 745786.	1.1	2
21272	lncRNA Hmrhl regulates expression of cancer related genes in chronic myelogenous leukemia through chromatin association. <i>NAR Cancer</i> , 2021, 3, zcab042.	1.6	7
21273	Identification and Validation of a Dysregulated miRNA-Associated mRNA Network in Temporal Lobe Epilepsy. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	4
21274	Interpreting the Entire Connectivity of Individual Neurons in Micropatterned Neural Culture With an Integrated Connectome Analyzer of a Neuronal Network (iCANN). <i>Frontiers in Neuroanatomy</i> , 2021, 15, 746057.	0.9	9
21275	Top Trends in Multiomics Research: Evaluation of 52 Published Studies and New Ways of Thinking Terminology and Visual Displays. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 681-692.	1.0	6
21276	Aberrant Methylation and Immune Microenvironment Are Associated With Overexpressed Fibronectin 1: A Diagnostic and Prognostic Target in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 753563.	1.6	10
21277	Genome profiles of pathologist-defined cell clusters by multiregional LCM and G&T-seq in one triple-negative breast cancer patient. <i>Cell Reports Medicine</i> , 2021, 2, 100404.	3.3	5
21278	Prognostic and Immune-Infiltrate Significance of miR-222-3p and Its Target Genes in Thyroid Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 710412.	1.1	6

#	ARTICLE	IF	CITATIONS
21279	The theater of fake news spreading, who plays which role? A study on real graphs of spreading on Twitter. <i>Expert Systems With Applications</i> , 2022, 189, 116110.	4.4	25
21280	Identification of a 17-gene-signature in Non-alcoholic Steatohepatitis and Its Relationship with Immune Cell Infiltration. <i>Hepatitis Monthly</i> , 2021, 21, .	0.1	0
21281	Genome Instability and Long Noncoding RNA Reveal Biomarkers for Immunotherapy and Prognosis and Novel Competing Endogenous RNA Mechanism in Colon Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 740455.	1.8	6
21282	Stable Soil Microbial Functional Structure Responding to Biodiversity Loss Based on Metagenomic Evidences. <i>Frontiers in Microbiology</i> , 2021, 12, 716764.	1.5	10
21283	Data-Driven Analysis of Fluorination of Ligands of Aminergic G Protein Coupled Receptors. <i>Biomolecules</i> , 2021, 11, 1647.	1.8	2
21285	Computational screening of miRNAs and their targets in saffron ( <i>Crocus sativus</i> L.) by transcriptome mining. <i>Planta</i> , 2021, 254, 117.	1.6	12
21286	Restorative potential of (âˆ”)-epicatechin in a rat model of Gulf War illness muscle atrophy and fatigue. <i>Scientific Reports</i> , 2021, 11, 21861.	1.6	6
21287	Breath and plasma metabolomics to assess inflammation in acute stroke. <i>Scientific Reports</i> , 2021, 11, 21949.	1.6	3
21288	Identification of Hypoxia Induced Metabolism Associated Genes in Pulmonary Hypertension. <i>Frontiers in Pharmacology</i> , 2021, 12, 753727.	1.6	12
21289	New tale on LianHuaQingWen: IL6R/IL6/IL6ST complex is a potential target for COVID-19 treatment. <i>Aging</i> , 2021, 13, 23913-23935.	1.4	5
21290	Endophytic colonization of entomopathogenic fungi increases plant disease resistance by changing the endophytic bacterial community. <i>Journal of Basic Microbiology</i> , 2021, 61, 1098-1112.	1.8	11
21292	Integrative analysis of Iso-Seq and RNA-seq data reveals transcriptome complexity and differentially expressed transcripts in sheep tail fat. <i>PeerJ</i> , 2021, 9, e12454.	0.9	16
21293	Integrative Analysis for Elucidating Transcriptomics Landscapes of Systemic Lupus Erythematosus. <i>Frontiers in Genetics</i> , 2021, 12, 782005.	1.1	1
21294	Molecular profiles of predictive biomarkers for platinum-based chemotherapy in Non-Small Cell Lung Cancer (NSCLC). <i>Meta Gene</i> , 2022, 31, 100993.	0.3	3
21295	Defining and identifying satellite cell-opathies within muscular dystrophies and myopathies. <i>Experimental Cell Research</i> , 2022, 411, 112906.	1.2	22
21297	Proximity-Labeling Reveals Novel Host and Parasite Proteins at the <i>Toxoplasma</i> Parasitophorous Vacuole Membrane. <i>MBio</i> , 2021, 12, e0026021.	1.8	26
21299	Computationally Reconstructed Interactome of Bradyrhizobium diazoefficiens USDA110 Reveals Novel Functional Modules and Protein Hubs for Symbiotic Nitrogen Fixation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11907.	1.8	0
21300	Cross-platform transcriptomic profiling of the response to recombinant human erythropoietin. <i>Scientific Reports</i> , 2021, 11, 21705.	1.6	5

#	ARTICLE	IF	CITATIONS
21301	Identification of Potential Key Genes in the Pathogenesis of Chronic Obstructive Pulmonary Disease Through Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 754569.	1.1	8
21302	Ovarian activation delays in peripubertal ewe lambs infected with <i>Haemonchus contortus</i> can be avoided by supplementing protein in their diets. <i>BMC Veterinary Research</i> , 2021, 17, 344.	0.7	2
21303	Comprehensive Analysis of m6A RNA Methylation Regulators in the Prognosis and Immune Microenvironment of Multiple Myeloma. <i>Frontiers in Oncology</i> , 2021, 11, 731957.	1.3	4
21305	Clinical prognosis and gene expression profiles of prostate cancer patients with bone and lymphatic metastases. <i>Food Science and Technology</i> , 0, , .	0.8	0
21306	Development and Verification of the Amino Metabolism-Related and Immune-Associated Prognosis Signature in Gliomas. <i>Frontiers in Oncology</i> , 2021, 11, 774332.	1.3	3
21307	Revealing the Mechanism of Friedelin in the Treatment of Ulcerative Colitis Based on Network Pharmacology and Experimental Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-14.	0.5	7
21308	Weighted gene co-expression network analysis to identify key modules and hub genes associated with paucigranulocytic asthma. <i>BMC Pulmonary Medicine</i> , 2021, 21, 343.	0.8	7
21309	Comparison of metabolic states using genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2021, 17, e1009522.	1.5	4
21310	Differential proteome profile, biological pathways, and network relationships of osteogenic proteins in calcified human aortic valves. <i>Heart and Vessels</i> , 2021, , 1.	0.5	2
21311	Identification of Potential Osteoporosis miRNA Biomarkers Using Bioinformatics Approaches. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-8.	0.7	3
21312	Candidate genes of SARS-CoV-2 gender susceptibility. <i>Scientific Reports</i> , 2021, 11, 21968.	1.6	14
21313	An Oxidative Stress-Related Gene Pair (CCNB1/PKD1), Competitive Endogenous RNAs, and Immune-Infiltration Patterns Potentially Regulate Intervertebral Disc Degeneration Development. <i>Frontiers in Immunology</i> , 2021, 12, 765382.	2.2	19
21315	Identification of DELLA Genes and Key Stage for GA Sensitivity in Bolting and Flowering of Flowering Chinese Cabbage. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12092.	1.8	19
21316	Integrin $\alpha$ 23 Induction Promotes Tubular Cell Senescence and Kidney Fibrosis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 733831.	1.8	11
21317	Bioinformatic Analysis and Integration of Transcriptome and Proteome Results Identify Key Coding and Noncoding Genes Predicting Malignancy in Intraductal Papillary Mucinous Neoplasms of the Pancreas. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	4
21319	Analysis of Differentially Expressed Genes That Aggravate Metabolic Diseases in Depression. <i>Life</i> , 2021, 11, 1203.	1.1	1
21320	Tubulin isotypes optimize distinct spindle positioning mechanisms during yeast mitosis. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	11
21321	Searching for bioactive compounds from Solanaceae: lethal and sublethal toxicity to <i>Spodoptera frugiperda</i> and untargeted metabolomics approaches. <i>Journal of Pest Science</i> , 2022, 95, 1317-1329.	1.9	5

#	ARTICLE	IF	CITATIONS
21323	Circulating <scp>microRNAs</scp> as indicators in the prediction of neoadjuvant chemotherapy response in luminal <scp>B</scp> breast cancer. <i>Thoracic Cancer</i> , 2021, 12, 3396-3406.	0.8	16
21324	Construction of a Ferroptosis-Related Long Non-coding RNA Prognostic Signature and Competing Endogenous RNA Network in Lung Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 751490.	1.8	13
21325	Shrimp AHPND Causing <i>Vibrio anguillarum</i> Infection: Quantitative Diagnosis and Identifying Antagonistic Bacteria. <i>Marine Biotechnology</i> , 2021, 23, 964-975.	1.1	12
21326	Proximity labeling identifies LOTUS domain proteins that promote the formation of perinuclear germ granules in <i>C. elegans</i> . <i>ELife</i> , 2021, 10, .	2.8	9
21327	Differed biotic interactions influenced by anthropogenic disturbances among trophic levels in fragmented wetlands. <i>Science of the Total Environment</i> , 2022, 809, 151179.	3.9	1
21328	Immune Infiltration-Related Signature Predicts Risk Stratification and Immunotherapy Efficacy in Grade II and III Gliomas. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 756005.	1.8	7
21329	Spike Formation Is a Turning Point Determining Wheat Root Microbiome Abundance, Structures and Functions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11948.	1.8	2
21330	Leptin Signaling in the Ovary of Diet-Induced Obese Mice Regulates Activation of NOD-Like Receptor Protein 3 Inflammasome. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 738731.	1.8	4
21331	Dietary Contamination with a Neonicotinoid (Clothianidin) Gradient Triggers Specific Dysbiosis Signatures of Microbiota Activity along the Honeybee ( <i>Apis mellifera</i> ) Digestive Tract. <i>Microorganisms</i> , 2021, 9, 2283.	1.6	9
21332	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. <i>Rice</i> , 2021, 14, 90.	1.7	23
21333	iTRAQ-Based Proteomics Analysis of Human Cytomegalovirus Latency and Reactivation in T98G Cells. <i>Journal of Virology</i> , 2022, 96, JVI0147621.	1.5	4
21334	Identification and Functional Analysis of lncRNAs Responsive to Hypoxia in <i>Eospalax fontanierii</i> . <i>Current Issues in Molecular Biology</i> , 2021, 43, 1889-1905.	1.0	0
21336	MiR-16-5p suppresses breast cancer proliferation by targeting ANLN. <i>BMC Cancer</i> , 2021, 21, 1188.	1.1	22
21337	Massive QTL analysis identifies pleiotropic genetic determinants for stress resistance, aroma formation, and ethanol, glycerol and isobutanol production in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2021, 14, 211.	6.2	7
21339	A genome-phenome association study in native microbiomes identifies a mechanism for cytosine modification in DNA and RNA. <i>ELife</i> , 2021, 10, .	2.8	6
21340	Multidimensional Single-Nuclei RNA-Seq Reconstruction of Adipose Tissue Reveals Adipocyte Plasticity Underlying Thermogenic Response. <i>Cells</i> , 2021, 10, 3073.	1.8	11
21341	Passages in culture and stimulation conditions influence protein expression of primary fibroblasts. <i>Proteomics</i> , 2021, , 2100116.	1.3	0
21343	Effect of exposure to antibiotics on the gut microbiome and biochemical indexes of pregnant women. <i>BMJ Open Diabetes Research and Care</i> , 2021, 9, e002321.	1.2	9



#	ARTICLE	IF	CITATIONS
21345	Identification of diagnostic signatures in ulcerative colitis patients via bioinformatic analysis integrated with machine learning. <i>Human Cell</i> , 2022, 35, 179-188.	1.2	9
21346	Integrated bioinformatics analysis reveals dynamic candidate genes and signaling pathways involved in the progression and prognosis of diffuse large B-cell lymphoma. <i>PeerJ</i> , 2021, 9, e12394.	0.9	3
21347	Control of osteocyte dendrite formation by Sp7 and its target gene osteocrin. <i>Nature Communications</i> , 2021, 12, 6271.	5.8	41
21348	Tissue Specific Transcriptome Changes Upon Influenza A Virus Replication in the Duck. <i>Frontiers in Immunology</i> , 2021, 12, 786205.	2.2	6
21349	Proteogenomic discovery of sORF-encoded peptides associated with bacterial virulence in <i>Yersinia pestis</i> . <i>Communications Biology</i> , 2021, 4, 1248.	2.0	10
21350	Interactions of the Intracellular Bacterium <i>Cardinium</i> with Its Host, the House Dust Mite <i>Dermatophagoides farinae</i> , Based on Gene Expression Data. <i>MSystems</i> , 2021, 6, e0091621.	1.7	7
21351	Trial Proteomic Qualitative and Quantitative Analysis of the Protein Matrix of Submandibular Sialoliths. <i>Molecules</i> , 2021, 26, 6725.	1.7	5
21354	Coupling plant litter quantity to a novel metric for litter quality explains C storage changes in a thawing permafrost peatland. <i>Global Change Biology</i> , 2021, , .	4.2	8
21355	An alternative splicing signature in human Crohn's disease. <i>BMC Gastroenterology</i> , 2021, 21, 420.	0.8	5
21356	Drug repurposing for coronavirus (SARS-CoV-2) based on gene co-expression network analysis. <i>Scientific Reports</i> , 2021, 11, 21872.	1.6	13
21357	Enterocyte-innate lymphoid cell crosstalk drives early IFN- $\beta$ -mediated control of <i>Cryptosporidium</i> . <i>Mucosal Immunology</i> , 2022, 15, 362-372.	2.7	26
21358	Potential biomarkers identified in plasma of patients with gestational diabetes mellitus. <i>Metabolomics</i> , 2021, 17, 99.	1.4	10
21359	A survey of substrate specificity among Auxiliary Activity Family 5 copper radical oxidases. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 8187-8208.	2.4	15
21360	Integrative analysis of DNA methylation and gene expression profiles to identify biomarkers of glioblastoma. <i>Cancer Genetics</i> , 2021, 258-259, 135-150.	0.2	12
21361	Corticosteroid treatment in COVID-19 modulates host inflammatory responses and transcriptional signatures of immune dysregulation. <i>Journal of Leukocyte Biology</i> , 2021, 110, 1225-1239.	1.5	4
21362	Comparison of the Proteomes of Porcine Macrophages and a Stable Porcine Cell Line after Infection with African Swine Fever Virus. <i>Viruses</i> , 2021, 13, 2198.	1.5	15
21363	Functional genomics and metabolomics advance the ethnobotany of the Samoan traditional medicine 'œmatalafi'. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
21364	Construction of a lncRNA-miRNA-mRNA network to determine the key regulators of the Th1/Th2 imbalance in multiple sclerosis. <i>Epigenomics</i> , 2021, 13, 1797-1815.	1.0	17

#	ARTICLE	IF	CITATIONS
21365	Ancestral sequences of a large promiscuous enzyme family correspond to bridges in sequence space in a network representation. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210389.	1.5	0
21366	Tumor relevant protein functional interactions identified using bipartite graph analyses. <i>Scientific Reports</i> , 2021, 11, 21530.	1.6	1
21367	Novel Targets in a High-Altitude Pulmonary Hypertension Rat Model Based on RNA-seq and Proteomics. <i>Frontiers in Medicine</i> , 2021, 8, 742436.	1.2	0
21368	Verification of the role of spiperone in the treatment of COPD through bioinformatics analysis. <i>International Immunopharmacology</i> , 2021, 101, 108308.	1.7	2
21370	Weighted gene co-expression network analysis to define pivotal modules and genes in diabetic heart failure. <i>Bioscience Reports</i> , 2020, 40, .	1.1	5
21377	A Study on the Mechanism of Lavender in the Treatment of Insomnia Based on Network Pharmacology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 419-432.	0.6	5
21381	Predicting Disease-related Genes Using Biomedical Literature Based on GloVe Word Embedding. <i>The Journal of Korean Institute of Information Technology</i> , 2020, 18, 1-14.	0.1	0
21386	A ferredoxin-dependent dihydropyrimidine dehydrogenase in <i>Clostridium chromiireducens</i> . <i>Bioscience Reports</i> , 2020, 40, .	1.1	0
21389	Screening potential microRNAs associated with pancreatic cancer: Data mining based on RNA sequencing and microarrays. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 2705-2715.	0.8	7
21393	Karmañ±k Añ± Analizi Kullanñ±larak Kitap ã–dñ±nñ± Alma Añ±nñ±n Analizi. <i>Bitlis Eren ãœniversitesi Fen Bilimleri Dergisi</i> , 0, , .	0.1	1
21395	Identification of potential gene associated with berberine in overcoming tamoxifen resistance by functional network analysis. <i>Journal of Applied Pharmaceutical Science</i> , 0, , .	0.7	1
21400	Key genes involved in cell cycle arrest and DNA damage repair identified in anaplastic thyroid carcinoma using integrated bioinformatics analysis. <i>Translational Cancer Research</i> , 2020, 9, 4188-4203.	0.4	4
21402	Screening and Interaction Analysis of Key Genes in miR-542-3p Over- Expressed Osteosarcoma Cells by Bioinformatics. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 411-418.	0.6	0
21404	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 0, , 173-194.		0
21405	Biclustering of DNA Microarray Data. , 0, , 513-551.		3
21406	Modules in Biological Networks. , 0, , 637-663.		0
21407	Efficient Techniques for Graph Searching and Biological Network Mining. <i>Advances in Data Mining and Database Management Book Series</i> , 0, , 89-111.	0.4	0
21408	Inferring the Origin of the Genetic Code. <i>Springer Optimization and Its Applications</i> , 2007, , 291-320.	0.6	0

#	ARTICLE	IF	CITATIONS
21410	GlycoBrowser: A Tool for Contextual Visualization of Biological Data and Pathways Using Ontologies. , 2008, , 305-316.		1
21413	iTRAQ-based proteomic analysis reveals potential regulatory networks in dust mite-related asthma treated with subcutaneous allergen immunotherapy. <i>Molecular Medicine Reports</i> , 2020, 22, 3607-3620.	1.1	2
21414	Argo Lite. , 2020, , .		5
21415	Integrated transcriptome meta-analysis of pancreatic ductal adenocarcinoma and matched adjacent pancreatic tissues. <i>PeerJ</i> , 2020, 8, e10141.	0.9	34
21434	Integrative genomics analysis identifies five promising genes implicated in insomnia risk based on multiple omics datasets. <i>Bioscience Reports</i> , 2020, 40, .	1.1	8
21435	Gene expression in urinary incontinence and pelvic organ prolapse: a review of literature. <i>Current Opinion in Obstetrics and Gynecology</i> , 2020, 32, 441-448.	0.9	2
21436	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	0.8	2
21448	Identification of potential key genes affecting soybean growth under salt stress via transcriptome study. <i>Biologia Plantarum</i> , 0, 64, 692-700.	1.9	2
21449	AMP-activated protein kinase family member 5 is an independent prognostic indicator of pancreatic adenocarcinoma: A study based on The Cancer Genome Atlas. <i>Molecular Medicine Reports</i> , 2020, 22, 4329-4339.	1.1	1
21450	A novel prognostic risk score model based on immune-related genes in patients with stage IV colorectal cancer. <i>Bioscience Reports</i> , 2020, 40, .	1.1	9
21451	An interactive network of alternative splicing events with prognostic value in geriatric lung adenocarcinoma via the regulation of splicing factors. <i>Bioscience Reports</i> , 2020, 40, .	1.1	2
21452	Identification of robust genes in transcriptional regulatory network of <i>Mycobacterium tuberculosis</i> . <i>IET Systems Biology</i> , 2020, 14, 292-296.	0.8	2
21468	RNA sequencing of whole blood in dogs with primary immune-mediated hemolytic anemia (IMHA) reveals novel insights into disease pathogenesis. <i>PLoS ONE</i> , 2020, 15, e0240975.	1.1	5
21469	From sequence to information. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190448.	1.8	5
21470	Soil fungal networks are more sensitive to grazing exclusion than bacterial networks. <i>PeerJ</i> , 2020, 8, e9986.	0.9	10
21471	Global insights to drought stress perturbed genes in oat ( <i>Avena sativa</i> L.) seedlings using RNA sequencing. <i>Plant Signaling and Behavior</i> , 2021, 16, 1845934.	1.2	2
21496	Construction of Protein Expression Network. <i>Methods in Molecular Biology</i> , 2021, 2189, 119-132.	0.4	1
21497	Studying Seed Microbiomes. <i>Methods in Molecular Biology</i> , 2021, 2232, 1-21.	0.4	5

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21498	Data Analysis for Antibody Arrays. <i>Methods in Molecular Biology</i> , 2021, 2237, 263-276.	0.4	0
21499	An Almost-Solvable Model of Complex Network Dynamics. <i>Russian Journal of Mathematical Physics</i> , 2020, 27, 469-476.	0.4	1
21500	NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. , 2020, , .		1
21501	Insight into CsWRKY gene family and their involvement in plant hormone response of <i>Cymbidium sinense</i> . <i>Acta Horticulturae</i> , 2020, , 471-480.	0.1	0
21502	Landscape of transcription and expression regulated by DNA methylation related to age of donor and cell passage in adipose-derived mesenchymal stem cells. <i>Aging</i> , 2020, 12, 21186-21201.	1.4	8
21503	Oncostatin M expression and TP53 mutation status regulate tumor-infiltration of immune cells and survival outcomes in cholangiocarcinoma. <i>Aging</i> , 2020, 12, 21518-21543.	1.4	5
21504	Upregulation of glutaminase 2 and neutrophil cytosolic factor 2 is associated with the poor prognosis of glioblastoma. <i>Biomarkers in Medicine</i> , 2020, 14, 1585-1597.	0.6	3
21505	Identifying citrus CBL and CIPK gene families and their expressions in response to drought and arbuscular mycorrhizal fungi colonization. <i>Biologia Plantarum</i> , 0, 64, 773-783.	1.9	10
21506	Re-construction of Co-expression Network of Genes Involved in Bacterial Cell Wall Synthesis and Their Role in Penicillin Resistance. <i>Avicenna Journal of Clinical Microbiology and Infection</i> , 2020, 7, 65-71.	0.2	3
21507	A framework for integrating functional and microbial data: The case of dark fermentation H <sub>2</sub> production. <i>International Journal of Hydrogen Energy</i> , 2020, 45, 31706-31718.	3.8	4
21508	<i>LSM3</i> , <i>NDUFB3</i> , and <i>PTGS2</i> may be potential biomarkers for <i>BRCA1</i> -mutation positive breast cancer. <i>Romanian Journal of Laboratory Medicine</i> , 2020, 28, 381-391.	0.1	0
21509	Modularity of the Personality Network. <i>European Journal of Psychological Assessment</i> , 2020, 36, 998-1008.	1.7	3
21510	Identification of Candidate Genetic Markers and a Novel 4-genes Diagnostic Model in Osteoarthritis through Integrating Multiple Microarray Data. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 805-813.	0.6	1
21511	Exploring the mechanism of resistance to sorafenib in two hepatocellular carcinoma cell lines. <i>Aging</i> , 2020, 12, 24255-24269.	1.4	3
21512	BioFabric Visualization of Network Alignments. , 2021, , 65-97.		0
21513	Sugar modulation of anaerobic-response networks in maize root tips. <i>Plant Physiology</i> , 2021, 185, 295-317.	2.3	7
21514	Protein-Protein Interaction Network Analysis for a Biomarker Panel Related to Human Esophageal Adenocarcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2017, 18, 3357-3363.	0.5	35
21515	An integrated dataset for in silico drug discovery. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	9

#	ARTICLE	IF	CITATIONS
21516	Computational Methods for Learning Bayesian Networks from High-Throughput Biological Data. , 0, , 385-400.		5
21519	CD138 <sup>&lt;sup&gt;-&lt;/sup&gt;</sup> multiple myeloma cells express high level of CHK1 which correlated to overall survival in MM patient. Aging, 2020, 12, 23067-23081.	1.4	4
21520	Public databases and software for the pathway analysis of cancer genomes. Cancer Informatics, 2007, 3, 379-97.	0.9	6
21521	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 439-50.	0.7	10
21522	A systems biology approach to study the phagosomal proteome modulated by mycobacterial infections. International Journal of Clinical and Experimental Medicine, 2009, 2, 233-47.	1.3	16
21523	Biomolecular Systems of Disease Buried Across Multiple GWAS Unveiled by Information Theory and Ontology. Summit on Translational Bioinformatics, 2010, 2010, 31-5.	0.7	5
21524	Consistent visualizations of changing knowledge. Summit on Translational Bioinformatics, 2009, 2009, 129-32.	0.7	1
21525	Exploring schizophrenia drug-gene interactions through molecular network and pathway modeling. AMIA ... Annual Symposium proceedings, 2011, 2011, 1127-33.	0.2	12
21526	Social network analysis of physician interactions: the effect of institutional boundaries on breast cancer care. AMIA ... Annual Symposium proceedings, 2011, 2011, 152-60.	0.2	11
21527	Biomarkers of the Hedgehog/Smoothed pathway in healthy volunteers. American Journal of Translational Research (discontinued), 2012, 4, 229-39.	0.0	2
21529	A chain reaction approach to modelling gene pathways. Translational Cancer Research, 2012, 1, 61-73.	0.4	2
21530	Quality assurance in LOINC using Description Logic. AMIA ... Annual Symposium proceedings, 2012, 2012, 1099-108.	0.2	7
21531	A method for probing disease relatedness using common clinical eligibility criteria. Studies in Health Technology and Informatics, 2013, 192, 481-5.	0.2	9
21532	Network analysis of unstructured EHR data for clinical research. AMIA Summits on Translational Science Proceedings, 2013, 2013, 14-8.	0.4	4
21533	Transcriptomic changes induced by mycophenolic acid in gastric cancer cells. American Journal of Translational Research (discontinued), 2013, 6, 28-42.	0.0	15
21535	Comparison of the gene expression profiles between gallstones and gallbladder polyps. International Journal of Clinical and Experimental Pathology, 2014, 7, 8016-23.	0.5	5
21536	Computational methods and opportunities for phosphorylation network medicine. Translational Cancer Research, 2014, 3, 266-278.	0.4	8
21537	Integrated regulatory mechanisms of miRNAs and targeted genes involved in colorectal cancer. International Journal of Clinical and Experimental Pathology, 2015, 8, 517-29.	0.5	12

#	ARTICLE	IF	CITATIONS
21539	Comparative Analysis of Prostate Cancer Gene Regulatory Networks via Hub Type Variation. <i>Avicenna Journal of Medical Biotechnology</i> , 2015, 7, 8-15.	0.2	2
21540	Using software to elicit user needs for clinical research visit scheduling. <i>AMIA Summits on Translational Science Proceedings</i> , 2014, 2014, 109-15.	0.4	0
21541	Screening feature genes of osteosarcoma with DNA microarray: a bioinformatic analysis. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 7134-42.	1.3	2
21542	Predicting New Target Conditions for Drug Retesting Using Temporal Patterns in Clinical Trials: A Proof of Concept. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 445-9.	0.4	0
21543	A Bibliometric Analysis on Cancer Population Science with Topic Modeling. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 102-6.	0.4	1
21544	Detecting Cancer Pathway Crosstalk with Distance Correlation. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 41-5.	0.4	0
21545	Protein-Protein Interaction Network could reveal the relationship between the breast and colon cancer. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2015, 8, 215-24.	0.6	42
21546	Identification of a novel miRNA-target gene regulatory network in osteosarcoma by integrating transcriptome analysis. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 8348-57.	0.5	9
21547	Screening feature genes of lung carcinoma with DNA microarray analysis. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 12161-71.	1.3	21
21548	Proteomics and bioinformatics analysis of mouse hypothalamic neurogenesis with or without EPHX2 gene deletion. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 12634-45.	0.5	3
21549	A six-microRNA set as prognostic indicators for bile duct cancer. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 17261-70.	1.3	25
21550	Analysis of differentially expressed genes based on microarray data of glioma. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 17321-32.	1.3	8
21551	The non-Geldanamycin Hsp90 inhibitors enhanced the antifungal activity of fluconazole. <i>American Journal of Translational Research (discontinued)</i> , 2015, 7, 2589-602.	0.0	21
21552	Using a Novel Ontology to Inform the Discovery of Therapeutic Peptides from Animal Venoms. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 209-18.	0.4	3
21553	In Search of 'Birth Month Genes': Using Existing Data Repositories to Locate Genes Underlying Birth Month-Disease Relationships. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 189-98.	0.4	1
21554	Phospho-Network Analysis Identifies and Quantifies Hepatitis C Virus (HCV)-induced Hepatocellular Carcinoma (HCC) Proteins Regulating Viral-mediated Tumor Growth. <i>Cancer Genomics and Proteomics</i> , 2016, 13, 339-57.	1.0	3
21555	Central Nodes in Protein Interaction Networks Drive Critical Functions in Transforming Growth Factor Beta-1 Stimulated Kidney Cells. <i>Cell Journal</i> , 2017, 18, 514-531.	0.2	7
21556	Protein-protein interaction network of celiac disease. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2016, 9, 268-277.	0.6	33



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21557	Introduction of inflammatory bowel disease biomarkers panel using protein-protein interaction (PPI) network analysis. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2016, 9, S8-S13.	0.6	12
21558	Bioinformatics Analysis Reveals Genes Involved in the Pathogenesis of Ameloblastoma and Keratocystic Odontogenic Tumor. <i>International Journal of Molecular and Cellular Medicine</i> , 2016, 5, 199-219.	1.1	5
21559	Identification of miR-101-3p targets and functional features based on bioinformatics, meta-analysis and experimental verification in hepatocellular carcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 2088-2105.	0.0	19
21560	Integrative network and transcriptomics-based approach predicts genotype-specific drug combinations for melanoma. <i>AMIA Summits on Translational Science Proceedings</i> , 2017, 2017, 247-256.	0.4	9
21561	Fluoxetine Regulates Ig Kappa Chain C Region Expression Levels in the Serum of Obsessive-Compulsive Disorder Patients: A proteomic Approach. <i>Iranian Journal of Pharmaceutical Research</i> , 2017, 16, 1264-1271.	0.3	8
21562	Exploring conserved mRNA-miRNA interactions in colon and lung cancers. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2017, 10, 184-193.	0.6	5
21563	A systems biology analysis protein-protein interaction of NASH and IBD based on comprehensive gene information. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2017, 10, 194-201.	0.6	26
21564	Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 536-547.	0.7	7
21565	Annotating gene sets by mining large literature collections with protein networks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 602-613.	0.7	6
21566	GeneDive: A gene interaction search and visualization tool to facilitate precision medicine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 590-601.	0.7	3
21567	Protein interaction mapping interpretation of none alcoholic fatty liver disease model of rats after fat diet feeding. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2017, 10, S146-S153.	0.6	9
21568	Protein-protein interaction analysis of Alzheimer's disease and NAFLD based on systems biology methods unhide common ancestor pathways. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2018, 11, 27-33.	0.6	24
21569	Add-On therapy with Chinese herb medicine Bo-Er-Ning capsule (BENC) improves outcomes of gastric cancer patients: a randomized clinical trial followed with bioinformatics-assisted mechanism study. <i>American Journal of Cancer Research</i> , 2018, 8, 1090-1105.	1.4	7
21570	Bioinformatics-based analysis of the involvement of AC005550.3, RP11-415D17.3, and RP1-140K8.5 in homocysteine-induced vascular endothelial injury. <i>American Journal of Translational Research (discontinued)</i> , 2018, 10, 2126-2136.	0.0	2
21571	EFNB2 acts as the target of miR-557 to facilitate cell proliferation, migration and invasion in pancreatic ductal adenocarcinoma by bioinformatics analysis and verification. <i>American Journal of Translational Research (discontinued)</i> , 2018, 10, 3514-3528.	0.0	11
21572	SFRP4 is a prognostic marker and correlated with Treg cell infiltration in pancreatic ductal adenocarcinoma. <i>American Journal of Cancer Research</i> , 2019, 9, 363-377.	1.4	8
21573	Investigation of health benefits of cocoa in human colorectal cancer cell line, HT-29 through interactome analysis. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2019, 12, 67-73.	0.6	17
21574	The bioinformatics aspects of gene screening of HT-29, human colon cell line treated with caffeic acid. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2019, 12, 246-253.	0.6	5

#	ARTICLE	IF	CITATIONS
21575	Prognostic alternative splicing signatures and underlying regulatory network in esophageal carcinoma. American Journal of Translational Research (discontinued), 2019, 11, 4010-4028.	0.0	7
21577	Expression profile of circular RNA s in TMJ osteoarthritis synovial tissues and potential functions of hsa_circ_0000448 with specific back-spliced junction. American Journal of Translational Research (discontinued), 2019, 11, 5357-5374.	0.0	8
21578	Bioinformatics analyses of publicly available NEPCa datasets. American Journal of Clinical and Experimental Urology, 2019, 7, 327-340.	0.4	11
21579	A pilot study comparing the genetic molecular biology of gestational and non-gestational choriocarcinoma. American Journal of Translational Research (discontinued), 2019, 11, 7049-7062.	0.0	5
21580	Using Transcriptional Signatures to Find Cancer Drivers with LURE. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 343-354.	0.7	1
21581	Cytochrome P450 family proteins as potential biomarkers for ovarian granulosa cell damage in mice with premature ovarian failure. International Journal of Clinical and Experimental Pathology, 2018, 11, 4236-4246.	0.5	1
21582	Serum proteomics study reveals candidate biomarkers for systemic lupus erythematosus. International Journal of Clinical and Experimental Pathology, 2017, 10, 10681-10694.	0.5	2
21583	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. Molecules and Cells, 2020, 43, 86-95.	1.0	6
21584	Gallbladder cancer integrated bioinformatics analysis of protein profile data. Gastroenterology and Hepatology From Bed To Bench, 2019, 12, S66-S73.	0.6	3
21585	and lactational 2,3,7,8-tetrachlorodibenzo-dioxin (TCDD) exposure exacerbates urinary dysfunction in hormone-treated C57BL/6J mice through a non-malignant mechanism involving proteomic changes in the prostate that differ from those elicited by testosterone and estradiol. American Journal of Clinical and Experimental Urology, 2020, 8, 59-72.	0.4	8
21586	Differentiation of -negative and positive gastric cancer via regulatory network analysis. Gastroenterology and Hepatology From Bed To Bench, 2020, 13, 161-167.	0.6	2
21587	Proteomic profiling and bioinformatics analysis identify key regulators during the process from fanconi anemia to acute myeloid leukemia. American Journal of Translational Research (discontinued), 2020, 12, 1415-1427.	0.0	1
21588	pSTAT3 Y705 is a prognostic biomarker identified from time-series gene expression profiles of a chemically induced mouse model of hepatocellular carcinoma. American Journal of Translational Research (discontinued), 2020, 12, 1443-1458.	0.0	0
21589	Response to fluoxetine in children and adolescents: a weighted gene co-expression network analysis of peripheral blood. American Journal of Translational Research (discontinued), 2020, 12, 2028-2040.	0.0	0
21590	Overexpressed gene signature of EPH receptor A/B family in cancer patients-comprehensive analyses from the public high-throughput database. International Journal of Clinical and Experimental Pathology, 2020, 13, 1220-1242.	0.5	11
21591	Identification of transcriptomic markers for developing idiopathic pulmonary fibrosis: an integrative analysis of gene expression profiles. International Journal of Clinical and Experimental Pathology, 2020, 13, 1698-1706.	0.5	4
21592	Advances in Text Mining and Visualization for Precision Medicine. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 559-565.	0.7	3
21593	High ADAMTS18 expression is associated with poor prognosis in stomach adenocarcinoma. Oncology Letters, 2020, 20, 211.	0.8	2

#	ARTICLE	IF	CITATIONS
21594	The modulation relationship of genomic pattern of intratumor heterogeneity and immunity microenvironment heterogeneity in hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 20, 233.	0.8	0
21595	Assessment for prognostic value of differentially expressed genes in immune microenvironment of clear cell renal cell carcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 5416-5432.	0.0	4
21596	Screening of autophagy genes as prognostic indicators for glioma patients. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 5320-5331.	0.0	4
21597	Investigating the expressions of miRNA-125b and in endometriosis. Does it underlie cancer-like features of endometriosis? A case-control study. <i>International Journal of Reproductive BioMedicine</i> , 2020, 18, 825-836.	0.5	1
21598	Inhibition of AURKB, regulated by pseudogene , confers synthetic lethality to PARP inhibition in skin cutaneous melanoma. <i>American Journal of Cancer Research</i> , 2020, 10, 3458-3474.	1.4	1
21599	Diagnostic and prognostic values of forkhead box D4 gene in colonic adenocarcinoma. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 2615-2627.	0.5	0
21600	Tumorigenesis-related key genes in adolescents and young adults with HR(+)/HER2(-) breast cancer. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 2701-2709.	0.5	3
21601	iTRAQ-based proteomic analysis of the interaction of A549 human lung epithelial cells with <i>Aspergillus fumigatus</i> conidia. <i>Molecular Medicine Reports</i> , 2020, 22, 4601-4610.	1.1	1
21602	Using mRNA deep sequencing to analyze differentially expressed genes during <i>Panax notoginseng</i> saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	0
21603	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	0
21604	Development of RNA binding proteins expression signature for prognosis prediction in gastric cancer patients. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 6775-6792.	0.0	1
21605	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	3
21606	Investigating the Effects of Ibuprofen on the Gene Expression Profile in Hippocampus of Mice Model of Alzheimer's Disease through Bioinformatics Analysis. <i>Iranian Journal of Pharmaceutical Research</i> , 2020, 19, 352-359.	0.3	3
21607	Investigating the human protein-host protein interactome of SARS-CoV-2 infection in the small intestine. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2020, 13, 374-387.	0.6	3
21608	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	0
21609	Identification of key genes in lung adenocarcinoma based on a competing endogenous RNA network. <i>Oncology Letters</i> , 2021, 21, 60.	0.8	2
21610	Î²-hydroxybutyrate does not alter the effects of glucose deprivation on breast cancer cells. <i>Oncology Letters</i> , 2021, 21, 65.	0.8	1
21611	Interaction network of immune-associated genes affecting the prognosis of patients with glioblastoma. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 61.	0.8	0

#	ARTICLE	IF	CITATIONS
21612	Identification of Dysregulated Genes for Late-Onset Alzheimer's Disease Using Gene Expression Data in Brain. , 2020, 10, .		0
21613	Transcriptomic analysis reveals a WNT signaling pathway-based gene signature prognostic for non-small cell carcinoma. Aging, 2020, 12, 19159-19172.	1.4	0
21614	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk based on multiple omics datasets. Aging, 2020, 12, 19173-19220.	1.4	2
21615	P4HB: A novel diagnostic and prognostic biomarker for bladder carcinoma. Oncology Letters, 2021, 21, 95.	0.8	9
21616	Single-cell transcriptomic profiling provides insights into retinal endothelial barrier properties. Molecular Vision, 2020, 26, 766-779.	1.1	2
21617	Oncogene enhances cellular invasion, migration and proliferation abilities via autophagy-related pathway resulting in poor prognosis in hepatocellular carcinoma. American Journal of Cancer Research, 2020, 10, 4178-4197.	1.4	2
21618	Identification of colorectal cancer-associated macrophage biomarkers by integrated bioinformatic analysis. International Journal of Clinical and Experimental Pathology, 2021, 14, 1-8.	0.5	2
21619	Showing NAFLD, as a key connector disease between Alzheimer's disease and diabetes via analysis of systems biology. Gastroenterology and Hepatology From Bed To Bench, 2020, 13, S89-S97.	0.6	0
21620	Proteomic study of advanced cirrhosis based on HCV to reveal potential biomarkers. Gastroenterology and Hepatology From Bed To Bench, 2020, 13, S113-S121.	0.6	0
21621	Integrated Network and Gene Ontology Analysis Identifies Key Genes and Pathways for Coronary Artery Diseases. Avicenna Journal of Medical Biotechnology, 2021, 13, 15-23.	0.2	1
21622	Proteomic Profiling of Lysine Acetylation Indicates Mitochondrial Dysfunction in the Hippocampus of Gut Microbiota-Absent Mice. Frontiers in Molecular Neuroscience, 2021, 14, 594332.	1.4	1
21623	Potential targets identified in adenoid cystic carcinoma point out new directions for further research. American Journal of Translational Research (discontinued), 2021, 13, 1085-1108.	0.0	0
21624	Centrality Analysis of Protein-Protein Interaction Networks and Molecular Docking Prioritize Potential Drug-Targets in Type 1 Diabetes. Iranian Journal of Pharmaceutical Research, 2020, 19, 121-134.	0.3	4
21625	Characterization of pathways involved in colorectal cancer using real-time RT-PCR gene expression data. Gastroenterology and Hepatology From Bed To Bench, 2021, 14, 123-131.	0.6	2
21626	Network pharmacology-guided mechanism study uncovers inhibitory effect of Mahuang Decoction on lung cancer growth by impeding Akt/ERK signaling pathways. American Journal of Translational Research (discontinued), 2021, 13, 2094-2110.	0.0	2
21627	Immune-related gene expression signatures in colorectal cancer. Oncology Letters, 2021, 22, 543.	0.8	1
21628	Evaluating of Gene Expression Alteration after Garlic Consumption, Analyzing through Bioinformatics Approach. Iranian Journal of Pharmaceutical Research, 2021, 20, 72-81.	0.3	0
21629	Identification of candidate targets for the diagnosis and treatment of atherosclerosis by bioinformatics analysis. American Journal of Translational Research (discontinued), 2021, 13, 4137-4151.	0.0	3

#	ARTICLE	IF	CITATIONS
21630	Topological Analysis of Regulatory Networks Reveals Functionally Key Genes and miRNAs Involved in the Differentiation of Mesenchymal Stem Cells. Iranian Journal of Biotechnology, 2021, 19, e2565.	0.3	0
21631	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. Iranian Journal of Biotechnology, 2021, 19, e2560.	0.3	0
21632	Dysbiotic gut microbiota in pancreatic cancer patients form correlation networks with the oral microbiota and prognostic factors. American Journal of Cancer Research, 2021, 11, 3163-3175.	1.4	4
21633	Identification of novel survival-related lncRNA-miRNA-mRNA competing endogenous RNA network associated with immune infiltration in colorectal cancer. American Journal of Translational Research (discontinued), 2021, 13, 5815-5834.	0.0	2
21634	Comparative Bioinformatics Characteristic of Bladder Cancer Stage 2 from Stage 4 Expression Profile: A Network-Based Study. Galen, 2018, 7, e1279.	0.6	0
21635	Prediction of Key Proteins Via Topological Analysis of Protein-Protein Interaction Network. Galen, 2018, 7, e1129.	0.6	1
21636	Integrative Network Analysis Revealed Genetic Impact of Pyruvate Kinase L/R on Hepatocyte Proliferation and Graft Survival after Liver Transplantation. Oxidative Medicine and Cellular Longevity, 2021, 2021, 7182914.	1.9	0
21637	Multi-Omics Analysis Identified TMED2 as a Shared Potential Biomarker in Six Subtypes of Human Cancer. International Journal of General Medicine, 2021, 14, 7025-7042.	0.8	2
21638	Gene Co-Expression Analysis Identified Preserved and Survival-Related Modules in Severe Blunt Trauma, Burns, Sepsis, and Systemic Inflammatory Response Syndrome. International Journal of General Medicine, 2021, 14, 7065-7076.	0.8	0
21639	Identification of mitochondria-related hub genes in sarcopenia and functional regulation of MFG-E8 on ROS-mediated mitochondrial dysfunction and cell cycle arrest. Food and Function, 2022, 13, 624-638.	2.1	9
21640	A deep learning model to identify gene expression level using cobinding transcription factor signals. Briefings in Bioinformatics, 2022, 23, .	3.2	12
21641	Heptad stereotypy, S/Q layering, and remote origin of the SARS-CoV-2 fusion core. Virus Evolution, 2021, 7, veab097.	2.2	2
21642	A comprehensive transcription factor and DNA-binding motif resource for the construction of gene regulatory networks in Botrytis cinerea and Trichoderma atroviride. Computational and Structural Biotechnology Journal, 2021, 19, 6212-6228.	1.9	6
21643	Development and Validation of a Novel Immune-Related Prognostic Model and the Potential Mechanism in Metastatic Synovial Sarcoma. SSRN Electronic Journal, 0, , .	0.4	0
21644	Construction of miRNA-mRNA network reveals crucial miRNAs and genes in acute myocardial infarction. Journal of Biomedical Research, 2021, 35, 425.	0.7	4
21645	Lesion covariance networks reveal proposed origins and pathways of diffuse gliomas. Brain Communications, 2021, 3, fcab289.	1.5	11
21646	Circular RNA transcriptome analysis responses to heat stress in the hypothalamus of sows. Journal of Applied Animal Research, 2021, 49, 440-446.	0.4	0
21647	AURKB as a Promising Prognostic Biomarker in Hepatocellular Carcinoma. Evolutionary Bioinformatics, 2021, 17, 117693432110575.	0.6	7

#	ARTICLE	IF	CITATIONS
21648	A TP53-associated immune prognostic signature for the prediction of the overall survival and therapeutic responses in pancreatic cancer. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 191-208.	1.0	4
21649	Proteomic dissection of rice cytoskeleton reveals the dominance of microtubule and microfilament proteins, and novel components in the cytoskeleton-bound polysome. <i>Plant Physiology and Biochemistry</i> , 2022, 170, 75-86.	2.8	1
21650	Coupling ecological network analysis with high-throughput sequencing-based surveys: Lessons from the next-generation biomonitoring project. <i>Advances in Ecological Research</i> , 2021, 65, 367-430.	1.4	5
21651	Molecular pathways involved in COVID-19 and potential pathway-based therapeutic targets. <i>Biomedicine and Pharmacotherapy</i> , 2022, 145, 112420.	2.5	78
21652	Introduction to basics of bioinformatics. , 2022, , 1-15.		5
21653	MMP modulated differentiation of mouse embryonic stem cells on engineered cell derived matrices. <i>Biomaterials</i> , 2022, 280, 121268.	5.7	3
21654	Chemoproteomic-enabled characterization of small GTPase Rab1a as a target of an <i>N</i> -arylbenzimidazole ligand's rescue of Parkinson's-associated cell toxicity. <i>RSC Chemical Biology</i> , 2022, 3, 96-111.	2.0	5
21655	Elucidation of the anti-inflammatory mechanism of Er Miao San by integrative approach of network pharmacology and experimental verification. <i>Pharmacological Research</i> , 2022, 175, 106000.	3.1	45
21656	Colonization characteristics of pioneer surface-associated eukaryotes during natural biofilm formation on PDMS-based composites via 18S rRNA gene sequencing methods. <i>International Biodeterioration and Biodegradation</i> , 2022, 166, 105341.	1.9	0
21657	Pathway modeling and simulation analysis. , 2022, , 409-423.		2
21658	Systems biomarkers for papillary thyroid cancer prognosis and treatment through multi-omics networks. <i>Archives of Biochemistry and Biophysics</i> , 2022, 715, 109085.	1.4	18
21659	Antibody ligation of CEACAM1, CEACAM3, and CEACAM6, differentially enhance the cytokine release of human neutrophils in responses to <i>Candida albicans</i> . <i>Cellular Immunology</i> , 2022, 371, 104459.	1.4	1
21660	Machine learning based predictive model and systems-level network of host-microbe interactions in post-COVID-19 mucormycosis. <i>Microbial Pathogenesis</i> , 2022, 162, 105324.	1.3	5
21661	Splicing factor SRSF1 controls distinct molecular programs in regulatory and effector T cells implicated in systemic autoimmune disease. <i>Molecular Immunology</i> , 2022, 141, 94-103.	1.0	6
21662	Applications and challenges of microarray and RNA-sequencing. , 2022, , 91-103.		9
21663	Identification of key genes involved in recovery from spinal cord injury in adult zebrafish. <i>Neural Regeneration Research</i> , 2022, 17, 1334.	1.6	5
21664	Neuroprotective effects of long noncoding RNAs involved in ischemic postconditioning after ischemic stroke. <i>Neural Regeneration Research</i> , 2022, 17, 1299.	1.6	3
21665	Edaphic factors override temperature in shaping soil bacterial diversity across an elevation-vegetation gradient in Himalaya. <i>Applied Soil Ecology</i> , 2022, 170, 104306.	2.1	5



#	ARTICLE	IF	CITATIONS
21666	Neogargarooligosaccharides modulate gut microbiota and alleviate body weight gain and metabolic syndrome in high-fat diet-induced obese rats. <i>Journal of Functional Foods</i> , 2022, 88, 104869.	1.6	16
21667	Influence of environmental variables on methane related microbial activities in a tropical bio-secured zero-exchange shrimp culture system. <i>Aquaculture Reports</i> , 2022, 22, 100950.	0.7	6
21668	Understanding aquaporin regulation defining silicon uptake and role in arsenic, antimony and germanium stress in pigeonpea ( <i>Cajanus cajan</i> ). <i>Environmental Pollution</i> , 2022, 294, 118606.	3.7	11
21669	Hydrogen cyanamide enhances flowering time in tea oil camellia ( <i>Camellia oleifera</i> Abel.). <i>Industrial Crops and Products</i> , 2022, 176, 114313.	2.5	10
21670	Fast and slow myofiber-specific expression profiles are affected by noncoding RNAs in Mongolian horses. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100942.	0.4	1
21671	Actinobacterial biofertilizer improves the yields of different plants and alters the assembly processes of rhizosphere microbial communities. <i>Applied Soil Ecology</i> , 2022, 171, 104345.	2.1	17
21672	Proteomic Profiling of Lysine Acetylation Indicates Mitochondrial Dysfunction in the Hippocampus of Gut Microbiota-Absent Mice. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 594332.	1.4	13
21673	Bioinformatics analysis of SARS-CoV-2 infection-associated immune injury and therapeutic prediction for COVID-19. <i>Emergency and Critical Care Medicine</i> , 2021, 1, 20-28.	0.1	0
21674	Augmenting Code Review Experience Through Visualization. , 2021, , .		1
21675	<i>Rhizoma polygonati</i> from Mount Tai: nutritional value and usefulness as a traditional Chinese medicine, source of herbzyme, and potential remediating agent for COVID-19 and chronic and hidden hunger. , 2021, 1, 31-38.		15
21677	Network Pharmacology-Based and Molecular Docking Analysis of Resveratrol's Pharmacological Effects on Type I Endometrial Cancer. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2022, 22, 1933-1944.	0.9	3
21678	The active lung microbiota landscape of COVID-19 patients through the metatranscriptome data analysis. <i>BiolImpacts</i> , 2021, 12, 139-146.	0.7	25
21679	Multi-Omics Analysis Identified TMED2 as a Shared Potential Biomarker in Six Subtypes of Human Cancer. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7025-7042.	0.8	7
21680	Construction of a circular <sc>RNA</sc>â€“<sc>microRNA</sc>â€“messenger <sc>RNA</sc> regulatory network of <sc>hsa_circ_0043256</sc> in lung cancer by integrated analysis. <i>Thoracic Cancer</i> , 2022, 13, 61-75.	0.8	4
21681	Transcriptomic Characterization of Cow, Donkey and Goat Milk Extracellular Vesicles Reveals Their Anti-Inflammatory and Immunomodulatory Potential. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12759.	1.8	27
21682	Defective cytokinin signaling reprograms lipid and flavonoid gene-to-metabolite networks to mitigate high salinity in <i>Arabidopsis</i>. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	34
21683	The Transcriptional Differences of Avian CD4+CD8+ Double-Positive T Cells and CD8+ T Cells From Peripheral Blood of ALV-J Infected Chickens Revealed by Smart-Seq2. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 747094.	1.8	6
21684	Identification and Validation of Prognostic Factors of Lipid Metabolism in Obstructive Sleep Apnea. <i>Frontiers in Genetics</i> , 2021, 12, 747576.	1.1	3

#	ARTICLE	IF	CITATIONS
21685	Transcriptome based identification and validation of heat stress transcription factors in wheat progenitor species <i>Aegilops speltoides</i> . <i>Scientific Reports</i> , 2021, 11, 22049.	1.6	9
21686	A systems genetics approach reveals PbrNSC as a regulator of lignin and cellulose biosynthesis in stone cells of pear fruit. <i>Genome Biology</i> , 2021, 22, 313.	3.8	32
21687	Centromere-Specific Retrotransposons and Very-Long-Chain Fatty Acid Biosynthesis in the Genome of Yellowhorn ( <i>Xanthoceras sorbifolium</i> , Sapindaceae), an Oil-Producing Tree With Significant Drought Resistance. <i>Frontiers in Plant Science</i> , 2021, 12, 766389.	1.7	6
21688	A Novel Lipid Prognostic Signature of ADCY2, LIPE, and OLR1 in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 735993.	1.3	8
21689	Integrated Strategy of UHPLC-Q-TOF-MS and Molecular Networking for Identification of Diterpenoids from <i>Euphorbia fischeriana</i> Steud. and Prediction of the Anti-Breast-Cancer Mechanism by the Network Pharmacological Method. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-19.	0.5	1
21690	The Transcriptome and Metabolome Reveal Stress Responses in Sulfur-Fumigated Cucumber ( <i>Cucumis</i> ) Tj ETQq1 1,0,784314,rgBT /O	1.7	8
21691	Leaf Size Development Differences and Comparative Transcriptome Analyses of Two Poplar Genotypes. <i>Genes</i> , 2021, 12, 1775.	1.0	15
21692	Proteomic dissection of large extracellular vesicle surfaceome unravels interactive surface platform. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12164.	5.5	40
21693	Diverse human astrocyte and microglial transcriptional responses to Alzheimer's pathology. <i>Acta Neuropathologica</i> , 2022, 143, 75-91.	3.9	80
21696	Vitis OneGenE: A Causality-Based Approach to Generate Gene Networks in <i>Vitis vinifera</i> Sheds Light on the Laccase and Dirigent Gene Families. <i>Biomolecules</i> , 2021, 11, 1744.	1.8	16
21697	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , 2021, 599, 485-490.	13.7	126
21698	Yap5 Competes With Hap4 for the Regulation of Iron Homeostasis Genes in the Human Pathogen <i>Candida glabrata</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 731988.	1.8	0
21699	Identification of Gene Co-Expression Modules and Core Genes Related to Immune Disorders in Major Depression Disorder. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7983-7993.	0.8	1
21700	CYCLON and NPM1 Cooperate within an Oncogenic Network Predictive of R-CHOP Response in DLBCL. <i>Cancers</i> , 2021, 13, 5900.	1.7	6
21701	Suppression and Activation of Intracellular Immune Response in Initial Severe Acute Respiratory Syndrome Coronavirus 2 Infection. <i>Frontiers in Microbiology</i> , 2021, 12, 768740.	1.5	1
21702	Molecular Insight Into the Therapeutic Potential of Long Non-coding RNA-Associated Competing Endogenous RNA Axes in Alzheimer's Disease: A Systematic Scoping Review. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 742242.	1.7	14
21703	Involvement of homeobox transcription factor Mohawk in palatogenesis. <i>Congenital Anomalies (discontinued)</i> , 2021, , .	0.3	2
21704	Genomic analysis to screen potential genes and mutations in children with non-syndromic early onset severe obesity: a multicentre study in Turkey. <i>Molecular Biology Reports</i> , 2021, , 1.	1.0	3

#	ARTICLE	IF	CITATIONS
21705	Single-Cell RNA Sequencing Analysis of the Heterogeneity in Gene Regulatory Networks in Colorectal Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 765578.	1.8	4
21706	Discovery and biosynthesis of cyclic plant peptides via autocatalytic cyclases. <i>Nature Chemical Biology</i> , 2022, 18, 18-28.	3.9	36
21707	A comparative study of pan-genome methods for microbial organisms: <i>Acinetobacter baumannii</i> pan-genome reveals structural variation in antimicrobial resistance-carrying plasmids. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
21708	Plasma-Derived Extracellular Vesicles Reveal Galectin-3 Binding Protein as Potential Biomarker for Early Detection of Glioma. <i>Frontiers in Oncology</i> , 2021, 11, 778754.	1.3	9
21709	Discovery of putative tumor suppressors from CRISPR screens reveals rewired lipid metabolism in acute myeloid leukemia cells. <i>Nature Communications</i> , 2021, 12, 6506.	5.8	13
21710	Circular RNA-associated ceRNA network involved in HIF-1 signalling in triple-negative breast cancer: circ_0047303 as a potential key regulator. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 11322-11332.	1.6	13
21711	POGZ promotes homology-directed DNA repair in an HP1-dependent manner. <i>EMBO Reports</i> , 2022, 23, e51041.	2.0	9
21712	Pharmacological Mechanism of Danggui-Sini Formula for Intervertebral Disc Degeneration: A Network Pharmacology Study. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	3
21713	A role of anterior cingulate cortex in the emergence of worker-parasite relationship. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	3
21714	Potential Molecular Targets of Tenofovir Disoproxil Fumarate for Alleviating Chronic Liver Diseases via a Non-Antiviral Effect in a Normal Mouse Model. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 763150.	1.6	4
21715	Genome-wide understanding of evolutionary and functional relationships of rice Yellow Stripe-Like (YSL) transporter family in comparison with other plant species. <i>Biologia (Poland)</i> , 2022, 77, 39-53.	0.8	11
21716	Role of FRG1 in predicting the overall survivability in cancers using multivariate based optimal model. <i>Scientific Reports</i> , 2021, 11, 22505.	1.6	2
21717	Treatment with mixed probiotics induced, enhanced and diversified modulation of the gut microbiome of healthy rats. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	4
21718	Proteome-Informed Machine Learning Studies of Cocaine Addiction. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 11122-11134.	2.1	8
21719	Transcriptomic Changes in Internode Explants of Stinging Nettle during Callogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12319.	1.8	1
21720	NETWORK INTERACTIONS OF GLOBAL SUPPLY CHAIN MEMBERS. <i>Journal of Business Economics and Management</i> , 2021, 22, 1593-1613.	1.1	2
21721	A genome-scale TF-DNA interaction network of transcriptional regulation of primary and specialized metabolism. <i>Molecular Systems Biology</i> , 2021, 17, e10625.	3.2	15
21722	A Colorectal Cancer 3D Bioprinting Workflow as a Platform for Disease Modeling and Chemotherapeutic Screening. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 755563.	2.0	17

#	ARTICLE	IF	CITATIONS
21723	CRISPR screens unveil signal hubs for nutrient licensing of T cell immunity. <i>Nature</i> , 2021, 600, 308-313.	13.7	36
21724	Trimethylamine-N-oxide-stimulated hepatocyte-derived exosomes promote inflammation and endothelial dysfunction through nuclear factor-kappa B signaling. <i>Annals of Translational Medicine</i> , 2021, 9, 1670-1670.	0.7	10
21725	Exploring the Therapeutic Mechanism of Tingli Dazao Xiefei Decoction on Heart Failure Based on Network Pharmacology and Experimental Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	4
21726	Air pollution-regulated E-cadherin mediates contact inhibition of proliferation via the hippo signaling pathways in emphysema. <i>Chemico-Biological Interactions</i> , 2022, 351, 109763.	1.7	8
21727	The O2-ZmGRAS11 transcriptional regulatory network orchestrates the coordination of endosperm cell expansion and grain filling in Maize. <i>Molecular Plant</i> , 2022, 15, 468-487.	3.9	25
21728	Network Medicine-Based Analysis of Association Between Gynecological Cancers and Metabolic and Hormonal Disorders. <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 323-338.	1.4	2
21730	Identification of tumour immune microenvironment-related alternative splicing events for the prognostication of pancreatic adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 1211.	1.1	7
21731	Effects of poor sleep on the immune cell landscape as assessed by single-cell analysis. <i>Communications Biology</i> , 2021, 4, 1325.	2.0	21
21732	Rugonidines A-F, Diastereomeric 1,6-Dioxo-7,9-diazaspiro[4.5]dec-7-en-8-amines from the Leaves of <i>Alchornea rugosa</i> . <i>Journal of Natural Products</i> , 2021, 84, 3055-3063.	1.5	4
21733	Metagenomics Analysis to Investigate the Microbial Communities and Their Functional Profile During Cyanobacterial Blooms in Lake Varese. <i>Microbial Ecology</i> , 2022, 83, 850-868.	1.4	15
21734	Feature-Based Molecular Networking—An Exciting Tool to Spot Species of the Genus <i>Cortinarius</i> with Hidden Photosensitizers. <i>Metabolites</i> , 2021, 11, 791.	1.3	4
21735	Identifying the Predictive Role of Oxidative Stress Genes in the Prognosis of Glioma Patients. <i>Medical Science Monitor</i> , 2021, 27, e934161.	0.5	8
21736	Comparing the epigenetic landscape in myonuclei purified with a PCM1 antibody from a fast/glycolytic and a slow/oxidative muscle. <i>PLoS Genetics</i> , 2021, 17, e1009907.	1.5	12
21737	In Silico Characterization and Expression Profiles of Heat Shock Transcription Factors (HSFs) in Maize ( <i>Zea mays</i> L.). <i>Agronomy</i> , 2021, 11, 2335.	1.3	13
21738	Whole-transcriptome sequencing reveals a vernalization-related ceRNA regulatory network in chinese cabbage ( <i>Brassica campestris</i> L. ssp. <i>pekinensis</i> ). <i>BMC Genomics</i> , 2021, 22, 819.	1.2	13
21739	Global identification and integrated analysis of heat-responsive long non-coding RNAs in contrasting rice cultivars. <i>Theoretical and Applied Genetics</i> , 2022, 135, 833-852.	1.8	7
21740	Joint GWAS and WGCNA uncover the genetic control of calcium accumulation under salt treatment in maize seedlings. <i>Physiologia Plantarum</i> , 2022, 174, e13606.	2.6	8
21741	Bioinformatics-Guided Expansion and Discovery of Graspetides. <i>ACS Chemical Biology</i> , 2021, 16, 2787-2797.	1.6	31

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21742	Analysis of the thaumatin-like genes of <i>Rosa chinensis</i> and functional analysis of the role of RcTLP6 in salt stress tolerance. <i>Planta</i> , 2021, 254, 118.	1.6	8
21743	<i>Staphylococcus aureus</i> injection drug use-associated bloodstream infections are propagated by community outbreaks of diverse lineages. <i>Communications Medicine</i> , 2021, 1, .	1.9	9
21744	Ancient hybridization patterns between bighorn and thinhorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	2.0	4
21745	Co-activation of Sonic hedgehog and Wnt signaling in murine retinal precursor cells drives ocular lesions with features of intraocular medulloepithelioma. <i>Oncogenesis</i> , 2021, 10, 78.	2.1	0
21746	Stress granule-associated TaMBF1c confers thermotolerance through regulating specific mRNA translation in wheat ( <i>Triticum aestivum</i> ). <i>New Phytologist</i> , 2022, 233, 1719-1731.	3.5	31
21748	Muscle transcriptome provides the first insight into the dynamics of gene expression with progression of age in sheep. <i>Scientific Reports</i> , 2021, 11, 22360.	1.6	11
21749	Unveiling Ecological and Genetic Novelty within Lytic and Lysogenic Viral Communities of Hot Spring Phototrophic Microbial Mats. <i>Microbiology Spectrum</i> , 2021, , e0069421.	1.2	4
21750	SARS-CoV-2 infection and replication in human gastric organoids. <i>Nature Communications</i> , 2021, 12, 6610.	5.8	47
21751	Identification of Unique Transcriptomic Signatures and Hub Genes Through RNA Sequencing and Integrated WGCNA and PPI Network Analysis in Nonerosive Reflux Disease. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 6143-6156.	1.6	6
21752	Increased Collagen Turnover Is a Feature of Fibromuscular Dysplasia and Associated With Hypertrophic Radial Remodeling: A Pilot, Urine Proteomic Study. <i>Hypertension</i> , 2022, 79, 93-103.	1.3	4
21753	Prognostic Significance of Alternative Splicing Genes in Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7933-7949.	0.8	1
21754	Biosynthesis of fluopsin C, a copper-containing antibiotic from <i>Pseudomonas aeruginosa</i> . <i>Science</i> , 2021, 374, 1005-1009.	6.0	50
21755	Phosphoproteomic Comparison of Four <i>Eimeria tenella</i> Life Cycle Stages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12110.	1.8	6
21756	Investigation on the antitumor effects of paeonol against renal cell carcinoma based on network pharmacology and experimental validation. <i>Journal of Ethnopharmacology</i> , 2022, 285, 114857.	2.0	7
21757	Mechanistic insights into the renoprotective role of curcumin in cisplatin-induced acute kidney injury: network pharmacology analysis and experimental validation. <i>Bioengineered</i> , 2021, 12, 11039-11054.	1.4	5
21758	Identification of proximal SUMO-dependent interactors using SUMO-ID. <i>Nature Communications</i> , 2021, 12, 6671.	5.8	27
21759	Identification of Two Long Non-Coding RNAs AC010082.1 and AC011443.1 as Biomarkers of Coronary Heart Disease Based on Logistic Stepwise Regression Prediction Model. <i>Frontiers in Genetics</i> , 2021, 12, 780431.	1.1	1
21760	Temporal and sequential order of nonoverlapping gene networks unraveled in mated female <i>Drosophila</i> . <i>Life Science Alliance</i> , 2022, 5, e202101119.	1.3	4

#	ARTICLE	IF	CITATIONS
21761	<i>ZNF76</i> predicts prognosis and response to platinum chemotherapy in human ovarian cancer. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
21762	A combined EM and proteomic analysis places HIV-1 Vpu at the crossroads of retromer and ESCRT complexes: PTPN23 is a Vpu-cofactor. <i>PLoS Pathogens</i> , 2021, 17, e1009409.	2.1	0
21763	Ion Channel and Ubiquitin Differential Expression during Erythromycin-Induced Anhidrosis in Foals. <i>Animals</i> , 2021, 11, 3379.	1.0	1
21766	Chikungunya Virus Infects the Heart and Induces Heart-Specific Transcriptional Changes in an Immunodeficient Mouse Model of Infection. <i>American Journal of Tropical Medicine and Hygiene</i> , 2022, 106, 99-104.	0.6	6
21767	A review on the role of epidermal growth factor signaling in the development, progression and treatment of cervical cancer. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 179-187.	3.6	13
21768	Decreasing molecular diversity of soil dissolved organic matter related to microbial community along an alpine elevation gradient. <i>Science of the Total Environment</i> , 2022, 818, 151823.	3.9	19
21769	Transporter Protein-Guided Genome Mining for Head-to-Tail Cyclized Bacteriocins. <i>Molecules</i> , 2021, 26, 7218.	1.7	7
21770	Fatty acid-binding protein 5 aggravates pulmonary artery fibrosis in pulmonary hypertension secondary to left heart disease via activating wnt/ $\beta$ -catenin pathway. <i>Journal of Advanced Research</i> , 2022, 40, 197-206.	4.4	14
21771	Occurrence and phylogenetic analysis of <i>Pseudanabaena</i> sp. producing 2-methylisoborneol in drinking water source of South Korea. <i>Environmental Microbiology Reports</i> , 2022, 14, 197-202.	1.0	6
21772	Prioritization of human well-being spectrum related GWAS-SNVs using ENCODE-based web-tools predict interplay between PSMC3, ITIH4, and SERPINC1 genes in modulating well-being. <i>Journal of Psychiatric Research</i> , 2022, 145, 92-101.	1.5	2
21773	In silico Methods for Identification of Potential Therapeutic Targets. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 285-310.	2.2	17
21775	Pan-Cancer Analyses Reveal Oncogenic and Immunological Role of Dickkopf-1 (DKK1). <i>Frontiers in Genetics</i> , 2021, 12, 757897.	1.1	9
21776	Construction of a Support Vector Machine-Based Classifier for Pulmonary Arterial Hypertension Patients. <i>Frontiers in Genetics</i> , 2021, 12, 781011.	1.1	2
21777	Loss-of-function mutation in <i>IKZF2</i> leads to immunodeficiency with dysregulated germinal center reactions and reduction of MAIT cells. <i>Science Immunology</i> , 2021, 6, eabe3454.	5.6	30
21778	Drug metabolism-related eight-gene signature can predict the prognosis of gastric adenocarcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24085.	0.9	10
21780	Verification of the Potential Targets of the Herbal Prescription Sochehwan for Drug Repurposing Processes as Deduced by Network Pharmacology. <i>Processes</i> , 2021, 9, 2034.	1.3	1
21781	Identifying the Effect of Ursolic Acid Against Triple-Negative Breast Cancer: Coupling Network Pharmacology With Experiments Verification. <i>Frontiers in Pharmacology</i> , 2021, 12, 685773.	1.6	4
21782	Galectin network in osteoarthritis: galectin-4 programs a pathogenic signature of gene and effector expression in human chondrocytes in vitro. <i>Histochemistry and Cell Biology</i> , 2021, .	0.8	2



#	ARTICLE	IF	CITATIONS
21783	Strong partitioning of soil bacterial community composition and co-occurrence networks along a small-scale elevational gradient on Zijin Mountain. <i>Soil Ecology Letters</i> , 2021, 3, 290-302.	2.4	13
21784	Diterpenes/Diterpenoids and Their Derivatives as Potential Bioactive Leads against Dengue Virus: A Computational and Network Pharmacology Study. <i>Molecules</i> , 2021, 26, 6821.	1.7	22
21785	Presence and Persistence of Putative Lytic and Temperate Bacteriophages in Vaginal Metagenomes from South African Adolescents. <i>Viruses</i> , 2021, 13, 2341.	1.5	8
21786	Mono-specific algal diets shape microbial networking in the gut of the sea urchin <i>Tripneustes gratilla elatensis</i> . <i>Animal Microbiome</i> , 2021, 3, 79.	1.5	7
21787	An ECHO of Cartilage: In Silico Prediction of Combinatorial Treatments to Switch Between Transient and Permanent Cartilage Phenotypes With Ex Vivo Validation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 732917.	2.0	3
21788	Study of Neuronal Apoptosis ceRNA Network in Hippocampal Sclerosis of Human Temporal Lobe Epilepsy by RNA-Seq. <i>Frontiers in Neuroscience</i> , 2021, 15, 770627.	1.4	11
21790	Genome-Wide Characterization of Salt-Responsive miRNAs, circRNAs and Associated ceRNA Networks in Tomatoes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12238.	1.8	12
21791	Wnt signaling mediates acquisition of blood-brain barrier properties in naïve endothelium derived from human pluripotent stem cells. <i>ELife</i> , 2021, 10, .	2.8	31
21792	PCNA in Cervical Intraepithelial Neoplasia and Cervical Cancer: An Interaction Network Analysis of Differentially Expressed Genes. <i>Frontiers in Oncology</i> , 2021, 11, 779042.	1.3	7
21793	IFN-Gamma and TNF-Alpha as a Priming Strategy to Enhance the Immunomodulatory Capacity of Secretomes from Menstrual Blood-Derived Stromal Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12177.	1.8	13
21794	Network-based identification of miRNAs and transcription factors and in silico drug screening targeting $\beta$ -secretase involved in Alzheimer's disease. <i>Heliyon</i> , 2021, 7, e08502.	1.4	4
21795	Oxandrastins: Antibacterial Meroterpenes from an Australian Mud Dauber Wasp Nest-Associated Fungus, <i>Penicillium</i> sp. CMB-MD14. <i>Molecules</i> , 2021, 26, 7144.	1.7	4
21797	Phylogenetic Analysis of the Membrane Attack Complex/Perforin Domain-Containing Proteins in <i>Gossypium</i> and the Role of GhMACPF26 in Cotton Under Cold Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 684227.	1.7	6
21798	Identification of the Active Constituents and Significant Pathways of Shen-qi-Yi-zhu Decoction on Antigastric Cancer: A Network Pharmacology Research and Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	3
21799	Deep analysis of neuroblastoma core regulatory circuitries using online databases and integrated bioinformatics shows their pan-cancer roles as prognostic predictors. <i>Discover Oncology</i> , 2021, 12, 56.	0.8	6
21800	HIV-1 genetic transmission networks among people living with HIV/AIDS in Sichuan, China: a genomic and spatial epidemiological analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 18, 100318.	1.3	9
21801	A conserved expression signature predicts growth rate and reveals cell & lineage-specific differences. <i>PLoS Computational Biology</i> , 2021, 17, e1009582.	1.5	4
21803	Predicting protein interaction network perturbation by alternative splicing with semi-supervised learning. <i>Cell Reports</i> , 2021, 37, 110045.	2.9	3

#	ARTICLE	IF	CITATIONS
21804	Identification of intrinsically disordered regions in hub genes of acute myeloid leukemia: A bioinformatics approach. <i>Biotechnology and Applied Biochemistry</i> , 2022, 69, 2304-2322.	1.4	2
21805	Distinct microbiota assembly mechanisms revealed in different reconstruction stages during gut regeneration in the sea cucumber <i>Apostichopus japonicus</i> . <i>MicrobiologyOpen</i> , 2021, 10, e1250.	1.2	5
21806	A System Pharmacology Model for Decoding the Synergistic Mechanisms of Compound Kushen Injection in Treating Breast Cancer. <i>Frontiers in Pharmacology</i> , 2021, 12, 723147.	1.6	0
21807	Inhibition of the renin-angiotensin system causes concentric hypertrophy of renal arterioles in mice and humans. <i>JCI Insight</i> , 2021, 6, .	2.3	16
21808	3-D vascularized breast cancer model to study the role of osteoblast in formation of a pre-metastatic niche. <i>Scientific Reports</i> , 2021, 11, 21966.	1.6	8
21809	A catalog of curated breast cancer genes. <i>Breast Cancer Research and Treatment</i> , 2022, 191, 431-441.	1.1	3
21810	Network medicine for disease module identification and drug repurposing with the NeDRex platform. <i>Nature Communications</i> , 2021, 12, 6848.	5.8	39
21811	Interrogation of the microenvironmental landscape in spinal ependymomas reveals dual functions of tumor-associated macrophages. <i>Nature Communications</i> , 2021, 12, 6867.	5.8	19
21812	Genome-wide identification and characterization of long noncoding RNAs in maize under rice black streaked dwarf virus infection. <i>Plant Pathology</i> , 0, , .	1.2	1
21813	Mechanism of Hip Arthropathy in Ankylosing Spondylitis: Abnormal Myeloperoxidase and Phagosome. <i>Frontiers in Immunology</i> , 2021, 12, 572592.	2.2	10
21814	Transcriptome and metabolome analysis to reveal major genes of saikosaponin biosynthesis in <i>Bupleurum chinense</i> . <i>BMC Genomics</i> , 2021, 22, 839.	1.2	9
21816	Bioinformatics screening of ETV4 transcription factor oncogenes and identifying small-molecular anticancer drugs. <i>Chemical Biology and Drug Design</i> , 2022, 99, 277-285.	1.5	3
21817	Identification of miRNAs and genes for predicting Barrett's esophagus progressing to esophageal adenocarcinoma using miRNA-mRNA integrated analysis. <i>PLoS ONE</i> , 2021, 16, e0260353.	1.1	2
21818	A network pharmacology-based strategy to explore the pharmacological mechanisms of <i>Antrodia camphorata</i> and antcin K for treating type II diabetes mellitus. <i>Phytomedicine</i> , 2022, 96, 153851.	2.3	9
21819	Investigation of the Proteomes of the Truffles <i>Tuber albidum</i> pico, <i>T. aestivum</i> , <i>T. indicum</i> , <i>T. magnatum</i> , and <i>T. melanosporum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 12999.	1.8	8
21820	Unravelling the Initial Triggers of <i>Botrytis cinerea</i> Infection: First Description of Its Surfactome. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1021.	1.5	1
21822	Identification of Key Dereglated RNA-Binding Proteins in Pancreatic Cancer by Meta-Analysis and Prediction of Their Role as Modulators of Oncogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 713852.	1.8	8
21823	Mycorrhiza-Induced Alterations in Metabolome of <i>Medicago lupulina</i> Leaves during Symbiosis Development. <i>Plants</i> , 2021, 10, 2506.	1.6	7

#	ARTICLE	IF	CITATIONS
21824	TP53 Mutation Infers a Poor Prognosis and Is Correlated to Immunocytes Infiltration in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 759154.	1.8	19
21825	Exploring the Role of Oxidative Stress in Sperm Motility: A Proteomic Network Approach. <i>Antioxidants and Redox Signaling</i> , 2022, 37, 501-520.	2.5	6
21826	Pan-genome analysis identifies intersecting roles for <i>Pseudomonas</i> specialized metabolites in potato pathogen inhibition. <i>ELife</i> , 2021, 10, .	2.8	25
21827	Involvement of immune system and Epithelial-Mesenchymal-Transition in increased invasiveness of clustered circulatory tumor cells in breast cancer. <i>BMC Medical Genomics</i> , 2021, 14, 273.	0.7	10
21828	Overexpression of Lin28A in neural progenitor cells in vivo does not lead to brain tumor formation but results in reduced spine density. <i>Acta Neuropathologica Communications</i> , 2021, 9, 185.	2.4	5
21829	Construction and Bioinformatics Analysis of the miRNA-mRNA Regulatory Network in Diabetic Nephropathy. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	4
21830	Identification of aquaporins and deciphering their role under salinity stress in pomegranate ( <i>Punica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	5
21831	The cell-surface 5'-nucleotidase CD73 defines a functional T memory cell subset that declines with age. <i>Cell Reports</i> , 2021, 37, 109981.	2.9	15
21832	Bioinformatics analyses of the pathogenesis and new biomarkers of chronic obstructive pulmonary disease. <i>Medicine (United States)</i> , 2021, 100, e27737.	0.4	2
21834	Identification of a novel prognosis-associated ceRNA network in lung adenocarcinoma via bioinformatics analysis. <i>BioMedical Engineering OnLine</i> , 2021, 20, 117.	1.3	4
21835	Future Challenges in Plant. <i>Methods in Molecular Biology</i> , 2022, 2395, 325-337.	0.4	0
21837	Effects of ultra-long fermentation time on the microbial community and flavor components of light-flavor Xiaoqu Baijiu based on fermentation tanks. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 3.	1.7	21
21838	A network pharmacology approach to reveal the pharmacological targets and biological mechanism of compound kushen injection for treating pancreatic cancer based on WGCNA and in vitro experiment validation. <i>Chinese Medicine</i> , 2021, 16, 121.	1.6	21
21839	The copper-linked <i>Escherichia coli</i> AZY operon: Structure, metal binding, and a possible physiological role in copper delivery. <i>Journal of Biological Chemistry</i> , 2022, 298, 101445.	1.6	1
21840	Protein-protein interactions: Methods, databases, and applications in virus-host study. <i>World Journal of Virology</i> , 2021, 10, 288-300.	1.3	10
21841	A systematic genome-wide mapping of oncogenic mutation selection during CRISPR-Cas9 genome editing. <i>Nature Communications</i> , 2021, 12, 6512.	5.8	24
21842	A Standardized Brain Molecular Atlas: A Resource for Systems Modeling and Simulation. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 604559.	1.4	3
21844	Dissection of the Complex Transcription and Metabolism Regulation Networks Associated with Maize Resistance to <i>Ustilago maydis</i> . <i>Genes</i> , 2021, 12, 1789.	1.0	11

#	ARTICLE	IF	CITATIONS
21845	Integrated Transcriptomics and Metabolomics Analysis Reveal Key Metabolism Pathways Contributing to Cold Tolerance in Peanut. <i>Frontiers in Plant Science</i> , 2021, 12, 752474.	1.7	25
21846	Alterations in T-Cell Transcription Factors and Cytokine Gene Expression in Late-Onset Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 645-665.	1.2	8
21847	Identification of miRNA-mRNA network and immune-related gene signatures in IgA nephropathy by integrated bioinformatics analysis. <i>BMC Nephrology</i> , 2021, 22, 392.	0.8	8
21848	Proximity-dependent biotinylation detects associations between SARS coronavirus nonstructural protein 1 and stress granule-associated proteins. <i>Journal of Biological Chemistry</i> , 2021, 297, 101399.	1.6	7
21849	Hidden diversity of double-stranded DNA phages in symbiotic <i>Rhizobium</i> species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200468.	1.8	5
21850	Mapping cis-regulatory elements in the midgestation mouse placenta. <i>Scientific Reports</i> , 2021, 11, 22331.	1.6	7
21851	Pre-existing chromatin accessibility and gene expression differences among naive CD4+ T cells influence effector potential. <i>Cell Reports</i> , 2021, 37, 110064.	2.9	20
21852	Unravelling lncRNA mediated gene expression as potential mechanism for regulating secondary metabolism in <i>Citrus limon</i> . <i>Food Bioscience</i> , 2022, 46, 101448.	2.0	9
21853	Searching for New Microbiome-Targeted Therapeutics through a Drug Repurposing Approach. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17277-17286.	2.9	4
21856	Identification and Validation of a 6-Metabolism-Related Gene Signature and Its Correlation With Immune Checkpoint in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 783934.	1.3	3
21857	Computational Network Pharmacology-Based Strategy to Capture Key Functional Components and Decode the Mechanism of Chai-Hu-Shu-Gan-San in Treating Depression. <i>Frontiers in Pharmacology</i> , 2021, 12, 782060.	1.6	6
21858	Identifying Two Novel Clusters in Calcium Oxalate Stones With Urinary Tract Infection Using 16S rDNA Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 723781.	1.8	3
21860	Identification of Prognostic Gene Biomarkers in Non-Small Cell Lung Cancer Progression by Integrated Bioinformatics Analysis. <i>Biology</i> , 2021, 10, 1200.	1.3	16
21861	Identification of a novel metabolism-related gene signature associated with the survival of bladder cancer. <i>BMC Cancer</i> , 2021, 21, 1267.	1.1	8
21862	An integrated host-microbiome response to atrazine exposure mediates toxicity in <i>Drosophila</i> . <i>Communications Biology</i> , 2021, 4, 1324.	2.0	10
21863	Mutation-Induced Long-Range Allosteric Interactions in the Spike Protein Determine the Infectivity of SARS-CoV-2 Emerging Variants. <i>ACS Omega</i> , 2021, 6, 31305-31320.	1.6	8
21865	Temporal Transcript Profiling Identifies a Role for Unfolded Protein Stress in Human Gut Ischemia-Reperfusion Injury. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 681-694.	2.3	10
21866	Genetic ancestry effects on the response to viral infection are pervasive but cell type specific. <i>Science</i> , 2021, 374, 1127-1133.	6.0	68

#	ARTICLE	IF	CITATIONS
21867	Potential Pathogenic Genes and Mechanism of Ankylosing Spondylitis: A Study Based on WGCNA and Bioinformatics Analysis. <i>World Neurosurgery</i> , 2022, 158, e543-e556.	0.7	2
21868	Diversification of plasmids in a genus of pathogenic and nitrogen-fixing bacteria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200466.	1.8	12
21870	Genome-Wide RNA-Sequencing Reveals Massive Circular RNA Expression Changes of the Neurotransmission Genes in the Rat Brain after Ischemiaâ€“Reperfusion. <i>Genes</i> , 2021, 12, 1870.	1.0	8
21871	LIMD2 is a Prognostic and Predictive Marker in Patients With Esophageal Cancer Based on a ceRNA Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 774432.	1.1	5
21872	Network Pharmacology Integrated Molecular Docking Revealed the Mechanism of Jianpi Yiqi Taohua Decoction Against Ulcerative Colitis. <i>Medical Science Monitor</i> , 2022, 28, e933537.	0.5	2
21873	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. <i>Nature Communications</i> , 2021, 12, 6761.	5.8	47
21874	Dynamic Protein Corona of Gold Nanoparticles with an Evolving Morphology. <i>ACS Applied Materials &amp; Interfaces</i> , 2021, 13, 58238-58251.	4.0	23
21876	Potential biomarkers of abnormal osseointegration of implants in type II diabetes mellitus. <i>BMC Oral Health</i> , 2021, 21, 583.	0.8	4
21877	Divergent Response Strategies of CsABF Facing Abiotic Stress in Tea Plant: Perspectives From Drought-Tolerance Studies. <i>Frontiers in Plant Science</i> , 2021, 12, 763843.	1.7	9
21878	Î²-Cyclocitral, a Master Regulator of Multiple Stress-Responsive Genes in <i>Solanum lycopersicum</i> L. Plants. <i>Plants</i> , 2021, 10, 2465.	1.6	6
21879	Targeting the spliceosome through RBM39 degradation results in exceptional responses in high-risk neuroblastoma models. <i>Science Advances</i> , 2021, 7, eabj5405.	4.7	32
21880	Hundreds of LncRNAs Display Circadian Rhythmicity in Zebrafish Larvae. <i>Cells</i> , 2021, 10, 3173.	1.8	1
21881	Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 768981.	1.8	1
21882	Transcriptional Profiles of Cell Fate Transitions Reveal Early Drivers of Neuronal Apoptosis and Survival. <i>Cells</i> , 2021, 10, 3238.	1.8	3
21883	Exploring the Mechanisms of Arsenic Trioxide (Pishuang) in Hepatocellular Carcinoma Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-9.	0.5	3
21884	Comprehensive analysis of miRNAâ€“mRNA regulatory network and potential drugs in chronic chagasic cardiomyopathy across human and mouse. <i>BMC Medical Genomics</i> , 2021, 14, 283.	0.7	13
21885	Transcriptome sequencing revealed the influence of blue light on the expression levels of light-stress response genes in <i>Centella asiatica</i> . <i>PLoS ONE</i> , 2021, 16, e0260468.	1.1	6
21887	A Bioactive Extract Rich in Triterpenic Acid and Polyphenols from <i>Olea europaea</i> Promotes Systemic Immunity and Protects Atlantic Salmon Smolts Against Furunculosis. <i>Frontiers in Immunology</i> , 2021, 12, 737601.	2.2	8

#	ARTICLE	IF	CITATIONS
21888	Dynamic Expression and Regulatory Network of Circular RNA for Abdominal Preadipocytes Differentiation in Chicken ( <i>Gallus gallus</i> ). <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 761638.	1.8	12
21889	Global mitochondrial protein import proteomics reveal distinct regulation by translation and translocation machinery. <i>Molecular Cell</i> , 2022, 82, 435-446.e7.	4.5	34
21891	Bacterial and Archaeal Community Distribution in Oilfield Water Re-injection Facilities and the Influences from Microorganisms in Injected Water. <i>Microbial Ecology</i> , 2021, , 1.	1.4	1
21892	Exploration of the Key Proteins of High-Grade Intraepithelial Neoplasia to Adenocarcinoma Sequence Using In-Depth Quantitative Proteomics Analysis. <i>Journal of Oncology</i> , 2021, 2021, 1-13.	0.6	5
21893	Expression Patterns and Regulation of Non-Coding RNAs during Synthesis of Cellulose in <i>Eucalyptus grandis</i> Hill. <i>Forests</i> , 2021, 12, 1565.	0.9	5
21894	Key Markers Involved in the Anticolon Cancer Response of CD8+ T Cells through the Regulation of Cholesterol Metabolism. <i>Journal of Oncology</i> , 2021, 2021, 1-11.	0.6	6
21895	MiR-574-5P, miR-1827, and miR-4429 as Potential Biomarkers for Schizophrenia. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 226-238.	1.1	16
21896	Intraocular Viral Communities Associated With Post-fever Retinitis. <i>Frontiers in Medicine</i> , 2021, 8, 724195.	1.2	6
21897	Construction of circRNA-miRNA-mRNA network and identification of novel potential biomarkers for non-small cell lung cancer. <i>Cancer Cell International</i> , 2021, 21, 611.	1.8	13
21898	Identification and Potential Mechanisms of a 7-MicroRNA Signature That Predicts Prognosis in Patients with Lower-Grade Glioma. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	4
21899	Genome-Wide Identification of CircRNAs of Infective Larvae and Adult Worms of Parasitic Nematode, <i>Haemonchus contortus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 764089.	1.8	8
21900	SKA3 Serves as a Biomarker for Poor Prognosis in Kidney Renal Papillary Cell Carcinoma. <i>International Journal of General Medicine</i> , 2021, Volume 14, 8591-8602.	0.8	10
21901	Gephyrin Interacts with the K-Cl Cotransporter KCC2 to Regulate Its Surface Expression and Function in Cortical Neurons. <i>Journal of Neuroscience</i> , 2022, 42, 166-182.	1.7	17
21902	Hif-1a suppresses ROS-induced proliferation of cardiac fibroblasts following myocardial infarction. <i>Cell Stem Cell</i> , 2022, 29, 281-297.e12.	5.2	71
21903	Manure Application Increases Soil Bacterial and Fungal Network Complexity and Alters Keystone Taxa. <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 607-618.	1.7	12
21904	Proteomic analysis reveals <i>Renibacterium salmoninarum</i> grown under iron-limited conditions induces iron uptake mechanisms and overproduction of the 57 kDa protein. <i>Journal of Fish Diseases</i> , 2021, 45, 289.	0.9	3
21905	Web-based transcriptome analysis determines a sixteen-gene signature and associated drugs on hearing loss patients: A bioinformatics approach. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24065.	0.9	6
21906	Proteomic Changes of Activated Hepatic Stellate Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12782.	1.8	8



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21907	Dendrochronological Provenance Patterns. Network Analysis of Tree-Ring Material Reveals Spatial and Economic Relations of Roman Timber in the Continental North-Western Provinces. <i>Journal of Computer Applications in Archaeology</i> , 2021, 4, 230.	0.8	1
21908	<i>Cyperus rotundus</i> L. reverses the olanzapine-induced weight gain and metabolic changes-outcomes from network and experimental pharmacology. <i>Computers in Biology and Medicine</i> , 2022, 141, 105035.	3.9	6
21909	Identification of <i>ITPR1</i> as a Hub Gene of Group 3 Medulloblastoma and Coregulated Genes with Potential Prognostic Values. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 633-641.	1.1	6
21911	Comparative proteomics reveals <i>Cryptosporidium parvum</i> manipulation of the host cell molecular expression and immune response. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009949.	1.3	6
21912	Identifying potential novel insights for COVID-19 pathogenesis and therapeutics using an integrated bioinformatics analysis of host transcriptome. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 770-780.	3.6	6
21914	The structure and functional profile of ruminal microbiota in young and adult reindeers ( <i>Rangifer</i> ) Tj ETQq1 1 0.784314 rgBT /Over e12389.	0.9	11
21915	Comprehensive Study of Human FBXW7 Deleterious nsSNPs Functional Inference and Susceptibility to Gynaecological Cancer. <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 407-433.	1.4	2
21916	Screening and Analysis of Key Genes in miRNA-mRNA Regulatory Network of Membranous Nephropathy. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-13.	1.1	3
21917	Weighted Gene Co-Expression Network Analysis and Treatment Strategies of Tumor Recurrence-Associated Hub Genes in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 756235.	1.1	6
21918	Global Transcriptome and Coexpression Network Analyses Reveal New Insights Into Somatic Embryogenesis in Hybrid Sweetgum ( <i>Liquidambar styraciflua</i> – <i>Liquidambar formosana</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 751866.	1.7	14
21919	Global miRNA expression of bone marrow mesenchymal stem/stromal cells derived from Fanconi anemia patients. <i>Human Cell</i> , 2022, 35, 111-124.	1.2	3
21920	Implication of proliferation gene biomarkers in pulmonary hypertension. <i>Animal Models and Experimental Medicine</i> , 2021, 4, 369-380.	1.3	11
21921	Single-cell transcriptomic profiles reveal changes associated with BCG-induced trained immunity and protective effects in circulating monocytes. <i>Cell Reports</i> , 2021, 37, 110028.	2.9	31
21922	Convergent molecular mechanisms underlying cognitive impairment in mucopolysaccharidosis type II. <i>Metabolic Brain Disease</i> , 2021, , 1.	1.4	2
21923	Machine learning of genomic features in organotropic metastases stratifies progression risk of primary tumors. <i>Nature Communications</i> , 2021, 12, 6692.	5.8	16
21924	Co-Regulation of Protein Coding Genes by Transcription Factor and Long Non-Coding RNA in SARS-CoV-2 Infected Cells: An In Silico Analysis. <i>Non-coding RNA</i> , 2021, 7, 74.	1.3	5
21926	Unexpected diversity among small-scale sample replicates of defined plant root compartments. <i>ISME Journal</i> , 2022, 16, 997-1003.	4.4	28
21927	A Co-Association Network Analysis Reveals Putative Regulators for Health-Related Traits in Pigs. <i>Frontiers in Immunology</i> , 2021, 12, 784978.	2.2	3

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21928	Potential Mechanism of Dingji Fumai Decoction Against Atrial Fibrillation Based on Network Pharmacology, Molecular Docking, and Experimental Verification Integration Strategy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 712398.	1.1	13
21929	Insights into the SARS-CoV-2-Mediated Alteration in the Stress Granule Protein Regulatory Networks in Humans. <i>Pathogens</i> , 2021, 10, 1459.	1.2	9
21931	CicerSpTEdb: A web-based database for high-resolution genome-wide identification of transposable elements in Cicer species. <i>PLoS ONE</i> , 2021, 16, e0259540.	1.1	5
21932	Calculation of Similarity Between 26 Autoimmune Diseases Based on Three Measurements Including Network, Function, and Semantics. <i>Frontiers in Genetics</i> , 2021, 12, 758041.	1.1	1
21933	MADS-box transcription factors determine the duration of temporary winter dormancy in closely related evergreen and deciduous <i>Iris</i> spp.. <i>Journal of Experimental Botany</i> , 2022, 73, 1429-1449.	2.4	6
21934	SNCA antisense transcript SNCA <sup>AS1</sup> regulates synapses and aging-related genes suggesting its implication in Parkinson's disease. <i>Aging Cell</i> , 2021, 20, e13504.	3.0	20
21935	Characterization of Constitutive Promoters for the Elicitation of Secondary Metabolites in Myxobacteria. <i>ACS Synthetic Biology</i> , 2021, 10, 2904-2909.	1.9	10
21936	Autocrine vitamin D signaling switches off pro-inflammatory programs of TH1 cells. <i>Nature Immunology</i> , 2022, 23, 62-74.	7.0	105
21937	Genome-wide identification and co-expression analysis of GDSL genes related to suberin formation during fruit russeting in pear. <i>Horticultural Plant Journal</i> , 2022, 8, 153-170.	2.3	7
21938	The Effects of Consuming White Button Mushroom <i>Agaricus bisporus</i> on the Brain and Liver Metabolome Using a Targeted Metabolomic Analysis. <i>Metabolites</i> , 2021, 11, 779.	1.3	2
21939	Microbiome of Field Grown Hemp Reveals Potential Microbial Interactions With Root and Rhizosphere Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 741597.	1.5	9
21940	Dynamically Accumulating Homologous Recombination Deficiency Score Served as an Important Prognosis Factor in High-Grade Serous Ovarian Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 762741.	1.6	6
21941	Integrative genomic analysis of PPP3R1 in Alzheimer's disease: a potential biomarker for predictive, preventive, and personalized medical approach. <i>EPMA Journal</i> , 2021, 12, 647-658.	3.3	2
21942	Candesartan prevents arteriopathy progression in cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy model. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	12
21944	Transcriptome Analysis of Insulin Signaling-Associated Transcription Factors in <i>C. elegans</i> Reveal Their Genome-Wide Target Genes Specificity and Complexity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12462.	1.8	3
21945	Network based analysis identifies TP53m-BRCA1/2wt-homologous recombination proficient (HRP) population with enhanced susceptibility to Vigil immunotherapy. <i>Cancer Gene Therapy</i> , 2022, 29, 993-1000.	2.2	4
21946	Transcriptome dynamics in developing testes of domestic cats and impact of age on tissue resilience to cryopreservation. <i>BMC Genomics</i> , 2021, 22, 847.	1.2	5
21947	Excess Heritability Contribution of Alcohol Consumption Variants in the "Missing Heritability" of Type 2 Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12318.	1.8	0

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21948	Analysis of subunit folding contribution of three yeast large ribosomal subunit proteins required for stabilisation and processing of intermediate nuclear rRNA precursors. <i>PLoS ONE</i> , 2021, 16, e0252497.	1.1	5
21949	Mechanistically Diverse Pathways for Sulfoquinovose Degradation in Bacteria. <i>ACS Catalysis</i> , 2021, 11, 14740-14750.	5.5	21
21950	Comprehensive analysis of human chorionic membrane extracts regulating mesenchymal stem cells during osteogenesis. <i>Cell Proliferation</i> , 2022, 55, e13160.	2.4	3
21951	Screening key prognostic factors and constructing survival prognostic risk prediction model based on ceRNA network in early lung adenocarcinoma. <i>Translational Cancer Research</i> , 2021, 10, 4652-4663.	0.4	1
21952	Rg1 Promotes the Proliferation and Adipogenic Differentiation of Human Adipose-Derived Stem Cells via FXR1/Lnc-GAS5-AS1 Pathway. <i>Current Stem Cell Research and Therapy</i> , 2022, 17, 815-824.	0.6	1
21953	UPLC-MS/MS and Network Pharmacology-Based Analysis of Bioactive Anti-Depression Compounds in Betel Nut. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 4827-4836.	2.0	13
21954	Transcriptome Analysis of Neuroendocrine Regulation of Ovine Hypothalamus-Pituitary-Ovary Axis during Ovine Anestrus and the Breeding Season. <i>Genes</i> , 2021, 12, 1861.	1.0	8
21955	A spatial-temporal understanding of gene regulatory networks and NtARF-mediated regulation of potassium accumulation in tobacco. <i>Planta</i> , 2022, 255, 9.	1.6	5
21956	In situ analysis of variations of arsenicals, microbiome and transcriptome profiles along murine intestinal tract. <i>Journal of Hazardous Materials</i> , 2022, 427, 127899.	6.5	7
21957	Overexpression of melanoma-associated antigen A2 has a clinical significance in embryonal carcinoma and is associated with tumor progression. <i>Journal of Cancer Research and Clinical Oncology</i> , 2022, 148, 609-631.	1.2	1
21958	Characterization of bacterial and archaeal community structure in deep subsurface sediments in the Shenhu area, northern South China Sea. <i>Marine and Petroleum Geology</i> , 2021, 136, 105468.	1.5	3
21959	Microenvironment-associated gene HSD11B1 may serve as a prognostic biomarker in clear cell renal cell carcinoma: a study based on TCGA, RT-qPCR, Western blotting, and immunohistochemistry. <i>Bioengineered</i> , 2021, 12, 10891-10904.	1.4	17
21960	Comparative analysis of the immune responses in cancer cells irradiated with X-ray, proton and carbon-ion beams. <i>Biochemical and Biophysical Research Communications</i> , 2021, 585, 55-60.	1.0	11
21961	Comprehensive Analysis of the Mechanism of Periodontitis-Related mRNA Expression Combined with Upstream Methylation and ceRNA Regulation. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 707-719.	0.3	1
21962	Concerted regulation of non-alcoholic fatty liver disease progression by microRNAs in apolipoprotein E-deficient mice. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	5
21963	Network Integration Analysis and Immune Infiltration Analysis Reveal Potential Biomarkers for Primary Open-Angle Glaucoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 793638.	1.8	10
21964	Prognostic Implications and Immune Infiltration Analysis of ALDOA in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 721021.	1.1	11
21965	Identification of genes related to tipburn resistance in Chinese cabbage and preliminary exploration of its molecular mechanism. <i>BMC Plant Biology</i> , 2021, 21, 567.	1.6	4

#	ARTICLE	IF	CITATIONS
21966	GFI1 tethers the NuRD complex to open and transcriptionally active chromatin in myeloid progenitors. <i>Communications Biology</i> , 2021, 4, 1356.	2.0	6
21967	Whole-transcriptome analysis of aluminum-exposed rat hippocampus and identification of ceRNA networks to investigate neurotoxicity of Al. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1401-1417.	2.3	12
21968	Transcriptome Analysis Reveals Sexual Disparities between Olfactory and Immune Gene Expression in the Olfactory Epithelium of <i>Megalobrama amblycephala</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 13017.	1.8	0
21969	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	5.8	55
21970	Integrated transcriptome and small RNA sequencing analyses reveal a drought stress response network in <i>Sophora tonkinensis</i> . <i>BMC Plant Biology</i> , 2021, 21, 566.	1.6	4
21971	Replica exchange molecular dynamics simulations reveal self-association sites in M-crystallin caused by mutations provide insights of cataract. <i>Scientific Reports</i> , 2021, 11, 23270.	1.6	4
21972	The possible mechanism of <i>Hippophae fructus</i> oil applied in tympanic membrane repair identified based on network pharmacology and molecular docking. <i>Journal of Clinical Laboratory Analysis</i> , 2021, , e24157.	0.9	4
21973	Altered gut bacterial and metabolic signatures and their interaction in inflammatory bowel disease. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 377-383.	1.8	2
21974	Network Pharmacology-Based Study on the Mechanism of Aloe Vera for Treating Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-8.	0.5	2
21975	A single dose of Ultraviolet-A induces proteome remodeling and senescence in primary human keratinocytes. <i>Scientific Reports</i> , 2021, 11, 23355.	1.6	7
21976	5-Methylcytosine RNA Methyltransferases-Related Long Non-coding RNA to Develop and Validate Biochemical Recurrence Signature in Prostate Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 775304.	1.6	19
21977	In silico study of missense variants of FANCA, FANCC and FANCG genes reveals high risk deleterious alleles predisposing to Fanconi anemia pathogenesis. <i>Gene</i> , 2022, 812, 146104.	1.0	3
21978	A Meta-Omics Analysis Unveils the Shift in Microbial Community Structures and Metabolomics Profiles in Mangrove Sediments Treated with a Selective Actinobacterial Isolation Procedure. <i>Molecules</i> , 2021, 26, 7332.	1.7	6
21979	Chemical Diversity and Antimicrobial Potential of Cultivable Fungi from Deep-Sea Sediments of the Gulf of Mexico. <i>Molecules</i> , 2021, 26, 7328.	1.7	4
21980	MicroRNA-Target Interaction Regulatory Network in Alzheimer's Disease. <i>Journal of Personalized Medicine</i> , 2021, 11, 1275.	1.1	11
21981	A Comparative Transcriptomic Meta-Analysis Revealed Conserved Key Genes and Regulatory Networks Involved in Drought Tolerance in Cereal Crops. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13062.	1.8	15
21982	Pan-cancer analysis of non-oncogene addiction to DNA repair. <i>Scientific Reports</i> , 2021, 11, 23264.	1.6	5
21983	Nucleus and chloroplast: A necessary understanding to overcome heat stress in <i>Pinus radiata</i> . <i>Plant, Cell and Environment</i> , 2022, 45, 446-458.	2.8	7

#	ARTICLE	IF	CITATIONS
21984	Screening of bioactivity-oriented extraction approach and quality control standards of lotus leaf extracts with dual functions. <i>Food Bioscience</i> , 2021, 44, 101462.	2.0	6
21985	Genome-Wide RNAi Screening Identifies Novel Pathways/Genes Involved in Oxidative Stress and Repurposable Drugs to Preserve Cystic Fibrosis Airway Epithelial Cell Integrity. <i>Antioxidants</i> , 2021, 10, 1936.	2.2	3
21986	The circular RNA expression profile in ovarian serous cystadenocarcinoma reveals a complex circRNA-miRNA regulatory network. <i>BMC Medical Genomics</i> , 2021, 14, 276.	0.7	3
21987	Kinase-dead mutation: A novel strategy for improving soybean resistance to soybean cyst nematode <i>Heterodera glycines</i> . <i>Molecular Plant Pathology</i> , 2022, 23, 417-430.	2.0	9
21988	Polyphenol Utilization Proteins in the Human Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0185121.	1.4	3
21989	Genome-wide identification and analysis of Oleosin gene family in four cotton species and its involvement in oil accumulation and germination. <i>BMC Plant Biology</i> , 2021, 21, 569.	1.6	7
21990	Transmembrane signaling molecules play a key role in the pathogenesis of IgA nephropathy: a weighted gene co-expression network analysis study. <i>BMC Immunology</i> , 2021, 22, 73.	0.9	9
21992	Identification of prognostic genes in the pancreatic adenocarcinoma immune microenvironment by integrated bioinformatics analysis. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 1757-1769.	2.0	8
21994	Identification of Hub Genes in Hemifacial Microsomia. <i>Journal of Craniofacial Surgery</i> , 2021, Publish Ahead of Print, .	0.3	4
21995	Metabolomics Tools Assisting Classic Screening Methods in Discovering New Antibiotics from Mangrove Actinomycetia in Leizhou Peninsula. <i>Marine Drugs</i> , 2021, 19, 688.	2.2	10
21996	Characterizing the Copy Number Variation of Non-Coding RNAs Reveals Potential Therapeutic Targets and Prognostic Markers of LUSC. <i>Frontiers in Genetics</i> , 2021, 12, 779155.	1.1	7
21997	Light-mediated discovery of surfaceome nanoscale organization and intercellular receptor interaction networks. <i>Nature Communications</i> , 2021, 12, 7036.	5.8	33
21999	Coupling Root Diameter With Rooting Depth to Reveal the Heterogeneous Assembly of Root-Associated Bacterial Communities in Soybean. <i>Frontiers in Microbiology</i> , 2021, 12, 783563.	1.5	4
22000	Bioinformatic reanalysis of public proteomics data reveals that nuclear proteins are recurrent in cancer secretomes. <i>Traffic</i> , 2022, 23, 98-108.	1.3	3
22002	Identification of immune features of HIV-infected patients with antiretroviral therapy through bioinformatics analysis. <i>Virology</i> , 2021, 566, 69-74.	1.1	1
22003	Pan-cancer multi-omics analyses reveal crosstalk between the Hippo and immune signaling pathways in the tumor microenvironment. <i>FEBS Letters</i> , 2021, , .	1.3	1
22004	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	2.8	11
22005	Time-series transcriptomic analysis of bronchoalveolar lavage cells from virulent and low virulent PRRSV-1-infected piglets. <i>Journal of Virology</i> , 2021, , JVI0114021.	1.5	6

#	ARTICLE	IF	CITATIONS
22006	The molecular phenotypes of injury, steatohepatitis, and fibrosis in liver transplant biopsies in the INTERLIVER study. <i>American Journal of Transplantation</i> , 2022, 22, 909-926.	2.6	4
22007	Broad Ultrastructural and Transcriptomic Changes Underlie the Multinucleated Giant Hemocyte Mediated Innate Immune Response against Parasitoids. <i>Journal of Innate Immunity</i> , 2022, 14, 335-354.	1.8	5
22008	Shared Molecular Mechanisms between Atherosclerosis and Periodontitis by Analyzing the Transcriptomic Alterations of Peripheral Blood Monocytes. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-28.	0.7	8
22011	OSMAC Strategy Integrated with Molecular Networking for Accessing Griseofulvin Derivatives from Endophytic Fungi of <i>Moquiniastrium polymorphum</i> (Asteraceae). <i>Molecules</i> , 2021, 26, 7316.	1.7	6
22012	Identification and Integrate Analysis of Key Biomarkers for Diagnosis and Prognosis of Non-Small Cell Lung Cancer Based on Bioinformatics Analysis. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110602.	0.8	17
22013	Systemic characterization of alternative splicing related to prognosis, immune infiltration, and drug sensitivity analysis in ovarian cancer. <i>Annals of Translational Medicine</i> , 2021, 10, 0-0.	0.7	1
22014	<i>In vivo</i> and <i>in silico</i> studies on the mechanisms of egg white peptides in relieving acute colitis symptoms. <i>Food and Function</i> , 2021, 12, 12774-12787.	2.1	7
22015	The Q41R mutation in the HCV-protease enhances the reactivity towards MAVS by suppressing non-reactive pathways. <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 2126-2138.	1.3	1
22016	Network Pharmacology-Based to Analyze Screen <i>Selaginella Doederleinii</i> ™s against Myocardial Ischemia. <i>Traditional Chinese Medicine</i> , 2021, 10, 840-854.	0.1	1
22017	Screening of Important Factors in the Early Sepsis Stage Based on the Evaluation of ssGSEA Algorithm and ceRNA Regulatory Network. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110584.	0.6	23
22018	Prognostic significance of ferroptosis-related genes and their methylation in AML. <i>Hematology</i> , 2021, 26, 919-930.	0.7	15
22019	Potential Molecular Mechanisms and Remdesivir Treatment for Acute Respiratory Syndrome Corona Virus 2 Infection/COVID 19 Through RNA Sequencing and Bioinformatics Analysis. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110673.	1.0	2
22020	A universal approach for integrating super large-scale single-cell transcriptomes by exploring gene rankings. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
22021	A transcriptomic analysis based on aberrant methylation levels revealed potential novel therapeutic targets for nasopharyngeal carcinoma. <i>Annals of Translational Medicine</i> , 2022, 10, 47-47.	0.7	4
22022	System Biology and Network Analysis Approaches on Oxidative Stress in Cancer. , 2021, , 1-18.		0
22023	Deciphering the potential anti-COVID-19 active ingredients in <i>Andrographis paniculata</i> (Burm. F.) Nees by combination of network pharmacology, molecular docking, and molecular dynamics. <i>RSC Advances</i> , 2021, 11, 36511-36517.	1.7	17
22024	Molecular Insights into the mechanisms of mucosal immunity induced by <i>Brucella abortus</i> infection in nasal-associated lymphoid tissues. <i>International Journal of Transgender Health</i> , 2021, 14, 809-818.	1.1	0
22025	Community Detection in Protein-Protein Interaction Networks and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 217-237.	1.9	11



#	ARTICLE	IF	CITATIONS
22026	Construction of a miRNA-mRNA-TFs Network Related to Diabetic Nephropathy. SSRN Electronic Journal, 0, , .	0.4	0
22028	Chemical profile of <i>Stachytarpheta schottiana</i> by LC-HRMS/MS dereplication and molecular networking. Rodriguesia, 0, 72, .	0.9	1
22029	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. Briefings in Bioinformatics, 2022, 23, .	3.2	10
22030	Decomposed Straw Mitigation of Soil N <sub>2</sub> o Emissions by Changing Dissolved Organic Matter and Denitrifying Bacterial Favoring Complete Denitrification. SSRN Electronic Journal, 0, , .	0.4	1
22031	Whole transcriptome analysis of high and low IFN $\alpha$ producers reveals differential response patterns following rhinovirus stimulation. Clinical and Translational Immunology, 2021, 10, e1356.	1.7	1
22032	Multimiomics Personalized Network Analyses Highlight Progressive Immune Disruption of Central Metabolism Associated with COVID-19 Severity. SSRN Electronic Journal, 0, , .	0.4	3
22033	Manufacturing T cells in hollow fiber membrane bioreactors changes their programming and enhances their potency. Oncoimmunology, 2021, 10, 1995168.	2.1	2
22034	Exploring the therapeutic mechanisms of <i>Cassia glauca</i> in diabetes mellitus through network pharmacology, molecular docking and molecular dynamics. RSC Advances, 2021, 11, 39362-39375.	1.7	16
22035	Analysis of the San Luis Obispo Bay Microbiome from a Network Perspective. Studies in Computational Intelligence, 2022, , 664-675.	0.7	1
22037	Evaluation of expression changes, proteins interaction network, and microRNAs targeting catalase and superoxide dismutase genes under cold stress in rapeseed ( <i>Brassica napus</i> L.). OCL - Oilseeds and Fats, Crops and Lipids, 2022, 29, 3.	0.6	4
22038	Identification of Candidate Gene Signatures and Regulatory Networks in Endometriosis and its Related Infertility by Integrated Analysis. Reproductive Sciences, 2022, 29, 411-426.	1.1	4
22039	Network pharmacology and <i>in vitro</i> experimental verification to explore the mechanism of Sanhua decoction in the treatment of ischaemic stroke. Pharmaceutical Biology, 2022, 60, 119-130.	1.3	13
22040	Blood transcriptome analysis revealed the immune changes and immunological adaptation of wildness training giant pandas. Molecular Genetics and Genomics, 2022, 297, 227-239.	1.0	4
22041	Multi-scale mechanism of antiviral drug-alike phytoligands from Ayurveda in managing COVID-19 and associated metabolic comorbidities: insights from network pharmacology. Molecular Diversity, 2022, 26, 2575-2594.	2.1	6
22042	Screening and analysis of RNAs associated with activated memory CD4 and CD8 T cells in liver cancer. World Journal of Surgical Oncology, 2022, 20, 2.	0.8	7
22043	Guanxin V Acts as an Antioxidant in Ventricular Remodeling. Frontiers in Cardiovascular Medicine, 2021, 8, 778005.	1.1	6
22044	Integration of Automatic Text Mining and Genomic and Proteomic Analysis to Unravel Prostate Cancer Biomarkers. Journal of Proteome Research, 2022, 21, 447-458.	1.8	5
22045	Identification of the Host Substratome of Leishmania-Secreted Casein Kinase 1 Using a SILAC-Based Quantitative Mass Spectrometry Assay. Frontiers in Cell and Developmental Biology, 2021, 9, 800098.	1.8	4

#	ARTICLE	IF	CITATIONS
22046	Integrative genomic analysis of a novel small nucleolar RNAs prognostic signature in patients with acute myelocytic leukemia. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 2424-2452.	1.0	4
22047	MAGEA6 positively regulates MSMO1 and promotes the migration and invasion of oesophageal cancer cells. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, 204.	0.8	4
22048	LncRNA functional annotation with improved false discovery rate achieved by disease associations. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 322-332.	1.9	4
22049	Gene Co-Expression Analysis Reveals Transcriptome Divergence between Wild and Cultivated Sugarcane under Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 569.	1.8	22
22050	Comparisons of the immunological landscape of COVID-19 patients based on sex and disease severity by multi-omics analysis. <i>Chemico-Biological Interactions</i> , 2022, 352, 109777.	1.7	1
22051	Omicron N501Y mutation among SARS-CoV-2 lineages: In silico analysis of potent binding to tyrosine kinase and hypothetical repurposed medicine. <i>Travel Medicine and Infectious Disease</i> , 2022, 45, 102242.	1.5	25
22052	Untargeted metabolomic analyses reveal the diversity and plasticity of the specialized metabolome in seeds of different <i>Camelina sativa</i> genotypes. <i>Plant Journal</i> , 2022, 110, 147-165.	2.8	9
22053	Mobile Genetic Elements Drive Antimicrobial Resistance Gene Spread in Pasteurellaceae Species. <i>Frontiers in Microbiology</i> , 2021, 12, 773284.	1.5	11
22054	Characterizing toxicity pathways of fluoxetine to predict adverse outcomes in adult fathead minnows ( <i>Pimephales promelas</i> ). <i>Science of the Total Environment</i> , 2022, 817, 152747.	3.9	5
22055	Reconstruction and analysis of transcriptome regulatory network of <i>Methanobrevibacter ruminantium</i> M1. <i>Gene Reports</i> , 2022, 26, 101489.	0.4	1
22056	Epithelial-mesenchymal transition related genes in unruptured aneurysms identified through weighted gene coexpression network analysis. <i>Scientific Reports</i> , 2022, 12, 225.	1.6	5
22057	BIRC2-BIRC3 amplification: a potentially druggable feature of a subset of head and neck cancers in patients with Fanconi anemia. <i>Scientific Reports</i> , 2022, 12, 45.	1.6	10
22058	Structural Identification of Metalloproteomes in Marine Diatoms, an Efficient Algae Model in Toxic Metals Bioremediation. <i>Molecules</i> , 2022, 27, 378.	1.7	10
22060	Multi-Omics Integration and Network Analysis Reveal Potential Hub Genes and Genetic Mechanisms Regulating Bovine Mastitis. <i>Current Issues in Molecular Biology</i> , 2022, 44, 309-328.	1.0	11
22061	Integrative omics analysis identifies biomarkers of idiopathic pulmonary fibrosis. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 66.	2.4	8
22062	Clinical Efficacy Evaluation and Potential Mechanism of Zhishe Tongluo Capsule in the Treatment of Cerebral Infarction by Meta-Analysis Associated with Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	1
22063	Deep Time Course Proteomics of SARS-CoV- and SARS-CoV-2-Infected Human Lung Epithelial Cells (Calu-3) Reveals Strong Induction of Interferon-Stimulated Gene Expression by SARS-CoV-2 in Contrast to SARS-CoV. <i>Journal of Proteome Research</i> , 2022, 21, 459-469.	1.8	16
22065	The System Research of the Molecular Mechanism of Quyushengxin Capsule in the Treatment of Osteonecrosis of the Femoral Head. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	2

#	ARTICLE	IF	CITATIONS
22066	Comprehensive analysis of the LncRNAs, MiRNAs, and MRNAs acting within the competing endogenous RNA network of LGG. <i>Genetica</i> , 2022, 150, 41.	0.5	1
22067	Immuno-genomic characterisation of high-grade serous ovarian cancer reveals immune evasion mechanisms and identifies an immunological subtype with a favourable prognosis and improved therapeutic efficacy. <i>British Journal of Cancer</i> , 2022, 126, 1570-1580.	2.9	18
22068	Proteomics Analysis of Exosomes From Patients With Active Tuberculosis Reveals Infection Profiles and Potential Biomarkers. <i>Frontiers in Microbiology</i> , 2021, 12, 800807.	1.5	13
22069	Artificial-Intelligence-Assisted Discovery of Genetic Factors for Precision Medicine of Antiplatelet Therapy in Diabetic Peripheral Artery Disease. <i>Biomedicines</i> , 2022, 10, 116.	1.4	5
22070	IL-17 Pathway Members as Potential Biomarkers of Effective Systemic Treatment and Cardiovascular Disease in Patients with Moderate-to-Severe Psoriasis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 555.	1.8	13
22071	Integrated microbiology and metabolomics analysis reveal responses of soil microorganisms and metabolic functions to phosphorus fertilizer on semiarid farm. <i>Science of the Total Environment</i> , 2022, 817, 152878.	3.9	40
22072	Immune-related gene expression in skin, inflamed and keloid tissue from patients with keloids. <i>Oncology Letters</i> , 2022, 23, 72.	0.8	6
22073	The Vulnerability of the Developing Brain: Analysis of Highly Expressed Genes in Infant C57BL/6 Mouse Hippocampus in Relation to Phenotypic Annotation Derived From Mutational Studies. <i>Bioinformatics and Biology Insights</i> , 2022, 16, 117793222110627.	1.0	1
22074	Genome-wide integrated analysis reveals functions of lncRNA-miRNA-mRNA interactions in Atlantic salmon challenged by <i>Aeromonas salmonicida</i> . <i>Genomics</i> , 2022, 114, 328-339.	1.3	9
22075	GhAPC8 regulates leaf blade angle by modulating multiple hormones in cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 1 0.784314 rgBT /Over	3.6	8
22076	Comparative Transcriptomic Analysis Reveals Diverse Expression Pattern Underlying Fatty Acid Composition among Different Beef Cuts. <i>Foods</i> , 2022, 11, 117.	1.9	6
22077	Comparative Transcriptomic Analyses of Different Jujube Cultivars Reveal the Co-Regulation of Multiple Pathways during Fruit Cracking. <i>Genes</i> , 2022, 13, 105.	1.0	8
22078	Genome-wide identification and functional analysis of circRNAs in <i>Trichophyton rubrum</i> conidial and mycelial stages. <i>BMC Genomics</i> , 2022, 23, 21.	1.2	3
22079	Systems scale characterization of circadian rhythm pathway in <i>Camellia sinensis</i> . <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 598-607.	1.9	5
22080	Impact of circ-0000221 in the Pathogenesis of Hepatocellular via Modulation of miR-661-PTPN11 mRNA Axis. <i>Pharmaceutics</i> , 2022, 14, 138.	2.0	1
22081	microRNA Profile Associated with Positive Lymph Node Metastasis in Early-Stage Cervical Cancer. <i>Current Oncology</i> , 2022, 29, 243-254.	0.9	4
22082	An in silico analysis of genome-wide expression profiles of the effects of exhaustive exercise identifies heat shock proteins as the key players. <i>Meta Gene</i> , 2022, 31, 101012.	0.3	1
22083	Trans cohort metabolic reprogramming towards glutaminolysis in long-term successfully treated HIV-infection. <i>Communications Biology</i> , 2022, 5, 27.	2.0	13

#	ARTICLE	IF	CITATIONS
22084	DNA Damage and Proteomic Profile Changes in Rat Salivary Glands After Chronic Exposure to Inorganic Mercury. <i>Biological Trace Element Research</i> , 2022, , 1.	1.9	1
22085	Analysis of the cells isolated from epithelial cell rests of Malassez through single-cell limiting dilution. <i>Scientific Reports</i> , 2022, 12, 382.	1.6	3
22086	Breath biomarkers of insulin resistance in pre-diabetic Hispanic adolescents with obesity. <i>Scientific Reports</i> , 2022, 12, 339.	1.6	8
22087	Altered succinylation of mitochondrial proteins, APP and tau in Alzheimer's disease. <i>Nature Communications</i> , 2022, 13, 159.	5.8	42
22088	Nitrogen fixing bacteria facilitate microbial biodegradation of a bio-based and biodegradable plastic in soils under ambient and future climatic conditions. <i>Environmental Sciences: Processes and Impacts</i> , 2022, 24, 233-241.	1.7	12
22089	Persistent coxsackievirus B1 infection triggers extensive changes in the transcriptome of human pancreatic ductal cells. <i>IScience</i> , 2022, 25, 103653.	1.9	3
22090	Integrated molecular networking strategy enhance the accuracy and visualization of components identification: A case study of Ginkgo biloba leaf extract. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2022, 209, 114523.	1.4	9
22091	Developing a molecular roadmap to Narasimha Rasayana: A system Polypharmacology approach. <i>Gene Reports</i> , 2022, 26, 101488.	0.4	0
22092	Identification of the GTPase IMAP family as an immune-related prognostic biomarker in the breast cancer tumor microenvironment. <i>Gene</i> , 2022, 812, 146094.	1.0	8
22093	Comparison between Heat-Clearing Medicine and Antirheumatic Medicine in Treatment of Gastric Cancer Based on Network Pharmacology, Molecular Docking, and Tumor Immune Infiltration Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-21.	0.5	3
22094	Quantitative proteomics reveals differential immunoglobulin-associated proteome (IgAP) in patients of acute myocardial infarction and chronic coronary syndromes. <i>Journal of Proteomics</i> , 2022, 252, 104449.	1.2	2
22095	Chemical constituents and antibacterial activity of <i>Bromelia laciniosa</i> (Bromeliaceae): Identification and structural characterization. <i>Phytomedicine Plus</i> , 2022, 2, 100215.	0.9	2
22096	Metagenomic features of traditional fermented milk products. <i>LWT - Food Science and Technology</i> , 2022, 155, 112945.	2.5	24
22097	Microplastic consumption induces inflammatory signatures in the colon and prolongs a viral arthritis. <i>Science of the Total Environment</i> , 2022, 809, 152212.	3.9	38
22098	Flud: A Hybrid Crowd's Algorithm Approach for Visualizing Biological Networks. <i>ACM Transactions on Computer-Human Interaction</i> , 2022, 29, 1-53.	4.6	2
22099	6-gingerol ameliorates metabolic disorders by inhibiting hypertrophy and hyperplasia of adipocytes in high-fat-diet induced obese mice. <i>Biomedicine and Pharmacotherapy</i> , 2022, 146, 112491.	2.5	14
22100	Cathepsin B is a potential therapeutic target for coronavirus disease 2019 patients with lung adenocarcinoma. <i>Chemico-Biological Interactions</i> , 2022, 353, 109796.	1.7	11
22101	A novel PAK4 inhibitor suppresses pancreatic cancer growth and enhances the inhibitory effect of gemcitabine. <i>Translational Oncology</i> , 2022, 16, 101329.	1.7	12

#	ARTICLE	IF	CITATIONS
22102	Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine. <i>Environmental Pollution</i> , 2022, 295, 118667.	3.7	10
22103	TNF signaling pathway-mediated microglial activation in the PFC underlies acute paradoxical sleep deprivation-induced anxiety-like behaviors in mice. <i>Brain, Behavior, and Immunity</i> , 2022, 100, 254-266.	2.0	21
22104	Chemical constituents from marine derived fungus <i>Talaromyces cellulolyticus</i> SHJ-3 and its chemotaxonomic significance. <i>Biochemical Systematics and Ecology</i> , 2022, 100, 104377.	0.6	4
22105	Re-aliment regains feed deprivation-induced microflora dysbiosis and immune stress in the gut of red swamp crayfish ( <i>Procambarus clarkii</i> ). <i>Aquaculture Reports</i> , 2022, 22, 100992.	0.7	4
22106	Prevalence of Actinobacteria in the production of 2-methylisoborneol and geosmin, over Cyanobacteria in a temperate eutrophic reservoir. <i>Chemical Engineering Journal Advances</i> , 2022, 9, 100226.	2.4	12
22107	A network-based integration for understanding racial disparity in prostate cancer. <i>Translational Oncology</i> , 2022, 17, 101327.	1.7	2
22108	Defining the interactomes of proteins involved in cytoskeletal dynamics using high-throughput proximity-dependent biotinylation in cellulose. <i>STAR Protocols</i> , 2022, 3, 101075.	0.5	4
22109	Use the Chinese herbal compound regulatory network to verify the relationship between the Jun, Chen, Zuo, and Shi of Xiaochaihu Decoction in treating hepatitis. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 2, 100023.	0.5	4
22110	Transcriptomic analysis of MA-10 tumor Leydig cells treated with adipose derived hormones adiponectin and resistin. <i>Reproductive Biology</i> , 2022, 22, 100598.	0.9	0
22111	Gut microbiome composition likely affects the growth of razor clam <i>Sinonovacula constricta</i> . <i>Aquaculture</i> , 2022, 550, 737847.	1.7	13
22112	The Screening and Identification of Key Biomarkers in Adrenocortical Carcinoma: Evidence from a Bioinformatics Analysis. <i>Journal of Biomaterials and Tissue Engineering</i> , 2022, 12, 523-532.	0.0	0
22113	Meta-analysis of genome-wide association studies for litter size in sheep. <i>Theriogenology</i> , 2022, 180, 103-112.	0.9	10
22114	Computational design of phage cocktails based on phage-bacteria infection networks. <i>Computers in Biology and Medicine</i> , 2022, 142, 105186.	3.9	5
22115	A new strategy for distinguishing menstrual blood from peripheral blood by the miR-451a/miR-21-5p ratio. <i>Forensic Science International: Genetics</i> , 2022, 57, 102654.	1.6	6
22116	Neuronetworks: Analysis of brain pathology in Mucopolysaccharidoses "A" A systems biology approach. <i>Neuroscience Informatics</i> , 2022, 2, 100036.	2.8	1
22117	Buyang Huanwu Decoction promotes angiogenesis in myocardial infarction through suppression of PTEN and activation of the PI3K/Akt signalling pathway. <i>Journal of Ethnopharmacology</i> , 2022, 287, 114929.	2.0	15
22118	The mechanism of FZXJJZ decoction suppresses colorectal liver metastasis via the VDR/TGF- $\beta$ 2/Snail1 signaling pathways based on network pharmacology-TCGA data-transcriptomics analysis. <i>Journal of Ethnopharmacology</i> , 2022, 287, 114904.	2.0	6
22119	<i>Perkinsus marinus</i> suppresses in vitro eastern oyster apoptosis via IAP-dependent and caspase-independent pathways involving TNFR, NF- $\kappa$ B, and oxidative pathway crosstalk. <i>Developmental and Comparative Immunology</i> , 2022, 129, 104339.	1.0	4

#	ARTICLE	IF	CITATIONS
22120	The use of the multidimensional protein identification technology (MudPIT) to analyze plasma proteome of astronauts collected before, during, and after spaceflights. <i>Acta Astronautica</i> , 2022, 193, 9-19.	1.7	5
22121	Differential responses of abomasal transcriptome to <i>Haemonchus contortus</i> infection between <i>Haemonchus</i> -selected and <i>Trichostrongylus</i> -selected merino sheep. <i>Parasitology International</i> , 2022, 87, 102539.	0.6	3
22122	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	6
22123	Using mRNA deep sequencing to analyze differentially expressed genes during <i>Panax notoginseng</i> saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	1
22124	Identification of key biomarkers and potential signaling pathway associated with poor progression of gastric cancer. <i>Translational Cancer Research</i> , 2020, 9, 5459-5472.	0.4	1
22125	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	1
22126	The modulation relationship of genomic pattern of intratumor heterogeneity and immunity microenvironment heterogeneity in hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	2
22127	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	4
22128	High ADAMTS18 expression is associated with poor prognosis in stomach adenocarcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	7
22129	Screening of potential genes and transcription factors involved in post-radiation cognitive dysfunction in mice via bioinformatics. <i>Translational Cancer Research</i> , 2020, 9, 6383-6391.	0.4	0
22132	Mathematical Model and Simulation for Nutrient-Plant Interaction Analysis. , 2020, , .		2
22133	Transcriptomic analysis reveals a WNT signaling pathway-based gene signature prognostic for non-small cell carcinoma. <i>Aging</i> , 2020, 12, 19159-19172.	1.4	0
22134	iTRAQ-based proteomic analysis of the interaction of A549 human lung epithelial cells with <i>Aspergillus fumigatus</i> conidia. <i>Molecular Medicine Reports</i> , 2020, 22, 4601-4610.	1.1	2
22135	Screening Potential Biomarkers of Breast Cancer Based on Bioinformatics. , 2020, , .		0
22136	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk based on multiple omics datasets. <i>Aging</i> , 2020, 12, 19173-19220.	1.4	6
22137	Investigating the expressions of miRNA-125b and TP53 in endometriosis. Does it underlie cancer-like features of endometriosis? A case-control study. <i>International Journal of Reproductive BioMedicine</i> , 2020, 18, 825-836.	0.5	5
22139	Interaction network of immune-associated genes affecting the prognosis of patients with glioblastoma. <i>Experimental and Therapeutic Medicine</i> , 2020, 21, 61.	0.8	4
22140	Hub Genes Identification in Brain Cancer with Gene Expression Data. , 2020, , .		0



#	ARTICLE	IF	CITATIONS
22141	Integrated Network and Gene Ontology Analysis Identifies Key Genes and Pathways for Coronary Artery Diseases. <i>Avicenna Journal of Medical Biotechnology</i> , 2021, 13, 15-23.	0.2	2
22143	TCF7 knockdown inhibits the imatinib resistance of chronic myeloid leukemia K562/G01 cells by neutralizing the Wnt/ $\beta$ -catenin/TCF7/ABC transporter signaling axis. <i>Oncology Reports</i> , 2020, 45, 557-568.	1.2	9
22144	Identification of key genes in lung adenocarcinoma based on a competing endogenous RNA network. <i>Oncology Letters</i> , 2020, 21, 60.	0.8	11
22145	Identification of key regulators in parathyroid adenoma using an integrative gene network analysis. <i>Bioinformatics</i> , 2020, 16, 910-922.	0.2	3
22146	$\beta$ -hydroxybutyrate does not alter the effects of glucose deprivation on breast cancer cells. <i>Oncology Letters</i> , 2020, 21, 65.	0.8	6
22147	Protein-Protein Interaction Networks Comparison Between Paediatric Neuroblastoma Cancer and Glioblastoma Multiforme Cancer with Gene Expression Data. , 2020, , .		0
22148	P4HB: A novel diagnostic and prognostic biomarker for bladder carcinoma. <i>Oncology Letters</i> , 2020, 21, 95.	0.8	27
22149	Investigation of molecular regulation mechanism under the pathophysiology of subarachnoid hemorrhage. <i>Open Life Sciences</i> , 2021, 16, 1377-1392.	0.6	4
22150	Study of Isopsoralen on the Postmenopausal Osteoporosis Based on the Network Pharmacology and Bioinformatics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22151	Advances in the elucidation of nuclear proteins in the model plant <i>Arabidopsis thaliana</i> : based on protein interactions and bioinformatics analysis. <i>Journal of Plant Interactions</i> , 2021, 16, 481-493.	1.0	5
22152	Genes and pathways of regulatory T cells regulated by adenosine A2A receptor: A bioinformatics study. <i>International Journal of Transgender Health</i> , 2021, 14, 1043-1053.	1.1	2
22153	Integration of transcriptomics and metabolomics to identify key coumarin biosynthetic genes in <i>Bupleurum chinense</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1858-1868.	0.5	2
22154	Gene Regulatory Networks Shape Developmental Plasticity of Root Cell Types Under Water Extremes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
22155	Combined screening analysis of aberrantly methylated-differentially expressed genes and pathways in hepatocellular carcinoma. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 311-325.	0.6	3
22156	High Expression of VAV Gene Family Predicts Poor Prognosis of Acute Myeloid Leukemia. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110658.	0.8	3
22157	Identifying Hub Genes and Key Pathways Associated with Thyroid Cancer by Integrated Bioinformatics Analysis. , 2021, , .		0
22158	Adenovirus Remodeling of the Host Proteome and Host Factors Associated with Viral Genomes. <i>MSystems</i> , 2021, 6, e0046821.	1.7	6
22159	Aryl Hydrocarbon Receptor Controls Skin Homeostasis, Regeneration, and Hair Follicle Cycling by Adjusting Epidermal Stem Cell Function. <i>Stem Cells</i> , 2021, 39, 1733-1750.	1.4	12

#	ARTICLE	IF	CITATIONS
22160	A Risk Signature Consisting of Eight m6A Methylation Regulators Predicts the Prognosis of Glioma. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 2733-2743.	1.7	10
22161	Multiomics Data Integration for Gene Regulatory Network Inference with Exponential Family Embeddings. , 2021, , .		1
22162	Integrative Network Analysis Revealed Genetic Impact of Pyruvate Kinase L/R on Hepatocyte Proliferation and Graft Survival after Liver Transplantation. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-31.	1.9	3
22163	Euxanthone inhibits lipopolysaccharide-induced injury, inflammatory response, and MUC5AC hypersecretion in human airway epithelial cells by the TLR4/MyD88 pathway. <i>Journal of Applied Toxicology</i> , 2022, 42, 671-682.	1.4	2
22164	Gene Co-Expression Analysis Identified Preserved and Survival-Related Modules in Severe Blunt Trauma, Burns, Sepsis, and Systemic Inflammatory Response Syndrome. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7065-7076.	0.8	9
22166	Network pharmacology-based strategy to investigate the active ingredients and molecular mechanisms of <i>Scutellaria Barbata</i> D. Don against radiation pneumonitis. <i>Medicine (United States)</i> , 2021, 100, e27957.	0.4	5
22167	In Silico Approaches in Bioremediation Research and Advancements. , 2022, , 221-238.		1
22168	Deep Proteomic Analysis on Biobanked Paraffine-Archived Melanoma with Prognostic/Predictive Biomarker Read-Out. <i>Cancers</i> , 2021, 13, 6105.	1.7	3
22169	The effect and mechanism of Jiao-tai-wan in the treatment of diabetes mellitus with depression based on network pharmacology and experimental analysis. <i>Molecular Medicine</i> , 2021, 27, 154.	1.9	11
22170	Comprehensive Analysis to Identify Key Genes Involved in Advanced Atherosclerosis. <i>Disease Markers</i> , 2021, 2021, 1-25.	0.6	6
22171	MiRNA-Regulated Pathways for Hypertrophic Cardiomyopathy: Network-Based Approach to Insight into Pathogenesis. <i>Genes</i> , 2021, 12, 2016.	1.0	3
22173	Phenylalanine Ammonia-Lyase (PAL) Genes Family in Wheat ( <i>Triticum aestivum</i> L.): Genome-Wide Characterization and Expression Profiling. <i>Agronomy</i> , 2021, 11, 2511.	1.3	28
22174	Identification of damage associated molecular patterns and extracellular matrix proteins as major constituents of the surface proteome of lung implantable silicone/nitinol devices. <i>Acta Biomaterialia</i> , 2022, 141, 209-218.	4.1	5
22175	Bioinformatic Analyses of the Ferroptosis-Related lncRNAs Signature for Ovarian Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 735871.	1.6	8
22176	Single-Cell RNA-Seq Reveals the Promoting Role of Ferroptosis Tendency During Lung Adenocarcinoma EMT Progression. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 822315.	1.8	19
22177	New Isoquinoline Alkaloids from <i>Paraphaeosphaeria sporulosa</i> F03, a Fungal Endophyte Isolated from <i>Paepalanthus planifolius</i> . <i>Planta Medica</i> , 2022, 88, 994-1003.	0.7	3
22178	Multi-omic profiling of histone variant H3.3 lysine 27 methylation reveals a distinct role from canonical H3 in stem cell differentiation. <i>Molecular Omics</i> , 2022, 18, 296-314.	1.4	2
22179	High-Mobility Group AT-Hook 1 Served as a Prognosis Biomarker and Associated with Immune Infiltrate in Hepatocellular Carcinoma. <i>International Journal of General Medicine</i> , 2022, Volume 15, 609-621.	0.8	7

#	ARTICLE	IF	CITATIONS
22180	SHMT2 is Associated with Tumor Purity, CD8+ T Immune Cells Infiltration, and a Novel Therapeutic Target in Four Different Human Cancers. <i>Current Molecular Medicine</i> , 2023, 23, 161-176.	0.6	5
22181	Clinical relevance of proteomic profiling in de novo pediatric acute myeloid leukemia: a Children's Oncology Group study. <i>Haematologica</i> , 2022, , .	1.7	7
22182	Integrated Proteome and Phosphoproteome Analyses Reveal Early- and Late-Stage Protein Networks of Traumatic Brain Injury. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 759-771.	1.1	1
22183	Integrated analysis of long non-coding RNAs and mRNAs reveals the regulatory network of maize seedling root responding to salt stress. <i>BMC Genomics</i> , 2022, 23, 50.	1.2	13
22184	Exosomal and Plasma Non-Coding RNA Signature Associated with Urinary Albumin Excretion in Hypertension. <i>International Journal of Molecular Sciences</i> , 2022, 23, 823.	1.8	9
22185	Secretome of Stressed Peripheral Blood Mononuclear Cells Alters Transcriptome Signature in Heart, Liver, and Spleen after an Experimental Acute Myocardial Infarction: An In Silico Analysis. <i>Biology</i> , 2022, 11, 116.	1.3	7
22186	Organochlorine contamination enriches virus-encoded metabolism and pesticide degradation associated auxiliary genes in soil microbiomes. <i>ISME Journal</i> , 2022, 16, 1397-1408.	4.4	45
22187	Prognostic Bone Metastasis-Associated Immune-Related Genes Regulated by Transcription Factors in Mesothelioma. <i>BioMed Research International</i> , 2022, 2022, 1-26.	0.9	1
22188	Molecular mechanism and candidate biomarkers of morphine for analgesia and addiction effects. <i>Annals of Translational Medicine</i> , 2022, 10, 89-89.	0.7	2
22189	The <i>Sinorhizobium meliloti</i> Nitrogen Stress Response Changes Radically in the Face of Concurrent Phosphate Stress. <i>Frontiers in Microbiology</i> , 2022, 13, 800146.	1.5	2
22190	Analysis and Visualization of Spatial Transcriptomic Data. <i>Frontiers in Genetics</i> , 2021, 12, 785290.	1.1	23
22191	Skin and heart allograft rejection solely by long-lived alloreactive T <sub>RM</sub> cells in skin of severe combined immunodeficient mice. <i>Science Advances</i> , 2022, 8, eabk0270.	4.7	14
22192	Co-expression of cancer stem cell markers, SALL4/ALDH1A1, is associated with tumor aggressiveness and poor survival in patients with serous ovarian carcinoma. <i>Journal of Ovarian Research</i> , 2022, 15, 17.	1.3	6
22193	A Molecular Networking Based Discovery of Diketopiperazine Heterodimers and Aspergillins from <i>Aspergillus caelatus</i> . <i>Journal of Natural Products</i> , 2022, 85, 25-33.	1.5	5
22194	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity. <i>Nature Microbiology</i> , 2022, 7, 262-276.	5.9	110
22195	Differences in the Accessory Genomes and Methylomes of Strains of <i>Streptococcus equi</i> subsp. <i>equi</i> and of <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Obtained from the Respiratory Tract of Horses from Texas. <i>Microbiology Spectrum</i> , 2022, 10, e0076421.	1.2	1
22196	Identification of Molecular Biomarkers and Key Pathways for Esophageal Carcinoma (EsC): A Bioinformatics Approach. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	4
22197	Transcriptomics and Functional Analysis of Copper Stress Response in the Sulfate-Reducing Bacterium <i>Desulfovibrio alaskensis</i> G20. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1396.	1.8	9

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22198	Laser microdissection transcriptome data derived gene regulatory networks of developing rice endosperm revealed tissue- and stage-specific regulators modulating starch metabolism. <i>Plant Molecular Biology</i> , 2022, 108, 443-467.	2.0	2
22199	Targeting HSP90 Inhibits Proliferation and Induces Apoptosis Through AKT1/ERK Pathway in Lung Cancer. <i>Frontiers in Pharmacology</i> , 2021, 12, 724192.	1.6	20
22200	Changes in the Transcriptome Profiles of Human Amnion-Derived Mesenchymal Stromal/Stem Cells Induced by Three-Dimensional Culture: A Potential Priming Strategy to Improve Their Properties. <i>International Journal of Molecular Sciences</i> , 2022, 23, 863.	1.8	15
22201	An integrated in silico analysis highlighted angiogenesis regulating miRNA-mRNA network in PCOS pathophysiology. <i>Journal of Assisted Reproduction and Genetics</i> , 2022, 39, 427-440.	1.2	12
22202	MiR-29a Increase in Aging May Function as a Compensatory Mechanism Against Cardiac Fibrosis Through SERPINH1 Downregulation. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 810241.	1.1	8
22203	TRPV1-Mediated Microglial Autophagy Attenuates Alzheimer's Disease-Associated Pathology and Cognitive Decline. <i>Frontiers in Pharmacology</i> , 2021, 12, 763866.	1.6	17
22204	Gentiana scabra Restrains Hepatic Pro-Inflammatory Macrophages to Ameliorate Non-Alcoholic Fatty Liver Disease. <i>Frontiers in Pharmacology</i> , 2021, 12, 816032.	1.6	5
22205	Inflammatory activation and immune cell infiltration are main biological characteristics of SARS-CoV-2 infected myocardium. <i>Bioengineered</i> , 2022, 13, 2486-2497.	1.4	5
22206	Illuminating the lineage-specific diversification of resin glycoside acylsugars in the morning glory (Convolvulaceae) family using computational metabolomics. <i>Horticulture Research</i> , 2022, 9, .	2.9	7
22207	Integrative multiomics and in silico analysis revealed the role of ARHGEF1 and its screened antagonist in mild and severe COVID-19 patients. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 673-690.	1.2	8
22208	Interactions Between Marine Group II Archaea and Phytoplankton Revealed by Population Correlations in the Northern Coast of South China Sea. <i>Frontiers in Microbiology</i> , 2021, 12, 785532.	1.5	6
22209	Kidney organoids recapitulate human basement membrane assembly in health and disease. <i>ELife</i> , 2022, 11, .	2.8	23
22211	Cocoa bean fingerprinting via correlation networks. <i>Npj Science of Food</i> , 2022, 6, 5.	2.5	3
22213	Immune Infiltrate and Tumor Microenvironment Transcriptional Programs Stratify Pediatric Osteosarcoma into Prognostic Groups at Diagnosis. <i>Cancer Research</i> , 2022, 82, 974-985.	0.4	14
22214	miR-200a/b-429 downregulation is a candidate biomarker of tumor radioresistance and independent of hypoxia in locally advanced cervical cancer. <i>Molecular Oncology</i> , 2022, 16, 1402-1419.	2.1	7
22216	Microbial communities in swamps of four mangrove reserves driven by interactions between physicochemical properties and microbe in the North Beibu Gulf, China. <i>Environmental Science and Pollution Research</i> , 2022, 29, 37582-37597.	2.7	5
22217	MetaNetwork Enhances Biological Insights from Quantitative Proteomics Differences by Combining Clustering and Enrichment Analyses. <i>Journal of Proteome Research</i> , 2022, 21, 410-419.	1.8	2
22218	Identifying Novel Genes and Proteins Involved in Salt Stress Perception and Signaling of Rice Seedlings. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 151-164.	1.0	3

#	ARTICLE	IF	CITATIONS
22219	Targeted isolation of photoactive pigments from mushrooms yielded a highly potent new photosensitizer: 7,7- $\beta$ -biphyscion. <i>Scientific Reports</i> , 2022, 12, 1108.	1.6	7
22220	Action Mechanism Underlying Improvement Effect of Fuzi Lizhong Decoction on Nonalcoholic Fatty Liver Disease: A Study Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-15.	0.5	4
22221	Data Integration Challenges for Machine Learning in Precision Medicine. <i>Frontiers in Medicine</i> , 2021, 8, 784455.	1.2	18
22222	Identification of Key Genes Related to Postnatal Testicular Development Based on Transcriptomic Data of Testis in Hu Sheep. <i>Frontiers in Genetics</i> , 2021, 12, 773695.	1.1	4
22223	Differential expression analysis of microRNAs and mRNAs in the mouse hippocampus of post-stroke depression (PSD) based on transcriptome sequencing. <i>Bioengineered</i> , 2022, 13, 3582-3596.	1.4	4
22224	Identification of bZIP transcription factors and their responses to brown spot in pear. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210175.	0.6	5
22225	Diverging metabolic effects of 2 energy-restricted diets differing in nutrient quality: a 12-week randomized controlled trial in subjects with abdominal obesity. <i>American Journal of Clinical Nutrition</i> , 2022, 116, 132-150.	2.2	15
22226	Phage JS02, a putative temperate phage, a novel biofilm-degrading agent for <i>Staphylococcus aureus</i> . <i>Letters in Applied Microbiology</i> , 2022, 75, 643-654.	1.0	9
22227	Decoding the signaling profile of hematopoietic progenitor kinase 1 (HPK1) in innate immunity: A proteomic approach. <i>European Journal of Immunology</i> , 2022, , .	1.6	1
22228	CircCCNB1 silencing acting as a miR-106b-5p sponge inhibited GPM6A expression to promote HCC progression by enhancing DYNC111 expression and activating the AKT/ERK signaling pathway. <i>International Journal of Biological Sciences</i> , 2022, 18, 637-651.	2.6	18
22229	Open chromatin interaction maps reveal functional regulatory elements and chromatin architecture variations during wheat evolution. <i>Genome Biology</i> , 2022, 23, 34.	3.8	22
22230	Pan-cancer analysis of biological events on cell cycle instability in gastrointestinal cancers with integrative scoring method. <i>Genomics</i> , 2022, 114, 253-265.	1.3	5
22233	Genome-wide annotation of protein-coding genes in pig. <i>BMC Biology</i> , 2022, 20, 25.	1.7	14
22234	Isolation and Characterization of a Novel Temperate <i>Escherichia coli</i> Bacteriophage, Kapi1, Which Modifies the O-Antigen and Contributes to the Competitiveness of Its Host during Colonization of the Murine Gastrointestinal Tract. <i>MBio</i> , 2022, 13, e0208521.	1.8	5
22235	Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology. <i>Journal of Hematology and Oncology</i> , 2022, 15, 5.	6.9	30
22236	Correlation between gene expression and MRI STIR signals in patients with chronic low-back pain and Modic changes indicates immune involvement. <i>Scientific Reports</i> , 2022, 12, 215.	1.6	6
22237	Medications Activating Tubular Fatty Acid Oxidation Enhance the Protective Effects of Roux-en-Y Gastric Bypass Surgery in a Rat Model of Early Diabetic Kidney Disease. <i>Frontiers in Endocrinology</i> , 2021, 12, 757228.	1.5	4
22238	Molecular Subgroup Classification in Alzheimer's Disease by Transcriptomic Profiles. <i>Journal of Molecular Neuroscience</i> , 2022, , 1.	1.1	2

#	ARTICLE	IF	CITATIONS
22239	miRNA and lncRNA Expression Networks Modulate Cell Cycle and DNA Repair Inhibition in Senescent Prostate Cells. <i>Genes</i> , 2022, 13, 208.	1.0	7
22240	Periodontal and Peri-Implant Microbiome Dysbiosis Is Associated With Alterations in the Microbial Community Structure and Local Stability. <i>Frontiers in Microbiology</i> , 2021, 12, 785191.	1.5	14
22241	Decoding gene regulation in the fly brain. <i>Nature</i> , 2022, 601, 630-636.	13.7	102
22242	Transcriptomics of receptive endometrium in women with sonographic features of adenomyosis. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, 2.	1.4	5
22243	Genome-wide identification and characterization of grapevine UFD1 genes during berry development and salt stress response. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 592-601.	0.9	1
22244	Proteomic analysis of descending thoracic aorta identifies unique and universal signatures of aneurysm and dissection. <i>JVS Vascular Science</i> , 2022, 3, 85-181.	0.4	5
22245	Central Role of C2H2-Type Zinc Finger-Containing Genes in Pediatric Brain Tumors. <i>Dna</i> , 2022, 2, 1-21.	0.4	0
22246	Novel Immune-Related Genetic Expression for Primary Sjögren's Syndrome. <i>Frontiers in Medicine</i> , 2021, 8, 719958.	1.2	1
22247	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. <i>BMC Genomics</i> , 2022, 23, 6.	1.2	1
22249	Identifying Cyclin A/Cdk1 Substrates in Mitosis in Human Cells. <i>Methods in Molecular Biology</i> , 2022, 2415, 175-182.	0.4	2
22251	Identification of potential genes correlated with breast cancer metastasis and prognosis. <i>International Journal of Transgender Health</i> , 2022, 15, 126-133.	1.1	1
22252	FOXO1 mediates GDF-15 dependent stemness and intrinsic drug resistance in breast cancer. <i>Molecular Biology Reports</i> , 2022, 49, 2877-2888.	1.0	12
22253	Exosomes Recovered From the Plasma of COVID-19 Patients Expose SARS-CoV-2 Spike-Derived Fragments and Contribute to the Adaptive Immune Response. <i>Frontiers in Immunology</i> , 2021, 12, 785941.	2.2	38
22254	Metabolome and Transcriptome Analyses Unravel the Molecular Regulatory Mechanisms Involved in Photosynthesis of <i>Cyclocarya paliurus</i> under Salt Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1161.	1.8	12
22255	Immunological Classification of Pancreatic Carcinomas to Identify Immune Index and Provide a Strategy for Patient Stratification. <i>Frontiers in Immunology</i> , 2021, 12, 719105.	2.2	4
22256	Microbiome profiling reveals that <i>Pseudomonas</i> antagonises parasitic nodule colonisation of cheater rhizobia in <i>Lotus</i> . <i>New Phytologist</i> , 2022, 234, 242-255.	3.5	16
22257	A Network Pharmacology Perspective Investigation of the Pharmacological Mechanisms of the Herbal Drug FDY003 in Gastric Cancer. <i>Natural Product Communications</i> , 2022, 17, 1934578X2110730.	0.2	0
22258	Identification of a ferroptosis-related gene pair biomarker with immune infiltration landscapes in ischemic stroke: a bioinformatics-based comprehensive study. <i>BMC Genomics</i> , 2022, 23, 59.	1.2	10



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22259	Extracellular vesicles produced by the human commensal gut bacterium <i>Bacteroides thetaiotaomicron</i> affect host immune pathways in a cell-type specific manner that are altered in inflammatory bowel disease. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12189.	5.5	33
22260	COL1A1 as a Potential Prognostic Marker and Therapeutic Target in Non-small Cell Lung Cancer. <i>Current Bioinformatics</i> , 2022, 17, 909-923.	0.7	1
22261	Transcriptomic and physiological analysis identifies a gene network module highly associated with brassinosteroid regulation in hybrid sweetgum tissues differing in the capability of somatic embryogenesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	13
22262	Co-expression of cancer-testis antigens of MAGE-A6 and MAGE-A11 is associated with tumor aggressiveness in patients with bladder cancer. <i>Scientific Reports</i> , 2022, 12, 599.	1.6	7
22263	Integrative analysis of immune-related multi-omics profiles identifies distinct prognosis and tumor microenvironment patterns in osteosarcoma. <i>Molecular Oncology</i> , 2022, 16, 2174-2194.	2.1	14
22264	Transcriptome analysis reveals upregulation of immune response pathways at the invasive tumour front of metastatic seminoma germ cell tumours. <i>British Journal of Cancer</i> , 2022, 126, 937-947.	2.9	8
22265	Qingwei San treats oral ulcer subjected to stomach heat syndrome in db/db mice by targeting TLR4/MyD88/NF- $\kappa$ B pathway. <i>Chinese Medicine</i> , 2022, 17, 1.	1.6	12
22266	Comprehensive Pan-Cancer Analyses of Pyroptosis-Related Genes to Predict Survival and Immunotherapeutic Outcome. <i>Cancers</i> , 2022, 14, 237.	1.7	9
22267	Construction of Light-Responsive Gene Regulatory Network for Growth, Development and Secondary Metabolite Production in <i>Cordyceps militaris</i> . <i>Biology</i> , 2022, 11, 71.	1.3	5
22268	NF- $\kappa$ B-Related Metabolic Gene Signature Predicts the Prognosis and Immunotherapy Response in Gastric Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-30.	0.9	1
22269	Genetic diversity in terrestrial subsurface ecosystems impacted by geological degassing. <i>Nature Communications</i> , 2022, 13, 284.	5.8	11
22270	Comprehensive Analysis of Hub Genes Associated With Competing Endogenous RNA Networks in Stroke Using Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 779923.	1.1	4
22271	An Overview of Transcriptional Responses of Schistosome-Susceptible (M line) or -Resistant (BS-90) <i>Biomphalaria glabrata</i> Exposed or Not to <i>Schistosoma mansoni</i> Infection. <i>Frontiers in Immunology</i> , 2021, 12, 805882.	2.2	10
22272	Management of Hypercholesterolemia Through Dietary $\beta$ -glucans—Insights From a Zebrafish Model. <i>Frontiers in Nutrition</i> , 2021, 8, 797452.	1.6	9
22273	RNA Sequencing Analysis of Gene Expression by Electroacupuncture in Guinea Pig Gallstone Models. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-10.	0.5	1
22275	A sorghum genome-wide association study (GWAS) identifies a WRKY transcription factor as a candidate gene underlying sugarcane aphid ( <i>Melanaphis sacchari</i> ) resistance. <i>Planta</i> , 2022, 255, 37.	1.6	10
22276	Identification of key tumor stroma-associated transcriptional signatures correlated with survival prognosis and tumor progression in breast cancer. <i>Breast Cancer</i> , 2022, , 1.	1.3	12
22277	Identification of Core Genes and Pathways in Melanoma Metastasis via Bioinformatics Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 794.	1.8	24

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22278	Identification of Diagnostic Markers for Breast Cancer Based on Differential Gene Expression and Pathway Network. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 811585.	1.8	12
22279	Land-use intensification differentially affects bacterial, fungal and protist communities and decreases microbiome network complexity. <i>Environmental Microbiomes</i> , 2022, 17, 1.	2.2	48
22280	Identifies Immune Feature Genes for Prediction of Chemotherapy Benefit in Cancer. <i>Journal of Cancer</i> , 2022, 13, 496-507.	1.2	3
22281	Communities of T4-like bacteriophages associated with bacteria in Lake Baikal: diversity and biogeography. <i>PeerJ</i> , 0, 10, e12748.	0.9	3
22282	Electrophilic thymol isobutyrate from <i>Inula nervosa</i> Wall. ( <i>Xiaoheiyao</i> ) ameliorates steatosis in HepG2 cells via Nrf2 activation. <i>Journal of Functional Foods</i> , 2022, 88, 104895.	1.6	4
22283	Plant Species-Driven Distribution of Individual Clades of Comammox Nitrospira in a Subtropical Estuarine Wetland. <i>Microbial Ecology</i> , 2023, 85, 209-220.	1.4	8
22284	Identification of the molecular subgroups in asthma by gene expression profiles: airway inflammation implications. <i>BMC Pulmonary Medicine</i> , 2022, 22, 29.	0.8	3
22285	Prognostic Value of Macrophage-Associated Long Non-Coding RNA Expression for Hepatocellular Carcinoma. <i>Cancer Management and Research</i> , 2022, Volume 14, 215-224.	0.9	2
22286	Single-cell architecture and functional requirement of alternative splicing during hematopoietic stem cell formation. <i>Science Advances</i> , 2022, 8, eabg5369.	4.7	12
22287	Gene expression profiling using targeted RNA-sequencing to elucidate the progression from histologically normal lung tissues to non-invasive lesions in invasive lung adenocarcinoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2022, , 1.	1.4	2
22288	Improving hemocompatibility of decellularized liver scaffold using Custodiol solution. <i>Materials Science and Engineering C</i> , 2022, , 112642.	3.8	4
22289	Overexpression of SKA Complex Is Associated With Poor Prognosis in Gliomas. <i>Frontiers in Neurology</i> , 2021, 12, 755681.	1.1	2
22290	Network Pharmacology and Molecular Docking-Based Mechanism Study to Reveal the Protective Effect of Salvianolic Acid C in a Rat Model of Ischemic Stroke. <i>Frontiers in Pharmacology</i> , 2021, 12, 799448.	1.6	16
22291	Bioinformatics approaches identified dasatinib and bortezomib inhibit the activity of MCM7 protein as a potential treatment against human cancer. <i>Scientific Reports</i> , 2022, 12, 1539.	1.6	16
22292	The deterioration of calcified cartilage integrity reflects the severity of osteoarthritis: A structural, molecular, and biochemical analysis. <i>FASEB Journal</i> , 2022, 36, e22142.	0.2	12
22293	Functional profiling of long intergenic non-coding RNAs in fission yeast. <i>ELife</i> , 2022, 11, .	2.8	7
22294	Gut microbiome and diet in populations with obesity: Role of the Na <sup>+</sup> /K <sup>+</sup> -ATPase transporter signaling in severe COVID-19. <i>Obesity</i> , 2022, 30, 869-873.	1.5	3
22295	The Identification and Validation of Hub Genes Associated with Acute Myocardial Infarction Using Weighted Gene Co-Expression Network Analysis. <i>Journal of Cardiovascular Development and Disease</i> , 2022, 9, 30.	0.8	5

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22296	Identification of an Immune-Related BAT Signature for Predicting Adjuvant Chemotherapy Response and Overall Survival in Patients with Resected Ductal Adenocarcinoma of the Pancreas. <i>Journal of Gastrointestinal Surgery</i> , 2022, 26, 869-886.	0.9	5
22297	Bioengineered models of Parkinson's disease using patient-derived dopaminergic neurons exhibit distinct biological profiles in a 3D microenvironment. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 78.	2.4	12
22298	Profiling of RNA-binding Proteins Interacting With Glucagon and Adipokinetic Hormone mRNAs. <i>Journal of Lipid and Atherosclerosis</i> , 2022, 11, 55.	1.1	0
22299	Dynamic Expression and Gene Regulation of MicroRNAs During Bighead Carp ( <i>Hypophthalmichthys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.1	3
22300	Combining Metabolomics and Experimental Evolution Reveals Key Mechanisms Underlying Longevity Differences in Laboratory Evolved <i>Drosophila melanogaster</i> Populations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1067.	1.8	7
22301	Transcriptomic Analysis Reveals a Link Between Hippo Signaling Pathway and Macrophages in Lungs of Mice with OVA-Induced Allergic Asthma. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 423-437.	1.6	4
22302	MeCOM: A Method for Comparing Three-Dimensional Metalloenzyme Active Sites. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 730-739.	2.5	3
22303	Genomic study of the resilience of buffalo cows to a negative energy balance. <i>Journal of Applied Genetics</i> , 2022, 63, 379.	1.0	0
22306	Changes in chemical composition, structural and functional microbiome during alfalfa ( <i>Medicago</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.1	13
22307	Overexpression of chaperonin containing TCP1 subunit 7 has diagnostic and prognostic value for hepatocellular carcinoma. <i>Aging</i> , 2022, 14, 747-769.	1.4	9
22308	The use of machine learning to discover regulatory networks controlling biological systems. <i>Molecular Cell</i> , 2022, 82, 260-273.	4.5	11
22309	Network Pharmacology and Molecular Docking Analysis on Pharmacological Mechanisms of <i>Astragalus membranaceus</i> in the Treatment of Gastric Ulcer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	3
22310	Hyperthermia promotes exosome secretion by regulating Rab7b while increasing drug sensitivity in adriamycin-resistant breast cancer. <i>International Journal of Hyperthermia</i> , 2022, 39, 246-257.	1.1	10
22312	Flavanol Consumption in Healthy Men Preserves Integrity of Immunological Endothelial Barrier Cell Functions: Nutri(epi)genomic Analysis. <i>Molecular Nutrition and Food Research</i> , 2022, 66, e2100991.	1.5	14
22313	Gene signature to predict prognostic survival of hepatocellular carcinoma. <i>Open Medicine (Poland)</i> , 2022, 17, 135-150.	0.6	7
22314	Unraveling unique and common cell type-specific mechanisms in glioblastoma multiforme. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 90-106.	1.9	2
22316	SPINK5 is a Prognostic Biomarker Associated With the Progression and Prognosis of Laryngeal Squamous Cell Carcinoma Identified by Weighted Gene Co-Expression Network Analysis. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432210771.	0.6	5
22317	Bioinformatic-based Identification of Genes Associated with Aortic Valve Stenosis. <i>Heart Surgery Forum</i> , 2022, 25, E069-E078.	0.2	1

#	ARTICLE	IF	CITATIONS
22318	Plant RNA-mediated gene regulatory network. <i>Genomics</i> , 2022, 114, 409-442.	1.3	17
22319	ggComp enables dissection of germplasm resources and construction of a multiscale germplasm network in wheat. <i>Plant Physiology</i> , 2022, 188, 1950-1965.	2.3	13
22320	An Integrated In Silico, In Vitro and Tumor Tissues Study Identified Selenoprotein S (SELENOS) and Valosin-Containing Protein (VCP/p97) as Novel Potential Associated Prognostic Biomarkers in Triple Negative Breast Cancer. <i>Cancers</i> , 2022, 14, 646.	1.7	5
22321	Identification of Circular RNA-Based Immunomodulatory Networks in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 779706.	1.3	3
22322	Neural responses to affective speech, including motherese, map onto clinical and social eye tracking profiles in toddlers with ASD. <i>Nature Human Behaviour</i> , 2022, 6, 443-454.	6.2	14
22323	Identification of Key microRNAs in Diabetes Mellitus Erectile Dysfunction Rats with Stem Cell Therapy by Bioinformatic Analysis of Deep Sequencing Data. <i>World Journal of Men's Health</i> , 2022, 40, 663.	1.7	5
22324	Molecular Network Analysis Reveals Transmission of HIV-1 Drug-Resistant Strains Among Newly Diagnosed HIV-1 Infections in a Moderately HIV Endemic City in China. <i>Frontiers in Microbiology</i> , 2021, 12, 797771.	1.5	14
22325	Allelic variation for alpha-Glucan Water Dikinase is associated with starch phosphate content in tetraploid potato. <i>Plant Molecular Biology</i> , 2022, 108, 469-480.	2.0	3
22326	New insights into aging-associated characteristics of female subcutaneous adipose tissue through integrative analysis of multi-omics data. <i>Bioengineered</i> , 2022, 13, 2044-2057.	1.4	6
22327	Integrative system biology and mathematical modeling of genetic networks identifies shared biomarkers for obesity and diabetes. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 2310-2329.	1.0	9
22329	Transcriptional Shift and Metabolic Adaptations during <i>Leishmania</i> Quiescence Using Stationary Phase and Drug Pressure as Models. <i>Microorganisms</i> , 2022, 10, 97.	1.6	7
22330	STIL Acts as an Oncogenetic Driver in a Primary Cilia-Dependent Manner in Human Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 804419.	1.8	5
22332	Inflammation Subtypes and Translating Inflammation-Related Genetic Findings in Schizophrenia and Related Psychoses: A Perspective on Pathways for Treatment Stratification and Novel Therapies. <i>Harvard Review of Psychiatry</i> , 2022, 30, 59-70.	0.9	45
22334	Comparative Analysis of the MADS-Box Genes Revealed Their Potential Functions for Flower and Fruit Development in Longan ( <i>Dimocarpus longan</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 813798.	1.7	12
22335	Cobalamin-Dependent Radical <i>S</i> -Adenosylmethionine Enzymes: Capitalizing on Old Motifs for New Functions. <i>ACS Bio &amp; Med Chem Au</i> , 2022, 2, 173-186.	1.7	24
22336	Adaptation of the periplasm to maintain spatial constraints essential for cell envelope processes and cell viability. <i>ELife</i> , 2022, 11, .	2.8	17
22337	The Natural Ligand for Metalloproteinase-A Multifaceted Drug Target. <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 1716-1739.	1.4	3
22338	Architecture and Dynamics of the Wounding-Induced Gene Regulatory Network During the Oolong Tea Manufacturing Process ( <i>Camellia sinensis</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 788469.	1.7	11

#	ARTICLE	IF	CITATIONS
22339	Identification of genes related to hydrolysis and assimilation of <i>Agave</i> fructans in <i>Candida apicola</i> NRRL Y-50540 and <i>Torulaspora delbrueckii</i> NRRL Y-50541 by <i>de novo</i> transcriptome analysis. <i>FEMS Yeast Research</i> , 2022, 22, .	1.1	4
22340	Redefining the coenzyme A transferase superfamily with a large set of manually annotated proteins. <i>Protein Science</i> , 2022, 31, 864-881.	3.1	9
22341	Integrated weighted gene co-expression network analysis reveals biomarkers associated with prognosis of high-grade serous ovarian cancer. <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, e24165.	0.9	4
22342	Exploration of the DARTable Genome- a Resource Enabling Data-Driven NAMs for Developmental and Reproductive Toxicity Prediction. <i>Frontiers in Toxicology</i> , 2021, 3, 806311.	1.6	3
22343	Spatiotemporal analysis identifies ABF2 and ABF3 as key hubs of endodermal response to nitrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	17
22344	A Preliminary Inquiry Into the Potential Mechanism of Huang-Lian-Jie-Du Decoction in Treating Rheumatoid Arthritis via Network Pharmacology and Molecular Docking. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 740266.	1.8	13
22345	Lung tumor MHCII immunity depends on in situ antigen presentation by fibroblasts. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	71
22346	STAT6 contributes to renal fibrosis by modulating PPAR $\alpha$ -mediated tubular fatty acid oxidation. <i>Cell Death and Disease</i> , 2022, 13, 66.	2.7	19
22347	The combination of transcriptome and metabolome reveals the molecular mechanism by which topping and salicylic acid treatment affect the synthesis of alkaloids in <i>Nicotiana tabacum</i> L.. <i>International Journal of Transgender Health</i> , 2022, 15, 147-159.	1.1	5
22348	Identification of Constituents and Exploring the Mechanism for Toutongning Capsule in the Treatment of Migraine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	0
22350	A New Prospect for the Treatment of Nephrotic Syndrome Based on Network Pharmacology Analysis. <i>Current Research in Physiology</i> , 2022, 5, 36-47.	0.8	7
22351	Distinct Phyllosphere Microbiome of Wild Tomato Species in Central Peru upon Dysbiosis. <i>Microbial Ecology</i> , 2023, 85, 168-183.	1.4	12
22352	Re-wiring and gene expression changes of AC025034.1 and ATP2B1 play complex roles in early-to-late breast cancer progression. <i>BMC Genomic Data</i> , 2022, 23, 6.	0.7	6
22353	Experimental Evidence of Intrinsic Disorder and Amyloid Formation by the Henipavirus W Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 923.	1.8	6
22354	The transcription factor HIF-1 $\alpha$ mediates plasticity of NKp46+ innate lymphoid cells in the gut. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	22
22355	Immunological and prognostic significance of novel ferroptosis-related genes in soft tissue sarcoma. <i>PLoS ONE</i> , 2022, 17, e0262234.	1.1	2
22356	Proteomic Identification of the SLC25A46 Interactome in Transgenic Mice Expressing SLC25A46-FLAG. <i>Journal of Proteome Research</i> , 2022, 21, 375-394.	1.8	4
22357	Identification of COPA as a potential prognostic biomarker and pharmacological intervention target of cervical cancer by quantitative proteomics and experimental verification. <i>Journal of Translational Medicine</i> , 2022, 20, 18.	1.8	4

#	ARTICLE	IF	CITATIONS
22358	HESML: a real-time semantic measures library for the biomedical domain with a reproducible survey. <i>BMC Bioinformatics</i> , 2022, 23, 23.	1.2	3
22359	Clinical, histological and molecular profiling of different stages of alcohol-related liver disease. <i>Gut</i> , 2022, 71, 1856-1866.	6.1	17
22360	Prognostic tumor microenvironment gene and the relationship with immune infiltration characteristics in metastatic breast cancer. <i>Biocell</i> , 2022, 46, 1215-1243.	0.4	1
22361	MicroRNA-365 regulates human cardiac action potential duration. <i>Nature Communications</i> , 2022, 13, 220.	5.8	15
22362	Deep immune phenotyping reveals similarities between aging, Down syndrome, and autoimmunity. <i>Science Translational Medicine</i> , 2022, 14, eabi4888.	5.8	20
22363	Ecological Role of Bacteria Involved in the Biogeochemical Cycles of Mangroves Based on Functional Genes Detected through GeoChip 5.0. <i>MSphere</i> , 2022, 7, e0093621.	1.3	29
22364	Multi-omics differential gene regulatory network inference for lung adenocarcinoma tumor progression biomarker discovery. <i>AICHE Journal</i> , 0, , .	1.8	2
22365	Prediction of Mechanosensitive Genes in Vascular Endothelial Cells Under High Wall Shear Stress. <i>Frontiers in Genetics</i> , 2021, 12, 796812.	1.1	8
22366	Genome-wide identification and expression profiling analysis of Wnt family genes affecting adipocyte differentiation in cattle. <i>Scientific Reports</i> , 2022, 12, 489.	1.6	8
22367	Producing Gold and Silver to Globalize the Economy during the Early Modern Era: San Luis Potosi and the Pacific Trade with Asia. <i>Asian Review of World Histories</i> , 2022, 10, 58-96.	0.1	0
22368	Single-Cell Profiles of Age-Related Osteoarthritis Uncover Underlying Heterogeneity Associated With Disease Progression. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 748360.	1.6	8
22369	The Cumulative Formation of R-loop Interacts with Histone Modifications to Shape Cell Reprogramming. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1567.	1.8	3
22370	Comparative Investigation of Gene Regulatory Processes Underlying Avian Influenza Viruses in Chicken and Duck. <i>Biology</i> , 2022, 11, 219.	1.3	3
22373	Comparative transcriptome analysis of genes and metabolic pathways involved in sporulation in <i>Ganoderma lingzhi</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
22374	DAMPs/PAMPs induce monocytic TLR activation and tolerance in COVID-19 patients; nucleic acid binding scavengers can counteract such TLR agonists. <i>Biomaterials</i> , 2022, 283, 121393.	5.7	34
22375	Transcriptomic Analysis Reveals Functional Interaction of mRNA, lncRNA, and miRNA in Steroidogenesis and Spermatogenesis of Gynogenetic Japanese Flounder ( <i>Paralichthys olivaceus</i> ). <i>Biology</i> , 2022, 11, 213.	1.3	8
22377	Transcriptome profiling provides preliminary molecular insights into adventitious bud formation in herbaceous peony ( <i>Paeonia A—</i> <i>â€™Coral Charmâ€™</i> ). <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 476-486.	0.9	2
22378	APOA1 Level is Negatively Correlated with the Severity of COVID-19. <i>International Journal of General Medicine</i> , 2022, Volume 15, 689-698.	0.8	5



#	ARTICLE	IF	CITATIONS
22379	Insights into the potential of withanolides as Phosphodiesterase-4 (PDE4D) inhibitors. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 2108-2117.	2.0	3
22380	Comparative transcriptomics and eQTL mapping of response to <i>Melampsora americana</i> in selected <i>Salix purpurea</i> F2 progeny. <i>BMC Genomics</i> , 2022, 23, 71.	1.2	5
22381	Trans-omic Analysis of Insulin Action Reveals a Sub-Network Required for Cell Growth Through Co-Regulated Gene Expression of Anabolic Processes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22382	Systems-level analysis of transcriptome reorganization during liver regeneration. <i>Molecular Omics</i> , 2022, 18, 315-327.	1.4	2
22383	The Anticancer Ruthenium Compound BOLD-100 Targets Glycolysis and Generates a Metabolic Vulnerability towards Glucose Deprivation. <i>Pharmaceutics</i> , 2022, 14, 238.	2.0	14
22384	Identification of key regulators in Sarcoidosis through multidimensional systems biological approach. <i>Scientific Reports</i> , 2022, 12, 1236.	1.6	4
22385	Inflammation of Gill Epithelia in Fish Causes Increased Permeation of Petrogenic Polar Organic Chemicals via Disruption of Tight Junctions. <i>Environmental Science &amp; Technology</i> , 2022, 56, 1820-1829.	4.6	4
22386	The role of SPI1-TYROBP-FCER1G network in oncogenesis and prognosis of osteosarcoma, and its association with immune infiltration. <i>BMC Cancer</i> , 2022, 22, 108.	1.1	8
22387	Colistin exposure enhances expression of eptB in colistin-resistant <i>Escherichia coli</i> co-harboring mcr-1. <i>Scientific Reports</i> , 2022, 12, 1348.	1.6	5
22388	Grapevine DMR6-1 Is a Candidate Gene for Susceptibility to Downy Mildew. <i>Biomolecules</i> , 2022, 12, 182.	1.8	14
22389	The role of IDH1 mutation on gene expression in glioblastoma. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100812.	1.9	3
22390	Insights Into the Molecular Mechanisms of Late Flowering in <i>Prunus sibirica</i> by Whole-Genome and Transcriptome Analyses. <i>Frontiers in Plant Science</i> , 2021, 12, 802827.	1.7	8
22391	Selective translation of epigenetic modifiers affects the temporal pattern and differentiation of neural stem cells. <i>Nature Communications</i> , 2022, 13, 470.	5.8	20
22392	Key genes in the liver fibrosis process are mined based on single-cell transcriptomics. <i>Biochemical and Biophysical Research Communications</i> , 2022, 598, 131-137.	1.0	3
22393	System Biology and Network Analysis Approaches on Oxidative Stress in Cancer. , 2022, , 1901-1918.		0
22394	Integrative proteomics and phosphoproteomics reveals phosphorylation networks involved in the maintenance and expression of embryogenic competence in sugarcane callus. <i>Journal of Plant Physiology</i> , 2022, 268, 153587.	1.6	3
22395	Developing an Amplification Refractory Mutation System-Quantitative Reverse Transcription-PCR Assay for Rapid and Sensitive Screening of SARS-CoV-2 Variants of Concern. <i>Microbiology Spectrum</i> , 2022, 10, e0143821.	1.2	11
22396	Systematic Review: microRNAs as Potential Biomarkers in Mild Cognitive Impairment Diagnosis. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 807764.	1.7	12

#	ARTICLE	IF	CITATIONS
22397	Antioxidant Effects and Potential Molecular Mechanism of Action of Limonium aureum Extract Based on Systematic Network Pharmacology. <i>Frontiers in Veterinary Science</i> , 2021, 8, 775490.	0.9	4
22398	Identification and functional characterization of transcriptional activators in human cells. <i>Molecular Cell</i> , 2022, 82, 677-695.e7.	4.5	64
22399	Integrated bioinformatics and network pharmacology to identify the therapeutic target and molecular mechanisms of Huangqin decoction on ulcerative Colitis. <i>Scientific Reports</i> , 2022, 12, 159.	1.6	28
22400	Transcriptomics and network analysis highlight potential pathways in the pathogenesis of pterygium. <i>Scientific Reports</i> , 2022, 12, 286.	1.6	5
22401	Neurodegeneration and neuroinflammation are linked, but independent of alpha-synuclein inclusions, in a seeding/spreading mouse model of Parkinson's disease. <i>Glia</i> , 2022, 70, 935-960.	2.5	30
22402	Full-Length Transcriptome of Red Swamp Crayfish Hepatopancreas Reveals Candidate Genes in Hif-1 and Antioxidant Pathways in Response to Hypoxia-Reoxygenation. <i>Marine Biotechnology</i> , 2022, 24, 55-67.	1.1	4
22403	Effect of dietary incorporation of <i>Chlorella vulgaris</i> and CAZyme supplementation on the hepatic proteome of finishing pigs. <i>Journal of Proteomics</i> , 2022, 256, 104504.	1.2	5
22404	Transcriptome shifts triggered by vitamin A and SCD genotype interaction in Duroc pigs. <i>BMC Genomics</i> , 2022, 23, 16.	1.2	2
22405	Prediction of the Mechanisms by Which Quercetin Enhances Cisplatin Action in Cervical Cancer: A Network Pharmacology Study and Experimental Validation. <i>Frontiers in Oncology</i> , 2021, 11, 780387.	1.3	9
22406	Identification of Hub Genes Associated with Immune Infiltration in Cardioembolic Stroke by Whole Blood Transcriptome Analysis. <i>Disease Markers</i> , 2022, 2022, 1-23.	0.6	2
22407	Suitability of high-resolution mass spectrometry in analytical toxicology: Focus on drugs of abuse. <i>Toxicologie Analytique Et Clinique</i> , 2022, 34, 29-41.	0.1	6
22408	Network analysis of host-pathogen protein interactions in microbe induced cardiovascular diseases. <i>In Silico Biology</i> , 2022, 14, 115-133.	0.4	1
22409	Bidirectional lncRNA Transfer between <i>Cuscuta</i> Parasites and Their Host Plant. <i>International Journal of Molecular Sciences</i> , 2022, 23, 561.	1.8	7
22410	Identification of potential biomarkers in hepatocellular carcinoma: A network-based approach. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100864.	1.9	4
22411	SPP1 in infliximab resistant ulcerative colitis and associated colorectal cancer. <i>European Journal of Gastroenterology and Hepatology</i> , 2022, Publish Ahead of Print, .	0.8	7
22412	Study on the Mechanism of Compound Kidney-Invigorating Granule for Osteoporosis based on Network Pharmacology and Experimental Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-20.	0.5	1
22413	Competing endogenous RNA network mediated by circ_3205 in SARS-CoV-2 infected cells. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 75.	2.4	15
22414	Oncogenic Mutation BRAF V600E Changes Phenotypic Behavior of THLE-2 Liver Cells through Alteration of Gene Expression. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1548.	1.8	1

#	ARTICLE	IF	CITATIONS
22415	Cobalt Neurotoxicity: Transcriptional Effect of Elevated Cobalt Blood Levels in the Rodent Brain. <i>Toxics</i> , 2022, 10, 59.	1.6	5
22416	Potential roles of hsa_circ_000839 and hsa_circ_0005986 in breast cancer. <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, e24263.	0.9	4
22417	Identification of Potential Key Genes and Molecular Mechanisms of Medulloblastoma Based on Integrated Bioinformatics Approach. <i>BioMed Research International</i> , 2022, 2022, 1-17.	0.9	8
22418	Regulation of fatty acid desaturase- and immunity gene-expression by mbk-1/DYRK1A in <i>Caenorhabditis elegans</i> . <i>BMC Genomics</i> , 2022, 23, 25.	1.2	4
22419	Bioinformatic Analysis Combined With Experimental Validation Reveals Novel Hub Genes and Pathways Associated With Focal Segmental Glomerulosclerosis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691966.	1.6	4
22420	Proteomic and Transcriptomic Analyses Indicate Reduced Biofilm-Forming Abilities in Cefiderocol-Resistant <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 778190.	1.5	10
22421	Identification and Validation of Immune-Related Prognostic Genes in the Tumor Microenvironment of Colon Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 778153.	1.1	0
22422	Molecular Mechanism of <i>Gelsemium elegans</i> (Gardner and Champ.) Benth. Against Neuropathic Pain Based on Network Pharmacology and Experimental Evidence. <i>Frontiers in Pharmacology</i> , 2021, 12, 792932.	1.6	11
22423	Immune microenvironment-related gene mapping predicts immunochemotherapy response and prognosis in diffuse large B-cell lymphoma. <i>Medical Oncology</i> , 2022, 39, 44.	1.2	5
22424	Metagenomic and metatranscriptomic analyses reveal minor-yet-crucial roles of gut microbiome in deep-sea hydrothermal vent snail. <i>Animal Microbiome</i> , 2022, 4, 3.	1.5	7
22425	New Association Between Diabetes Mellitus and Pancreatic Cancer. <i>Current Diabetes Reviews</i> , 2022, 18, .	0.6	0
22426	Aerial View of the Association Between m6A-Related LncRNAs and Clinicopathological Characteristics of Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 812785.	1.3	5
22427	Peppermint oil effects on the gut microbiome in children with functional abdominal pain. <i>Clinical and Translational Science</i> , 2022, 15, 1036-1049.	1.5	6
22428	Universal gene co-expression network reveals receptor-like protein genes involved in broad-spectrum resistance in pepper ( <i>Capsicum annuum</i> L.). <i>Horticulture Research</i> , 2022, , .	2.9	10
22429	Identification of potential core genes at single-cell level contributing to pathogenesis of pancreatic ductal adenocarcinoma through bioinformatics analysis. <i>Cancer Biomarkers</i> , 2022, , 1-12.	0.8	1
22432	Lifespan prolonging mechanisms and insulin upregulation without fat accumulation in long-lived reproductives of a higher termite. <i>Communications Biology</i> , 2022, 5, 44.	2.0	27
22433	microRNA-Based Network and Pathway Analysis for Neuropathic Pain in Rodent Models. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 780730.	1.6	1
22434	Identification of Molecular Subtypes and Potential Small-Molecule Drugs for Esophagus Cancer Treatment Based on m6A Regulators. <i>Journal of Oncology</i> , 2022, 2022, 1-13.	0.6	1

#	ARTICLE	IF	CITATIONS
22435	Comprehensive Analyses of Glucose Metabolism in Glioma Reveal the Glioma-Promoting Effect of GALM. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 717182.	1.8	1
22436	PBK/TOPK Inhibitor Suppresses the Progression of Prolactinomas. <i>Frontiers in Endocrinology</i> , 2021, 12, 706909.	1.5	1
22437	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics. <i>Frontiers in Plant Science</i> , 2021, 12, 769700.	1.7	4
22438	A Broad m6A Modification Landscape in Inflammatory Bowel Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 782636.	1.8	14
22439	Bioinformatics Characterization of Candidate Genes Associated with Gene Network and miRNA Regulation in Esophageal Squamous Cell Carcinoma Patients. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 1083.	1.3	0
22440	Bioinformatic Approach to Unveil Key Differentially Expressed Proteins in Human Sperm After Slow and Rapid Cryopreservation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 759354.	1.8	5
22441	Targeting pancreatic cancer by TAK-981: a SUMOylation inhibitor that activates the immune system and blocks cancer cell cycle progression in a preclinical model. <i>Gut</i> , 2022, 71, 2266-2283.	6.1	35
22442	CX3CR1 Acts as a Protective Biomarker in the Tumor Microenvironment of Colorectal Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 758040.	2.2	15
22443	A functional module states framework reveals transcriptional states for drug and target prediction. <i>Cell Reports</i> , 2022, 38, 110269.	2.9	1
22444	MODalyseRâ€”a novel software for inference of disease module hub regulators identified a putative multiple sclerosis regulator supported by independent eQTL data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	1
22445	Glenthenamines Aâ€”F: Enamine Pyranonaphthoquinones from the Australian Pasture Plant Derived <i>Streptomyces</i> sp. CMB-PB042. <i>Journal of Natural Products</i> , 2022, , .	1.5	3
22446	Dissecting the heterogeneity of the microenvironment in primary and recurrent nasopharyngeal carcinomas using single-cell RNA sequencing. <i>Oncolmmunology</i> , 2022, 11, 2026583.	2.1	15
22447	LRRK2 correlates with macrophage infiltration in pan-cancer. <i>Genomics</i> , 2022, 114, 316-327.	1.3	10
22448	Causal Biological Network Model for Inflammasome Signaling Applied for Interpreting Transcriptomic Changes in Various Inflammatory States. <i>International Journal of Inflammation</i> , 2022, 2022, 1-13.	0.9	1
22449	Gene and metabolite expression dependence on body mass index in human myocardium. <i>Scientific Reports</i> , 2022, 12, 1425.	1.6	3
22450	Role of key-stone microbial taxa in algae amended soil for mediating nitrogen transformation. <i>Science of the Total Environment</i> , 2022, 823, 153547.	3.9	6
22451	An Integrative Network Approach to Identify Common Genes for the Therapeutics in Tuberculosis and Its Overlapping Non-Communicable Diseases. <i>Frontiers in Pharmacology</i> , 2021, 12, 770762.	1.6	11
22452	From communities to protein complexes: A local community detection algorithm on PPI networks. <i>PLoS ONE</i> , 2022, 17, e0260484.	1.1	8

#	ARTICLE	IF	CITATIONS
22453	Gene regulatory network inference in long-lived <i>C.Âlegans</i> reveals modular properties that are predictive of novel aging genes. <i>IScience</i> , 2022, 25, 103663.	1.9	4
22454	Definition of the Metagenomic Profile of Ocean Water Samples From the Gulf of Mexico Based on Comparison With Reference Samples From Sites Worldwide. <i>Frontiers in Microbiology</i> , 2021, 12, 781497.	1.5	3
22455	Elucidation of the hepatoprotective effect and mechanism of <i>Melastoma dodecandrum</i> Lour. based on network pharmacology and experimental validation. <i>Journal of Traditional Chinese Medical Sciences</i> , 2022, 9, 47-58.	0.1	0
22456	A major yellow-seed QTL on chromosome A09 significantly increases the oil content and reduces the fiber content of seed in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 1293-1305.	1.8	26
22457	Dereplication and Quantification of Major Compounds of <i>Convolvulus arvensis</i> L. Extracts and Assessment of Their Effect on LPS-Activated J774 Macrophages. <i>Molecules</i> , 2022, 27, 963.	1.7	11
22458	Interplay between mitochondrial reactive oxygen species, oxidative stress and hypoxic adaptation in facioscapulohumeral muscular dystrophy: Metabolic stress as potential therapeutic target. <i>Redox Biology</i> , 2022, 51, 102251.	3.9	31
22459	Purification and structural elucidation of a cobalamin-dependent radical SAM enzyme. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
22460	Identification of Ferroptosis-Related Biomarkers for Prognosis and Immunotherapy in Patients With Glioma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 817643.	1.8	8
22462	Effects of Yeast Species and Processing on Intestinal Health and Transcriptomic Profiles of Atlantic Salmon ( <i>Salmo salar</i> ) Fed Soybean Meal-Based Diets in Seawater. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1675.	1.8	3
22463	A multi-omics approach unravels metagenomic and metabolic alterations of a probiotic and synbiotic additive in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Microbiome</i> , 2022, 10, 21.	4.9	25
22464	Exploring correlations between MS and NMR for compound identification using essential oils: A pilot study. <i>Phytochemical Analysis</i> , 2022, , .	1.2	6
22465	TMAO-Activated Hepatocyte-Derived Exosomes Impair Angiogenesis via Repressing CXCR4. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 804049.	1.8	10
22466	Distinguishing the molecular diversity, nutrient content, and energetic potential of exometabolomes produced by macroalgae and reef-building corals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	28
22467	Genome-wide RNAi screen identifies novel players in human 60S subunit biogenesis including key enzymes of polyamine metabolism. <i>Nucleic Acids Research</i> , 2022, 50, 2872-2888.	6.5	11
22468	Metabolomics study of COVID-19 patients in four different clinical stages. <i>Scientific Reports</i> , 2022, 12, 1650.	1.6	58
22469	Nocturnal Light Pollution Induces Weight Gain in Mice and Reshapes the Structure, Functions, and Interactions of Their Colonic Microbiota. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1673.	1.8	3
22470	Identification of Serum-Predictive Biomarkers for Subclinical Mastitis in Dairy Cows and New Insights into the Pathobiology of the Disease. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 1724-1746.	2.4	5
22471	Highâ€­intensity interval training along with spirulina algae consumption and caloric restriction ameliorated the Nrf1/Tfam/Mgmt and ATP5A1 pathway in the heart tissue of obese rats. <i>Journal of Food Biochemistry</i> , 2022, 46, e14061.	1.2	0

#	ARTICLE	IF	CITATIONS
22472	Exploiting Interdata Relationships in Prostate Cancer Proteomes: Clinical Significance of HO-1 Interactors. <i>Antioxidants</i> , 2022, 11, 290.	2.2	2
22473	Weaning differentially affects the maturation of piglet peripheral blood and jejunal Peyer's patches. <i>Scientific Reports</i> , 2022, 12, 1604.	1.6	3
22474	Splicing is an alternate oncogenic pathway activation mechanism in glioma. <i>Nature Communications</i> , 2022, 13, 588.	5.8	17
22475	An Integrative Analysis Framework for Identifying the Prognostic Markers from Multidimensional RNA Data of Clear Cell Renal Cell Carcinoma. <i>American Journal of Pathology</i> , 2022, 192, 671-686.	1.9	0
22476	Screening and Identification of Novel Potential Biomarkers for Breast Cancer Brain Metastases. <i>Frontiers in Oncology</i> , 2021, 11, 784096.	1.3	4
22477	Validated In Silico Model for Biofilm Formation in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 713-731.	1.9	3
22478	Reconstruction and exploratory analysis of mTORC1 signalling pathway and its applications to various diseases using Network based approach. <i>Journal of Microbiology and Biotechnology</i> , 2022, 32, .	0.9	1
22479	Comparative Analysis of Proanthocyanidin Metabolism and Genes Regulatory Network in Fresh Leaves of Two Different Ecotypes of <i>Tetrastigma hemsleyanum</i> . <i>Plants</i> , 2022, 11, 211.	1.6	3
22480	How Far Are We from the Completion of the Human Protein Interactome Reconstruction?. <i>Biomolecules</i> , 2022, 12, 140.	1.8	11
22481	Identification and Verification of Five Potential Biomarkers Related to Skin and Thermal Injury Using Weighted Gene Co-Expression Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 781589.	1.1	1
22482	Transcriptome Analysis of Atlantic Salmon ( <i>Salmo salar</i> ) Skin in Response to Sea Lice and Infectious Salmon Anemia Virus Co-Infection Under Different Experimental Functional Diets. <i>Frontiers in Immunology</i> , 2021, 12, 787033.	2.2	6
22483	Epigenetic modifications in pancreas development, diabetes, and therapeutics. <i>Medicinal Research Reviews</i> , 2022, 42, 1343-1371.	5.0	20
22484	Identification of novel proteins and mechanistic pathways associated with early-onset hypertension by deep proteomic mapping of resistance arteries. <i>Journal of Biological Chemistry</i> , 2022, 298, 101512.	1.6	8
22485	A Single-Cell Omics Network Model of Cell Crosstalk during the Formation of Primordial Follicles. <i>Cells</i> , 2022, 11, 332.	1.8	5
22486	Construction of a potential microRNA and messenger RNA regulatory network of acute lung injury in mice. <i>Scientific Reports</i> , 2022, 12, 777.	1.6	4
22487	Investigating the Molecular Mechanism of Xijiao Dihuang Decoction for the Treatment of SLE Based on Network Pharmacology and Molecular Docking Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-20.	0.9	5
22488	Pre-transplant Transcriptional Signature in Peripheral Blood Mononuclear Cells of Acute Renal Allograft Rejection. <i>Frontiers in Medicine</i> , 2021, 8, 799051.	1.2	0
22489	Downregulation of PIK3CB Involved in Alzheimer's Disease via Apoptosis, Axon Guidance, and FoxO Signaling Pathway. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	1.9	5



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22490	Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data. <i>Scientific Reports</i> , 2022, 12, 120.	1.6	12
22491	Computational analyses of mechanism of action (MoA): data, methods and integration. <i>RSC Chemical Biology</i> , 2022, 3, 170-200.	2.0	32
22492	The Prognostic and Molecular Landscape of Autophagy-Related Long Noncoding RNA in Colorectal Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-27.	0.9	2
22493	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	13.5	114
22494	Transcriptomic Landscape of Herbivore Oviposition in Arabidopsis: A Systematic Review. <i>Frontiers in Plant Science</i> , 2021, 12, 772492.	1.7	3
22495	Molecular structures and functional exploration of NDA family genes respond tolerant to alkaline stress in <i>Gossypium hirsutum</i> L. <i>Biological Research</i> , 2022, 55, 4.	1.5	4
22496	Regional and temporal coordinated mutation patterns in SARS-CoV-2 spike protein revealed by a clustering and network analysis. <i>Scientific Reports</i> , 2022, 12, 1128.	1.6	28
22498	&lt;i>Ex situ</i> Visualization and Network Analysis of Water Distribution in Gas Diffusion Layer of Polymer Electrolyte Fuel Cells by Synchrotron X-Ray Computed Tomography under Water Injection. <i>Journal of Chemical Engineering of Japan</i> , 2022, 55, 71-76.	0.3	0
22499	A Workflow of Integrated Resources to Catalyze Network Pharmacology Driven COVID-19 Research. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 718-729.	2.5	2
22500	Computational techniques for studying protein-protein interactions. , 2022, , 125-135.		1
22501	The Identification of Prognostic and Metastatic Alternative Splicing in Skin Cutaneous Melanoma. <i>Cancer Control</i> , 2022, 29, 107327482110515.	0.7	2
22502	Co-occurrence Interaction Networks of Extremophile Species Living in a Copper Mining Tailing. <i>Frontiers in Microbiology</i> , 2021, 12, 791127.	1.5	6
22503	Functional Prediction of Biological Profile During Eutrophication in Marine Environment. <i>Bioinformatics and Biology Insights</i> , 2022, 16, 117793222110639.	1.0	1
22504	Network pharmacology and GEO database-based analysis of Sini powder in the prevention of depression among shift workers. <i>International Journal of Transgender Health</i> , 2022, 15, 74-87.	1.1	2
22505	Deep distributed computing to reconstruct extremely large lineage trees. <i>Nature Biotechnology</i> , 2022, 40, 566-575.	9.4	14
22506	Identification of cardiomyopathy-related core genes through human metabolic networks and expression data. <i>BMC Genomics</i> , 2022, 23, 47.	1.2	2
22507	Integrated weighted gene coexpression network analysis identifies Frizzled 2 (FZD2) as a key gene in invasive malignant pleomorphic adenoma. <i>Journal of Translational Medicine</i> , 2022, 20, 15.	1.8	3
22508	In silico analysis of carotenoid biosynthesis pathway in cassava ( <i>Manihot esculenta</i> Crantz). <i>Journal of Genetics</i> , 2022, 101, 1.	0.4	4

#	ARTICLE	IF	CITATIONS
22509	Genome-Resolved Metagenomic Insights into Massive Seasonal Ammonia-Oxidizing Archaea Blooms in San Francisco Bay. <i>MSystems</i> , 2022, 7, e0127021.	1.7	11
22510	Integrative Lipidomics and Metabolomics for System-Level Understanding of the Metabolic Syndrome in Long-Term Treated HIV-Infected Individuals. <i>Frontiers in Immunology</i> , 2021, 12, 742736.	2.2	11
22511	Molecular Mechanisms of Cardiac Injury Associated With Myocardial SARS-CoV-2 Infection. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 643958.	1.1	10
22512	Bioinformatics analysis of recurrent deletion regions in neuroblastoma. <i>Medical Oncology</i> , 2022, 39, 31.	1.2	1
22513	Microbial Communities Influence Soil Dissolved Organic Carbon Concentration by Altering Metabolite Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 799014.	1.5	17
22514	Induction of Isochromanones by Co-Cultivation of the Marine Fungus <i>Cosmospora</i> sp. and the Phytopathogen <i>Magnaporthe oryzae</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 782.	1.8	9
22515	Simple But Efficacious Enrichment of Integral Membrane Proteins and Their Interactions for In-Depth Membrane Proteomics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100206.	2.5	20
22516	Ubiquitylomes and proteomes analyses provide a new interpretation of the molecular mechanisms of rice leaf senescence. <i>Planta</i> , 2022, 255, 43.	1.6	2
22517	Study on diverse pathological characteristics of heart failure in different stages based on proteomics. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 1169-1182.	1.6	3
22519	Periostin promotes the proliferation and metastasis of osteosarcoma by increasing cell survival and activates the PI3K/Akt pathway. <i>Cancer Cell International</i> , 2022, 22, 34.	1.8	4
22520	Afatinib and Pembrolizumab for Recurrent or Metastatic Head and Neck Squamous Cell Carcinoma (ALPHA Study): A Phase II Study with Biomarker Analysis. <i>Clinical Cancer Research</i> , 2022, 28, 1560-1571.	3.2	33
22521	Exploring the potential biomarkers for prognosis of glioblastoma via weighted gene co-expression network analysis. <i>PeerJ</i> , 2022, 10, e12768.	0.9	1
22522	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. <i>Communications Biology</i> , 2022, 5, 80.	2.0	12
22523	<i>Wolbachia</i> Utilizes lncRNAs to Activate the Anti-Dengue Toll Pathway and Balance Reactive Oxygen Species Stress in <i>Aedes aegypti</i> Through a Competitive Endogenous RNA Network. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 823403.	1.8	11
22524	Circadian transcription factor NPAS2 and the NAD <sup>+</sup> -dependent deacetylase SIRT1 interact in the mouse nucleus accumbens and regulate reward. <i>European Journal of Neuroscience</i> , 2022, 55, 675-693.	1.2	9
22526	FOXO1 cooperates with C/EBP $\beta$ and ATF4 to regulate skeletal muscle atrophy transcriptional program during fasting. <i>FASEB Journal</i> , 2022, 36, e22152.	0.2	22
22527	Comparison of Growth Performance, Immunity, Antioxidant Capacity, and Liver Transcriptome of Calves between Whole Milk and Plant Protein-Based Milk Replacer under the Same Energy and Protein Levels. <i>Antioxidants</i> , 2022, 11, 270.	2.2	6
22528	Reprogramming of phytopathogen transcriptome by a non-bactericidal pesticide residue alleviates its virulence in rice. <i>Fundamental Research</i> , 2022, 2, 198-207.	1.6	11

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22529	Genome-Wide Identification of Maize Aquaporin and Functional Analysis During Seed Germination and Seedling Establishment. <i>Frontiers in Plant Science</i> , 2022, 13, 831916.	1.7	6
22530	Identification of Key Genes and Pathways Involved in Circulating Tumor Cells in Colorectal Cancer. <i>Analytical Cellular Pathology</i> , 2022, 2022, 1-11.	0.7	3
22531	Myeloid-Biased HSC Require Semaphorin 4A From the Bone Marrow Niche for Self-Renewal Under Stress and Life-Long Persistence. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22532	Obesity modulates cell-cell interactions during ovarian folliculogenesis. <i>IScience</i> , 2022, 25, 103627.	1.9	12
22533	Revealing the differential protein profiles behind the nitrogen use efficiency in popcorn ( <i>Zea mays</i> var.) Tj ETQq0 0 0 ggBT /Overlock 10 T	1.6	6
22534	Genome-Wide Association Study of Root System Architecture in Maize. <i>Genes</i> , 2022, 13, 181.	1.0	13
22535	The Potential Bioactive Components of Nine TCM Prescriptions Against COVID-19 in Lung Cancer Were Explored Based on Network Pharmacology and Molecular Docking. <i>Frontiers in Medicine</i> , 2021, 8, 813119.	1.2	6
22536	Nitrogen application and differences in leaf number retained after topping affect the tobacco ( <i>Nicotiana tabacum</i> ) transcriptome and metabolome. <i>BMC Plant Biology</i> , 2022, 22, 38.	1.6	5
22537	Development of a CAFs-related gene signature to predict survival and drug response in bladder cancer. <i>Human Cell</i> , 2022, 35, 649-664.	1.2	11
22538	Genomic Diversity of Bacteriophages Infecting the Genus <i>Acinetobacter</i> . <i>Viruses</i> , 2022, 14, 181.	1.5	12
22539	An Immune Feature-Based, Three-Gene Scoring System for Prognostic Prediction of Head-and-Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 739182.	1.3	2
22540	Exploring Toxins for Hunting SARS-CoV-2 Main Protease Inhibitors: Molecular Docking, Molecular Dynamics, Pharmacokinetic Properties, and Reactome Study. <i>Pharmaceuticals</i> , 2022, 15, 153.	1.7	13
22541	Antimicrobial Peptides from Human Microbiome Against Multidrug Efflux Pump of <i>Pseudomonas aeruginosa</i> : a Computational Study. <i>Probiotics and Antimicrobial Proteins</i> , 2022, 14, 180-188.	1.9	3
22542	The miR-23b/27b/24-1 Cluster Inhibits Hepatic Fibrosis by Inactivating Hepatic Stellate Cells. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 1393-1412.	2.3	1
22543	High complement protein C1q levels in pulmonary fibrosis and non-small cell lung cancer associated with poor prognosis. <i>BMC Cancer</i> , 2022, 22, 110.	1.1	12
22544	A molecular map of long non-coding RNA expression, isoform switching and alternative splicing in osteoarthritis. <i>Human Molecular Genetics</i> , 2022, 31, 2090-2105.	1.4	15
22545	Doxycycline Alters the Porcine Renal Proteome and Degradome during Hypothermic Machine Perfusion. <i>Current Issues in Molecular Biology</i> , 2022, 44, 559-577.	1.0	1
22546	Proteome-scale mapping of binding sites in the unstructured regions of the human proteome. <i>Molecular Systems Biology</i> , 2022, 18, e10584.	3.2	33

#	ARTICLE	IF	CITATIONS
22547	Exposure to aerosolized staphylococcal enterotoxin B potentiated by lipopolysaccharide modifies lung transcriptomes and results in lung injury in the mouse model. <i>Journal of Applied Toxicology</i> , 2022, , .	1.4	2
22548	Mechanism of Rhubarb for Diabetic Kidney Disease through the AMPK/NF- $\kappa$ B Signaling Pathway Based on Network Pharmacology. <i>ChemistrySelect</i> , 2022, 7, .	0.7	2
22550	Transcriptome Analysis Reveals Olfactory System Expression Characteristics of Aquatic Snakes. <i>Frontiers in Genetics</i> , 2022, 13, 825974.	1.1	6
22551	Aulosirazoles B and C from the Cyanobacterium <i>Nostoc</i> sp. UIC 10771: Analogues of an Isothiazolonaphthoquinone Scaffold that Activate Nuclear Transcription Factor FOXO3a in Ovarian Cancer Cells. <i>Journal of Natural Products</i> , 2022, 85, 540-546.	1.5	4
22552	Pathway Driven Target Selection in <i>Klebsiella pneumoniae</i> : Insights Into Carbapenem Exposure. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 773405.	1.8	4
22554	Protein-protein interactions network model underlines a link between hormonal and neurological disorders. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100866.	1.9	0
22555	MiR-182-5p Modulates Prostate Cancer Aggressive Phenotypes by Targeting EMT Associated Pathways. <i>Biomolecules</i> , 2022, 12, 187.	1.8	7
22556	Construction of dynamic protein interaction network based on gene expression data and quartile one principle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, , .	1.5	0
22557	Sheep in wolves'™ clothing: Temperate T7-like bacteriophages and the origins of the Autographiviridae. <i>Virology</i> , 2022, 568, 86-100.	1.1	12
22560	Exosomal lncRNA and mRNA profiles in polycystic ovary syndrome: bioinformatic analysis reveals disease-related networks. <i>Reproductive BioMedicine Online</i> , 2022, 44, 777-790.	1.1	8
22561	A clinical and in-silico study of MicroRNA-21 and growth differentiation factor-15 expression in pre-diabetes, type 2 diabetes and diabetic nephropathy. <i>Minerva Endocrinology</i> , 2022, , .	0.6	4
22562	The MicroRNAs-Transcription Factors-mRNA Regulatory Network Plays an Important Role in Resistance to Cold Stress in the Pearl Grouper. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	5
22563	Transcriptome Analysis of Peripheral Blood Mononuclear Cells in SARS-CoV-2 Naïve and Recovered Individuals Vaccinated With Inactivated Vaccine. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 821828.	1.8	8
22564	Comparative transcriptomic analysis reveals potential mechanisms for high tolerance to submergence in arbor willows. <i>PeerJ</i> , 2022, 10, e12881.	0.9	3
22565	Identification of Prognostic lncRNA Related to the Immune Microenvironment of Soft Tissue Sarcoma. <i>BioMed Research International</i> , 2022, 2022, 1-15.	0.9	0
22566	Characterization of Cell Cycle-Related Competing Endogenous RNAs Using Robust Rank Aggregation as Prognostic Biomarker in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 2022, 12, 807367.	1.3	3
22567	Surface Characteristics Together With Environmental Conditions Shape Marine Biofilm Dynamics in Coastal NW Mediterranean Locations. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	3
22568	SU086, an inhibitor of HSP90, impairs glycolysis and represents a treatment strategy for advanced prostate cancer. <i>Cell Reports Medicine</i> , 2022, 3, 100502.	3.3	18

#	ARTICLE	IF	CITATIONS
22569	Cytoplasmic switch of ARS2 isoforms promotes nonsense-mediated mRNA decay and arsenic sensitivity. <i>Nucleic Acids Research</i> , 2022, 50, 1620-1638.	6.5	2
22570	Student biocuration projects as a learning environment. <i>F1000Research</i> , 0, 10, 1023.	0.8	0
22571	<i>CHEK1</i> : a hub gene related to poor prognosis for lung adenocarcinoma. <i>Biomarkers in Medicine</i> , 2022, 16, 83-100.	0.6	2
22572	Identification of Potential Candidate Genes From Co-Expression Module Analysis During Preadipocyte Differentiation in Landrace Pig. <i>Frontiers in Genetics</i> , 2021, 12, 753725.	1.1	2
22574	A practical guide to interpreting and generating bottom-up proteomics data visualizations. <i>Proteomics</i> , 2022, 22, e2100103.	1.3	16
22575	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	2.2	29
22576	Characterization of Pyridomycin B Reveals the Formation of Functional Groups in Antimycobacterial Pyridomycin. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0203521.	1.4	2
22577	Characterization of Interplay Between Autophagy and Ferroptosis and Their Synergistical Roles on Manipulating Immunological Tumor Microenvironment in Squamous Cell Carcinomas. <i>Frontiers in Immunology</i> , 2021, 12, 739039.	2.2	35
22580	Mechanical phenotyping reveals unique biomechanical responses in retinoic acid-resistant acute promyelocytic leukemia. <i>IScience</i> , 2022, 25, 103772.	1.9	4
22581	Integrated RNA- and miRNA-sequencing analysis identifies molecular basis for stress-induced heart injury in mouse models. <i>International Journal of Cardiology</i> , 2022, 349, 115-122.	0.8	2
22582	BIRC5 promotes cancer progression and predicts prognosis in laryngeal squamous cell carcinoma. <i>PeerJ</i> , 2022, 10, e12871.	0.9	6
22583	Integrated Metabolomics and Network Pharmacology Revealed Hong-Hua-Xiao-Yao Tablet's Effect of Mediating Hormone Synthesis in the Treatment of Mammary Gland Hyperplasia. <i>Frontiers in Pharmacology</i> , 2022, 13, 788019.	1.6	4
22584	Characterization and immobilization of <i>Pycnoporus cinnabarinus</i> carboxylic acid reductase, PccAR2. <i>Journal of Biotechnology</i> , 2022, 345, 47-54.	1.9	7
22585	Prediction the Molecular Mechanism of Shengmai Injection in Acute Treatment of COVID-19 Based on Network Pharmacology. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210750.	0.2	7
22586	New Insight Into the Interspecies Shift of Anammox Bacteria <i>Ca. Brocadia</i> and <i>Ca. Jettenia</i> in Reactors Fed With Formate and Folate. <i>Frontiers in Microbiology</i> , 2021, 12, 802201.	1.5	13
22587	Uveal Melanoma Cell Line Proliferation Is Inhibited by Ricolinostat, a Histone Deacetylase Inhibitor. <i>Cancers</i> , 2022, 14, 782.	1.7	12
22588	RNA-Seq with a novel glabrous-ZM24fl reveals some key lncRNAs and the associated targets in fiber initiation of cotton. <i>BMC Plant Biology</i> , 2022, 22, 61.	1.6	5
22589	A new blood-based RNA signature (R9), for monitoring effectiveness of tuberculosis treatment in a South Indian longitudinal cohort. <i>IScience</i> , 2022, 25, 103745.	1.9	1

#	ARTICLE	IF	CITATIONS
22590	Cross-species metabolomic analysis identifies uridine as a potent regeneration promoting factor. <i>Cell Discovery</i> , 2022, 8, 6.	3.1	50
22591	Glutamine-Fructose-6-Phosphate Transaminase 2 (GFPT2) Is Upregulated in Breast Epithelialâ€Mesenchymal Transition and Responds to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100185.	2.5	12
22592	Comparative microbiome analysis reveals bacterial communities associated with <i>Candidatus Liberibacter asiaticus</i> infection in the Huanglongbing insect vector <i>Diaphorina citri</i> . <i>Journal of Asia-Pacific Entomology</i> , 2022, 25, 101884.	0.4	5
22593	The Multi-Omics Analysis of Key Genes Regulating EGFR-TKI Resistance, Immune Infiltration, SCLC Transformation in EGFR-Mutant NSCLC. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 649-667.	1.6	11
22594	Diatom Biogeography, Temporal Dynamics, and Links to Bacterioplankton across Seven Oceanographic Time-Series Sites Spanning the Australian Continent. <i>Microorganisms</i> , 2022, 10, 338.	1.6	5
22595	Increase in ADAR1p110 activates the canonical Wnt signaling pathway associated with aggressive phenotype in triple negative breast cancer cells. <i>Gene</i> , 2022, 819, 146246.	1.0	4
22596	NF-ÎB perturbation reveals unique immunomodulatory functions in Prx1 <sup>+</sup> fibroblasts that promote development of atopic dermatitis. <i>Science Translational Medicine</i> , 2022, 14, eabj0324.	5.8	22
22597	A Calmodulin-Like Gene (GbCML7) for Fiber Strength and Yield Improvement Identified by Resequencing Core Accessions of a Pedigree in <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 815648.	1.7	4
22598	Yoghurt consumption is associated with changes in the composition of the human gut microbiome and metabolome. <i>BMC Microbiology</i> , 2022, 22, 39.	1.3	31
22599	Identifying Potential Biomarkers of Prognostic Value in Colorectal Cancer via Tumor Microenvironment Data Mining. <i>Frontiers in Genetics</i> , 2021, 12, 787208.	1.1	4
22600	Different gene co-expression patterns of aortic intima-media and adventitia in thoracic aortic aneurysm. <i>Gene</i> , 2022, 819, 146233.	1.0	0
22602	A cluster of transcripts identifies a transition stage initiating leafy head growth in heading morphotypes of <i>Brassica</i> . <i>Plant Journal</i> , 2022, 110, 688-706.	2.8	7
22603	A pan-CRISPR analysis of mammalian cell specificity identifies ultra-compact sgRNA subsets for genome-scale experiments. <i>Nature Communications</i> , 2022, 13, 625.	5.8	2
22604	Identification of the Cesa Subfamily and Functional Analysis of GhMCesA35 in <i>Gossypium hirsutum</i> L.. <i>Genes</i> , 2022, 13, 292.	1.0	4
22605	Characterization of the AGR2 Interactome Uncovers New Players of Protein Disulfide Isomerase Network in Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100188.	2.5	11
22606	Artificial intelligence analysis to explore synchronize exercise, cobalamin, and magnesium as new actors to therapeutic of migraine symptoms: a randomized, placebo-controlled trial. <i>Neurological Sciences</i> , 2022, 43, 4413-4424.	0.9	11
22607	Herbal Formula Modified Bu-Shen-Huo-Xue Decoction Attenuates Intervertebral Disc Degeneration via Regulating Inflammation and Oxidative Stress. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-12.	0.5	2
22608	Structure of a B12-dependent radical SAM enzyme in carbapenem biosynthesis. <i>Nature</i> , 2022, 602, 343-348.	13.7	36



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22609	FUS-DDIT3 Fusion Oncoprotein Expression Affects JAK-STAT Signaling in Myxoid Liposarcoma. <i>Frontiers in Oncology</i> , 2022, 12, 816894.	1.3	7
22610	Differential Regulation and Production of Secondary Metabolites among Isolates of the Fungal Wheat Pathogen <i>Zymoseptoria tritici</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0229621.	1.4	9
22611	Autism genes converge on asynchronous development of shared neuron classes. <i>Nature</i> , 2022, 602, 268-273.	13.7	180
22612	Deciphering the influence of multiple anthropogenic inputs on taxonomic and functional profiles of the microbial communities in Yitong River, Northeast China. <i>Environmental Science and Pollution Research</i> , 2022, 29, 39973-39984.	2.7	3
22613	Proteomic landscape of SARS-CoV-2 and MERS-CoV infected primary human renal epithelial cells. <i>Life Science Alliance</i> , 2022, 5, e202201371.	1.3	5
22614	Tree decline and mortality following pathogen invasion alters the diversity, composition and network structure of the soil microbiome. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108560.	4.2	16
22615	Fruit transcriptional profiling of the contrasting genotypes for shelf life reveals the key candidate genes and molecular pathways regulating post-harvest biology in cucumber. <i>Genomics</i> , 2022, 114, 110273.	1.3	7
22616	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108550.	4.2	19
22617	Common genetic aspects between COVID-19 and sarcoidosis: A network-based approach using gene expression data. <i>Biochemistry and Biophysics Reports</i> , 2022, 29, 101219.	0.7	0
22618	Identification of multiple sclerosis-related genes regulated by EBV-encoded microRNAs in B cells. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 59, 103563.	0.9	4
22619	Rapid 3D bioprinting of a multicellular model recapitulating pterygium microenvironment. <i>Biomaterials</i> , 2022, 282, 121391.	5.7	13
22620	Integrated proteome and phosphoproteome analysis of interscapular brown adipose and subcutaneous white adipose tissues upon high fat diet feeding in mouse. <i>Journal of Proteomics</i> , 2022, 255, 104500.	1.2	4
22621	Evolution of sulfate reduction behavior in leachate saturated zones in landfills. <i>Waste Management</i> , 2022, 141, 52-62.	3.7	10
22622	Deep 2-Hydroxyisobutyrylome in mouse liver expands the roles of lysine 2-hydroxyisobutyrylation pathway. <i>Bioorganic and Medicinal Chemistry</i> , 2022, 57, 116634.	1.4	3
22623	Polygenic networks in peripheral leukocytes indicate patterns associated with HIV infection and context-dependent effects of cannabis use. <i>Brain, Behavior, &amp; Immunity - Health</i> , 2022, 20, 100414.	1.3	4
22624	Identification of core microbiota in the fermented grains of a Chinese strong-flavor liquor from Sichuan. <i>LWT - Food Science and Technology</i> , 2022, 158, 113140.	2.5	19
22625	Weighted genome-wide association study reveals new candidate genes related to boar taint compounds 1. <i>Livestock Science</i> , 2022, 257, 104845.	0.6	2
22626	Recoupled-STOCSY-based co-expression network analysis to extract phenotype-driven metabolite modules in NMR-based metabolomics dataset. <i>Analytica Chimica Acta</i> , 2022, 1197, 339528.	2.6	4

#	ARTICLE	IF	CITATIONS
22627	Phylogenomic classification and synteny network analyses deciphered the evolutionary landscape of aldol-keto reductase (AKR) gene superfamily in the plant kingdom. <i>Gene</i> , 2022, 816, 146169.	1.0	4
22628	Landscape of keratinocytes transcriptome alterations in response to Trichophyton mentagrophytes infection. <i>Microbial Pathogenesis</i> , 2022, 164, 105426.	1.3	3
22629	System biology-based investigation of Silymarin to trace hepatoprotective effect. <i>Computers in Biology and Medicine</i> , 2022, 142, 105223.	3.9	19
22630	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immuninformatics</i> , 2022, 5, 100009.	1.2	27
22631	Triplication is the main evolutionary driving force of NLP transcription factor family in Chinese cabbage and related species. <i>International Journal of Biological Macromolecules</i> , 2022, 201, 492-506.	3.6	4
22632	SARS-CoV-2 causes a significant stress response mediated by small RNAs in the blood of COVID-19 patients. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 751-762.	2.3	12
22633	Constructing mRNA, miRNA, circRNA and lncRNA regulatory network by Analysis of microarray data in breast cancer. <i>Gene Reports</i> , 2022, 26, 101510.	0.4	2
22634	Untangling the placentome gene network of beef heifers in early gestation. <i>Genomics</i> , 2022, 114, 110274.	1.3	3
22635	Identification of the hormetic dose-response and regulatory network of multiple metals co-exposure-related hypertension via integration of metallomics and adverse outcome pathways. <i>Science of the Total Environment</i> , 2022, 817, 153039.	3.9	7
22636	Low-intensity blast induces acute glutamatergic hyperexcitability in mouse hippocampus leading to long-term learning deficits and altered expression of proteins involved in synaptic plasticity and serine protease inhibitors. <i>Neurobiology of Disease</i> , 2022, 165, 105634.	2.1	7
22637	HIF-1 $\alpha$ inhibition promotes the efficacy of immune checkpoint blockade in the treatment of non-small cell lung cancer. <i>Cancer Letters</i> , 2022, 531, 39-56.	3.2	37
22638	Genome-wide identification, expression pattern and subcellular localization analysis of the JAZ gene family in <i>Toona ciliata</i> . <i>Industrial Crops and Products</i> , 2022, 178, 114582.	2.5	8
22639	Role of systems biology and multi-omics analyses in delineating spatial interconnectivity and temporal dynamicity of ER stress mediated cellular responses. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022, 1869, 119210.	1.9	0
22640	Molecular dissemination of emerging antibiotic, biocide, and metal co-resistomes in the Himalayan hot springs. <i>Journal of Environmental Management</i> , 2022, 307, 114569.	3.8	8
22641	Reconstruction of regulatory network predicts transcription factors driving the dynamics of zebrafish heart regeneration. <i>Gene</i> , 2022, 819, 146242.	1.0	0
22642	RBM20S639G mutation is a high genetic risk factor for premature death through RNA-protein condensates. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 165, 115-129.	0.9	14
22643	Systems pharmacology-based drug discovery and active mechanism of natural products for coronavirus pneumonia (COVID-19): An example using flavonoids. <i>Computers in Biology and Medicine</i> , 2022, 143, 105241.	3.9	15
22645	Transcriptome and miRNAome analysis reveals components regulating tissue differentiation of bamboo shoots. <i>Plant Physiology</i> , 2022, 188, 2182-2198.	2.3	16

#	ARTICLE	IF	CITATIONS
22646	Comprehensive Investigation of Genes Associated Cell Cycle Pathways for Prognosis and Immunotherapy in Bladder Urothelial Carcinoma. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2022, , .	0.6	0
22647	A computational model revealing the immune-related hub genes and key pathways involved in rheumatoid arthritis (RA). <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 129, 247-273.	1.0	12
22648	Schisandrin <sup>AB</sup> suppresses osteosarcoma lung metastasis <sup>in vivo</sup> by inhibiting the activation of the Wnt/ $\beta$ -catenin and PI3K/Akt signaling pathways. <i>Oncology Reports</i> , 2022, 47, .	1.2	9
22649	Identification of inflammatory response and alternative splicing in acute kidney injury and experimental verification of the involvement of RNA-binding protein RBFOX1 in this disease. <i>International Journal of Molecular Medicine</i> , 2022, 49, .	1.8	10
22650	Molecular networking in infectious disease models. <i>Methods in Enzymology</i> , 2022, 663, 341-375.	0.4	1
22651	Thrombocytopenia in COVID-19 and vaccine-induced thrombotic thrombocytopenia. <i>International Journal of Molecular Medicine</i> , 2022, 49, .	1.8	4
22652	Identification of key pathways and genes in vestibular schwannoma using bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, 217.	0.8	0
22653	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. <i>Cell</i> , 2022, 185, 916-938.e58.	13.5	164
22654	PSINDB: the postsynaptic protein-protein interaction database. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	3
22655	Understanding the Biomass Conversion Processes of Bovine Gut Microbiota Through Community-Wide Metabolic Interaction Network. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22658	Quantitative Proteomics Reveals the Role of Lysine 2-Hydroxyisobutyrylation Pathway Mediated by Tip60. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-13.	1.9	4
22659	Identification of Hypoxia-Immune-Related Gene Signatures and Construction of a Prognostic Model in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 796156.	1.8	4
22660	Metabolomics Approaches to Dereplicate Natural Products from Coral-Derived Bioactive Bacteria. <i>Journal of Natural Products</i> , 2022, 85, 462-478.	1.5	14
22661	CTCFL regulates the PI3K-Akt pathway and it is a target for personalized ovarian cancer therapy. <i>Npj Systems Biology and Applications</i> , 2022, 8, 5.	1.4	5
22662	Mutation of MUC16 Is Associated With Tumor Mutational Burden and Lymph Node Metastasis in Patients With Gastric Cancer. <i>Frontiers in Medicine</i> , 2022, 9, 836892.	1.2	4
22663	Plasma Concentration of Tumor Necrosis Factor-Stimulated Gene-6 as a Novel Diagnostic and 3-Month Prognostic Indicator in Non-Cardioembolic Acute Ischemic Stroke. <i>Frontiers in Immunology</i> , 2022, 13, 713379.	2.2	6
22664	Identification of potential target endoribonuclease <i>NSP15</i> inhibitors of SARS-CoV-2 from natural products through high-throughput virtual screening and molecular dynamics simulation. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	8
22665	The P522R protective variant of <i>PLCG2</i> promotes the expression of antigen presentation genes by human microglia in an Alzheimer's disease mouse model. <i>Alzheimer's and Dementia</i> , 2022, 18, 1765-1778.	0.4	19

#	ARTICLE	IF	CITATIONS
22666	Ploidy and local environment drive intraspecific variation in endoreduplication in <i>Arabidopsis arenosa</i> . <i>American Journal of Botany</i> , 2022, 109, 259-271.	0.8	5
22667	LPIN1 Is a Regulatory Factor Associated With Immune Response and Inflammation in Sepsis. <i>Frontiers in Immunology</i> , 2022, 13, 820164.	2.2	13
22669	An investigation of mechanisms underlying mouse blastocyst hatching: a ribonucleic acid sequencing study. <i>F&amp;S Science</i> , 2022, 3, 35-48.	0.5	1
22670	Developmental Regulation and Functional Prediction of microRNAs in an Expanded <i>Fasciola hepatica</i> miRNome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 811123.	1.8	9
22671	Aldehyde Dehydrogenase 2 Family Member (ALDH2) Is a Therapeutic Index for Oxaliplatin Response on Colorectal Cancer Therapy with Dysfunction p53. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	1
22673	ADAR1- and ADAR2-mediated regulation of maturation and targeting of miR-376b to modulate GABA neurotransmitter catabolism. <i>Journal of Biological Chemistry</i> , 2022, 298, 101682.	1.6	5
22674	Transcriptome characterization of candidate genes for heat tolerance in perennial ryegrass after exogenous methyl Jasmonate application. <i>BMC Plant Biology</i> , 2022, 22, 68.	1.6	10
22675	Reckoning apigenin and kaempferol as a potential multi-targeted inhibitor of EGFR/HER2-MEK pathway of metastatic colorectal cancer identified using rigorous computational workflow. <i>Molecular Diversity</i> , 2022, 26, 3337-3356.	2.1	6
22676	Dissecting miRNA-Gene Networks to Map Clinical Utility Roads of Pharmacogenomics-Guided Therapeutic Decisions in Cardiovascular Precision Medicine. <i>Cells</i> , 2022, 11, 607.	1.8	11
22677	Decreased Expression of circ_0000160 in Breast Cancer With Axillary Lymph Node Metastasis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 690826.	1.6	1
22678	Chemical-induced chromatin remodeling reprograms mouse ESCs to totipotent-like stem cells. <i>Cell Stem Cell</i> , 2022, 29, 400-418.e13.	5.2	68
22679	Time-course analysis and transcriptomic identification of key response strategies of <i>Nelumbo nucifera</i> to complete submergence. <i>Horticulture Research</i> , 2022, 9, .	2.9	9
22680	Human transcription factor protein interaction networks. <i>Nature Communications</i> , 2022, 13, 766.	5.8	59
22681	Hepatitis C Virus NS3/4A Inhibition and Host Immunomodulation by Tannins from <i>Terminalia chebula</i> : A Structural Perspective. <i>Molecules</i> , 2022, 27, 1076.	1.7	13
22682	Lactate Rewires Lipid Metabolism and Sustains a Metabolic-Epigenetic Axis in Prostate Cancer. <i>Cancer Research</i> , 2022, 82, 1267-1282.	0.4	52
22683	Clinical and molecular assessment of an onco-immune signature with prognostic significance in patients with colorectal cancer. <i>Cancer Medicine</i> , 2022, 11, 1573-1586.	1.3	6
22684	Protein phase separation hotspots at the presynapse. <i>Open Biology</i> , 2022, 12, 210334.	1.5	6
22685	Diagnostic, Therapeutic, and Prognostic Value of the m6A Writer Complex in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 822011.	1.8	11

#	ARTICLE	IF	CITATIONS
22686	Impacts of the STING-IRF1-STAT1-IRF1 pathway on the cellular immune reaction induced by fractionated irradiation. <i>Cancer Science</i> , 2022, 113, 1352-1361.	1.7	7
22688	Phytogenics From Sage and Lemon Verbena Promote Growth, Systemic Immunity and Disease Resistance in Atlantic Salmon ( <i>Salmo salar</i> ). <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
22689	Identification of circular RNAs and functional competing endogenous RNA networks in human proximal tubular epithelial cells treated with sodium-glucose cotransporter 2 inhibitor dapagliflozin in diabetic kidney disease. <i>Bioengineered</i> , 2022, 13, 3911-3929.	1.4	8
22690	Identification of Ferroptosis-Related Genes in Alzheimer's Disease Based on Bioinformatic Analysis. <i>Frontiers in Neuroscience</i> , 2022, 16, 823741.	1.4	24
22691	Refinement of four major QTL for oil content in <i>Brassica napus</i> by integration of genome resequencing and transcriptomics. <i>Crop Journal</i> , 2022, 10, 627-637.	2.3	8
22692	Morphological and transcriptional evaluation of multiple facial cutaneous hyperpigmented spots. <i>Skin Health and Disease</i> , 2022, 2, .	0.7	3
22693	Research on the Mechanism of Kaempferol for Treating Senile Osteoporosis by Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-12.	0.5	7
22694	Prediction of occult tumor progression via platelet RNAs in a mouse melanoma model: a potential new platform for early detection of cancer. <i>Journal of Translational Medicine</i> , 2022, 20, 71.	1.8	1
22695	Identification of Subtypes and a Delayed Graft Function Predictive Signature Based on Ferroptosis in Renal Ischemia-Reperfusion Injury. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 800650.	1.8	7
22696	Mining GEO and TCGA Database for Immune Microenvironment of Lung Squamous Cell Carcinoma Patients With or Without Chemotherapy. <i>Frontiers in Oncology</i> , 2022, 12, 835225.	1.3	4
22697	The Toggle Switch Model for Gene Expression Change during the Prenatal-to-Postnatal Transition in Mammals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	2
22698	Transcriptome shock in interspecific F1 allotriploid hybrids between <i>Brassica</i> species. <i>Journal of Experimental Botany</i> , 2022, , .	2.4	4
22699	Fibroblast mechanotransduction network predicts targets for mechano-adaptive infarct therapies. <i>ELife</i> , 2022, 11, .	2.8	10
22700	Repurposing Ayush-64 for COVID-19: A Computational Study Based on Network Pharmacology and Molecular Docking. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 2089-2102.	0.6	1
22701	Endogenous CRISPR-Cas Systems in Group I <i>Clostridium botulinum</i> and <i>Clostridium sporogenes</i> Do Not Directly Target the Botulinum Neurotoxin Gene Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 787726.	1.5	8
22702	Increased IRF9-STAT2 Signaling Leads to Adaptive Resistance toward Targeted Therapy in Melanoma by Restraining GSDME-Dependent Pyroptosis. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2476-2487.e9.	0.3	15
22705	A metagenomics study of hexabromocyclododecane degradation with a soil microbial community. <i>Journal of Hazardous Materials</i> , 2022, 430, 128465.	6.5	16
22706	A Network Pharmacology Study to Uncover the Mechanism of FDY003 for Ovarian Cancer Treatment. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210754.	0.2	1

#	ARTICLE	IF	CITATIONS
22707	Combined transcriptomic and metabolomic analysis reveals the potential mechanism of seed germination and young seedling growth in <i>Tamarix hispida</i> . <i>BMC Genomics</i> , 2022, 23, 109.	1.2	8
22708	Relationship of Subcutaneous Adipose Tissue Inflammation-Related Gene Expression With Ectopic Lipid Deposition in Persons With HIV. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 90, 175-183.	0.9	6
22709	Forgotten Actors: Glycoside Hydrolases During Elongation Growth of Maize Primary Root. <i>Frontiers in Plant Science</i> , 2021, 12, 802424.	1.7	9
22710	Selected by bioinformatics and molecular docking analysis, Dhea and 2-14,15-Eg are effective against cholangiocarcinoma. <i>PLoS ONE</i> , 2022, 17, e0260180.	1.1	1
22712	Integrative OMICS Data-Driven Procedure Using a Derivatized Meta-Analysis Approach. <i>Frontiers in Genetics</i> , 2022, 13, 828786.	1.1	4
22713	Widespread discrepancy in Nnt genotypes and genetic backgrounds complicates granzyme A and other knockout mouse studies. <i>ELife</i> , 2022, 11, .	2.8	16
22714	The Lipid Droplet Knowledge Portal: A resource for systematic analyses of lipid droplet biology. <i>Developmental Cell</i> , 2022, 57, 387-397.e4.	3.1	22
22715	Clinical utility of cerebrospinal fluid-derived circular RNAs in lung adenocarcinoma patients with brain metastases. <i>Journal of Translational Medicine</i> , 2022, 20, 74.	1.8	6
22716	Differences in liver microRNA profiling in pigs with low and high feed efficiency. <i>Journal of Animal Science and Technology</i> , 2022, 64, 312-329.	0.8	2
22718	Identifying gene network patterns and associated cellular immune responses in children with or without nut allergy. <i>World Allergy Organization Journal</i> , 2022, 15, 100631.	1.6	5
22719	As a prognostic biomarker of clear cell renal cell carcinoma RUFY4 predicts immunotherapy responsiveness in a PDL1-related manner. <i>Cancer Cell International</i> , 2022, 22, 66.	1.8	2
22721	Longitudinal Plasma Proteomics Analysis Reveals Novel Candidate Biomarkers in Acute COVID-19. <i>Journal of Proteome Research</i> , 2022, 21, 975-992.	1.8	27
22722	Alpha B-Crystallin in Muscle Disease Prevention: The Role of Physical Activity. <i>Molecules</i> , 2022, 27, 1147.	1.7	10
22724	Comparative Flower Transcriptome Network Analysis Reveals DEGs Involved in Chickpea Reproductive Success during Salinity. <i>Plants</i> , 2022, 11, 434.	1.6	10
22725	EGR1 and KLF4 as Diagnostic Markers for Abdominal Aortic Aneurysm and Associated With Immune Infiltration. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 781207.	1.1	7
22726	Protein Level Defense Responses of <i>Theobroma cacao</i> Interaction With <i>Phytophthora palmivora</i> . <i>Frontiers in Agronomy</i> , 2022, 4, .	1.5	2
22727	A systems genetics approach delineates the role of Bcl2 in leukemia pathogenesis. <i>Leukemia Research</i> , 2022, 114, 106804.	0.4	2
22728	Development of gene signature and nomogram for diagnosis and prognosis of oral carcinoma. <i>Archives of Oral Biology</i> , 2022, 136, 105375.	0.8	1



#	ARTICLE	IF	CITATIONS
22731	Enriched and Decreased Intestinal Microbes in Active VKH Patients. , 2022, 63, 21.		9
22732	A DNA-Methylation-Driven Genes Based Prognostic Signature Reveals Immune Microenvironment in Pancreatic Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 803962.	2.2	13
22733	Network Pharmacology Combined with Molecular Docking and Experimental Verification Reveals the Bioactive Components and Potential Targets of Danlong Dingchuan Decoction against Asthma. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	5
22734	Identification of Potential Targets Linked to the Cardiovascular/Alzheimerâ€™s Axis through Bioinformatics Approaches. <i>Biomedicines</i> , 2022, 10, 389.	1.4	2
22735	Targeting Protein Tyrosine Phosphatase 1B in Obesityâ€“associated Colon Cancer: Possible Role of Sweet Potato ( <i>Ipomoea batatas</i> ). <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, , .	1.5	0
22736	Well-differentiated liver cancers reveal the potential link between ACE2 dysfunction and metabolic breakdown. <i>Scientific Reports</i> , 2022, 12, 1859.	1.6	6
22737	Analysis of Genetic Variants and the ceRNA Network of miR-9 in Non-Small Cell Lung Cancer. <i>DNA and Cell Biology</i> , 2022, 41, 142-150.	0.9	1
22738	A systematically derived overview of the non-ubiquitous pathways and genes that define the molecular and genetic signature of the healthy trabecular meshwork. <i>Genomics</i> , 2022, , 110280.	1.3	1
22739	Genome-Wide Analysis of U-box E3 Ubiquitin Ligase Family in Response to ABA Treatment in <i>Salvia miltiorrhiza</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 829447.	1.7	5
22740	Root Membrane Ubiquitinome under Short-Term Osmotic Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1956.	1.8	7
22741	Predicting Diagnostic Gene Biomarkers Associated With Immune Checkpoints, N6-Methyladenosine, and Ferroptosis in Patients With Acute Myocardial Infarction. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 836067.	1.1	10
22742	Phage Genome Diversity in a Biogas-Producing Microbiome Analyzed by Illumina and Nanopore GridION Sequencing. <i>Microorganisms</i> , 2022, 10, 368.	1.6	8
22743	WormBase in 2022â€”data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 220, .	1.2	128
22745	Integrated bioinformatic analysis of key biomarkers and signalling pathways in psoriasis. <i>Scottish Medical Journal</i> , 2022, 67, 7-17.	0.7	6
22746	Autophagy-related prognostic signature for survival prediction of triple negative breast cancer. <i>PeerJ</i> , 2022, 10, e12878.	0.9	1
22748	Cryptochrome-mediated blue-light signal contributes to lignin biosynthesis in stone cells in pear fruit. <i>Plant Science</i> , 2022, 318, 111211.	1.7	17
22749	Kaempferol and Apigenin suppresses the stemness properties of TNBC cells by modulating Sirtuins. <i>Molecular Diversity</i> , 2022, 26, 3225-3240.	2.1	11
22750	Metabolomic selection for enhanced fruit flavor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	66

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22753	Identifying significant genes and functionally enriched pathways in familial hypercholesterolemia using integrated gene co-expression network analysis. Saudi Journal of Biological Sciences, 2022, 29, 3287-3299.	1.8	4
22754	Proteome analysis of the circadian clock protein PERIOD2. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1315-1330.	1.5	6
22755	Rhizosphere bacteriome structure and functions. Nature Communications, 2022, 13, 836.	5.8	280
22756	Identification of Molecular Signatures and Candidate Drugs in Vascular Dementia by Bioinformatics Analyses. Frontiers in Molecular Neuroscience, 2022, 15, 751044.	1.4	10
22761	Dimensionality Reduction and Louvain Agglomerative Hierarchical Clustering for Cluster-Specified Frequent Biomarker Discovery in Single-Cell Sequencing Data. Frontiers in Genetics, 2022, 13, 828479.	1.1	10
22762	Cranberry Proanthocyanidin and Its Microbial Metabolite 3,4-Dihydroxyphenylacetic Acid, but Not 3-(4-Hydroxyphenyl)propionic Acid, Partially Reverse Pro-inflammatory microRNA Responses in Human Intestinal Epithelial Cells. Molecular Nutrition and Food Research, 2022, 66, e2100853.	1.5	5
22764	Multi-omics data identified <i>TP53</i> and <i>LRP1B</i> as key regulatory gene related to immune phenotypes via <i>EPCAM</i> in <i>HCC</i> . Cancer Medicine, 2022, 11, 2145-2158.	1.3	2
22765	Shifts in Bacterial Community Composition and Functional Traits at Different Time Periods Post-deglaciation of Gangotri Glacier, Himalaya. Current Microbiology, 2022, 79, 91.	1.0	7
22767	Old blood from heterochronic parabionts accelerates vascular aging in young mice: transcriptomic signature of pathologic smooth muscle remodeling. GeroScience, 2022, 44, 953-981.	2.1	15
22768	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. Cell, 2022, 185, 493-512.e25.	13.5	122
22769	Environmental structure impacts microbial composition and secondary metabolism. ISME Communications, 2022, 2, .	1.7	19
22770	Dynamic 3D genome architecture of cotton fiber reveals subgenome-coordinated chromatin topology for 4-staged single-cell differentiation. Genome Biology, 2022, 23, 45.	3.8	18
22771	Differential expression of long non-coding RNAs under <i>Peste des petits ruminants virus</i> (PPRV) infection in goats. Virulence, 2022, 13, 310-322.	1.8	2
22772	Transcriptome-wide changes in gene expression, splicing, and lncRNAs in response to a live attenuated dengue virus vaccine. Cell Reports, 2022, 38, 110341.	2.9	7
22773	Microeukaryotic gut parasites in wastewater treatment plants: diversity, activity, and removal. Microbiome, 2022, 10, 27.	4.9	15
22774	Comparative transcriptomics and multiple phytohormone profiling reveals the molecular immune response of <i>Arabidopsis thaliana</i> to the pathogen <i>Ralstonia solanacearum</i> type III effector RipN. Journal of Plant Pathology, 2022, 104, 591-603.	0.6	1
22775	Theta-Defensins to Counter COVID-19 as Furin Inhibitors: In Silico Efficiency Prediction and Novel Compound Design. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-15.	0.7	8
22776	Identification of Potential Biomarkers of Type 2 Diabetes Mellitus-Related Immune Infiltration Using Weighted Gene Coexpression Network Analysis. BioMed Research International, 2022, 2022, 1-14.	0.9	7

#	ARTICLE	IF	CITATIONS
22777	Effects of ZmHIPP on lead tolerance in maize seedlings: Novel ideas for soil bioremediation. <i>Journal of Hazardous Materials</i> , 2022, 430, 128457.	6.5	17
22779	Transcriptomic Response to Acidosis Reveals Its Contribution to Bone Metastasis in Breast Cancer Cells. <i>Cells</i> , 2022, 11, 544.	1.8	3
22782	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease. <i>Cell Systems</i> , 2022, 13, 304-320.e5.	2.9	15
22784	Network analysis of TCGA and GTEx gene expression datasets for identification of trait-associated biomarkers in human cancer. <i>STAR Protocols</i> , 2022, 3, 101168.	0.5	6
22785	Insights into the molecular basis of hypergravity-induced root growth phenotype in bread wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2022, 114, 110307.	1.3	4
22786	Comparative transcriptome analysis reveals potential anti-viral immune pathways of turbot ( <i>Scophthalmus maximus</i> ) subverted by megalocytivirus RBIV-C1 for immune evasion. <i>Fish and Shellfish Immunology</i> , 2022, 122, 153-161.	1.6	6
22787	Taking a whole-of-system approach to food packaging reduction. <i>Journal of Cleaner Production</i> , 2022, 338, 130632.	4.6	2
22788	The dynamic immune responses of Mandarin fish ( <i>Siniperca chuatsi</i> ) to ISKNV in early infection based on full-length transcriptome analysis and weighted gene co-expression network analysis. <i>Fish and Shellfish Immunology</i> , 2022, 122, 191-205.	1.6	8
22789	Comparative physiological and transcriptomic analyses reveal key regulatory networks and potential hub genes controlling peanut chilling tolerance. <i>Genomics</i> , 2022, 114, 110285.	1.3	10
22790	Comparative transcriptome study of the elongating internode in elephant grass ( <i>Cenchrus purpureus</i> ) seedlings in response to exogenous gibberellin applications. <i>Industrial Crops and Products</i> , 2022, 178, 114653.	2.5	10
22791	In silico analysis of Leishmania proteomes and protein-protein interaction network: Prioritizing therapeutic targets and drugs for repurposing to treat leishmaniasis. <i>Acta Tropica</i> , 2022, 229, 106337.	0.9	6
22792	Identification of differentially expressed genes in early-postmortem Semimembranosus muscle of Italian Large White heavy pigs divergent for glycolytic potential. <i>Meat Science</i> , 2022, 187, 108754.	2.7	3
22793	Analysis of antibiotic resistance genes reveals their important roles in influencing the community structure of ocean microbiome. <i>Science of the Total Environment</i> , 2022, 823, 153731.	3.9	8
22794	Identification and functional analysis of circRNAs in the skeletal muscle of juvenile and adult largemouth bass ( <i>Micropterus salmoides</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100969.	0.4	4
22795	Association of Circulating miR-145-5p and miR-let7c and Atherosclerotic Plaques in Hypertensive Patients. <i>Biomolecules</i> , 2021, 11, 1840.	1.8	4
22796	Long Non-Coding RNA- Associated Competing Endogenous RNA Axes in T-Cells in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2021, 12, 770679.	2.2	6
22798	Calcitriol ameliorates damage in high-salt diet-induced hypertension: Evidence of communication with the gut-kidney axis. <i>Experimental Biology and Medicine</i> , 2022, 247, 624-640.	1.1	3
22799	Circulating Transcriptional Profile Modulation in Response to Metabolic Unbalance Due to Long-Term Exercise in Equine Athletes: A Pilot Study. <i>Genes</i> , 2021, 12, 1965.	1.0	5

#	ARTICLE	IF	CITATIONS
22800	Interactions between phenolic constituents of <i>Scutellaria salviifolia</i> and key targets associated with inflammation: network pharmacology, molecular docking analysis and <i>in vitro</i> assays. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 1281-1294.	2.0	2
22801	Comprehensive Analyses of the Expression, Genetic Alteration, Prognosis Significance, and Interaction Networks of m6A Regulators Across Human Cancers. <i>Frontiers in Genetics</i> , 2021, 12, 771853.	1.1	3
22802	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. <i>Human Genetics</i> , 2022, 141, 147-173.	1.8	22
22803	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. <i>Cell</i> , 2021, 184, 6262-6280.e26.	13.5	125
22804	RadicalSAM.org: A Resource to Interpret Sequence-Function Space and Discover New Radical SAM Enzyme Chemistry. <i>ACS Bio &amp; Med Chem Au</i> , 2022, 2, 22-35.	1.7	61
22805	Single cell atlas for 11 non-model mammals, reptiles and birds. <i>Nature Communications</i> , 2021, 12, 7083.	5.8	32
22806	Genetic determinants of endophytism in the Arabidopsis root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	5.8	58
22807	A single-cell transcriptomic landscape of the lungs of patients with COVID-19. <i>Nature Cell Biology</i> , 2021, 23, 1314-1328.	4.6	91
22808	Excavating novel diagnostic and prognostic long non-coding RNAs (lncRNAs) for head and neck squamous cell carcinoma: an integrated bioinformatics analysis of competing endogenous RNAs (ceRNAs) and gene co-expression networks. <i>Bioengineered</i> , 2021, 12, 12821-12838.	1.4	13
22810	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	6.0	369
22811	Cargo Genes of Tn7-Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. <i>MBio</i> , 2021, 12, e0293821.	1.8	34
22813	Understanding Gene Expression and Transcriptome Profiling of COVID-19: An Initiative Towards the Mapping of Protective Immunity Genes Against SARS-CoV-2 Infection. <i>Frontiers in Immunology</i> , 2021, 12, 724936.	2.2	17
22814	Energy at Origins: Favorable Thermodynamics of Biosynthetic Reactions in the Last Universal Common Ancestor (LUCA). <i>Frontiers in Microbiology</i> , 2021, 12, 793664.	1.5	23
22815	Identification of Key Genes in "Luang Pratahn", Thai Salt-Tolerant Rice, Based on Time-Course Data and Weighted Co-expression Networks. <i>Frontiers in Plant Science</i> , 2021, 12, 744654.	1.7	8
22816	Cytoplasmic dynein-1 cargo diversity is mediated by the combinatorial assembly of FTS"Hook"FHIP complexes. <i>ELife</i> , 2021, 10, .	2.8	27
22817	Alterations in gut bacterial and fungal microbiomes are associated with bacterial Keratitis, an inflammatory disease of the human eye. <i>Journal of Biosciences</i> , 2018, 43, 835-856.	0.5	17
22818	Interaction network analysis of YBX1 for identification of therapeutic targets in adenocarcinomas. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	1
22819	Analysis of chickpea gene co-expression networks and pathways during heavy metal stress. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	0

#	ARTICLE	IF	CITATIONS
22820	Visual exploration of microbiome data. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	1
22821	Comprehensive molecular insights into the stress response dynamics of rice ( <i>L.</i> ) during rice tungro disease by RNA-seq-based comparative whole transcriptome analysis. <i>Journal of Biosciences</i> , 2020, 45, .	0.5	1
22822	Melanoma susceptibility: an update on genetic and epigenetic findings. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2021, 12, 71-89.	0.4	2
22823	Identification of key pathways and RNAs associated with skeletal muscle atrophy after spinal cord injury. <i>Journal of Musculoskeletal Neuronal Interactions</i> , 2021, 21, 550-559.	0.1	0
22824	Patient-matched analysis identifies deregulated networks in prostate cancer to guide personalized therapeutic intervention. <i>American Journal of Cancer Research</i> , 2021, 11, 5299-5318.	1.4	0
22825	Identification of genes and pathways leading to poor prognosis of non-small cell lung cancer using integrated bioinformatics analysis. <i>Translational Cancer Research</i> , 2022, 11, 710-724.	0.4	1
22826	Probabilistic Graphical Models Applied to Biological Networks. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 119-130.	0.8	0
22827	Exploration of Combinational Therapeutic Strategies for HCC Based on TCGA HCC Database. <i>Oncologie</i> , 2022, 24, 101-111.	0.2	5
22829	Neuronal Differentiation Pathways and Compound-Induced Developmental Neurotoxicity in the Human Neural Progenitor Cell Test (Hnpt) Revealed by Rna-Seq. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22830	Therapeutic Targets and Signaling Mechanisms of Epimedium Activity Against Acute Myocardial Infarction. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22831	Single-Cell Proteo-Genomic Mapping Reveals Cytosolic Spliceosome as a Major Player for Cell Division and Ciliogenesis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22832	Network pharmacology combined with metabolomics and lipidomics to reveal the hypolipidemic mechanism of <i>Alismatis rhizoma</i> in hyperlipidemic mice. <i>Food and Function</i> , 2022, 13, 4714-4733.	2.1	16
22833	Biochemical and structural characterization of <i>Haemophilus influenzae</i> nitroreductase in metabolizing nitroimidazoles. <i>RSC Chemical Biology</i> , 2022, 3, 436-446.	2.0	3
22834	Identification of molecular signatures and pathways common to blood cells and brain tissue based RNA-Seq datasets of bipolar disorder: Insights from comprehensive bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2022, 29, 100881.	1.9	6
22835	Ensemble Methods for Identifying RNA Operons and Regulons in the Clock Network of <i>Neurospora Crassa</i> . <i>IEEE Access</i> , 2022, 10, 32510-32524.	2.6	3
22836	Viral Derived Mirnas in OrNV- &Oryctes Rhinoceros& Interaction. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
22837	Variation and Influential Factors Underlying P Cycling in Rhizosphere Microbial Communities Along Water Gradients in an Arid Desert Region. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22838	Evaluating the predictive accuracy of curated biological pathways in a public knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	2

#	ARTICLE	IF	CITATIONS
22839	Cryptochrome-Mediated Blue-Light Signal Contributes to Lignin Biosynthesis in Stone Cells in Pear Fruit. SSRN Electronic Journal, 0, , .	0.4	0
22840	Data-driven identification of inherent features of eukaryotic stress-responsive genes. NAR Genomics and Bioinformatics, 2022, 4, lqac018.	1.5	1
22841	Network Approaches for Precision Oncology. Advances in Experimental Medicine and Biology, 2022, 1361, 199-213.	0.8	1
22842	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. Zoological Research, 2022, 43, 367-379.	0.9	6
22843	Nextcast: A software suite to analyse and model toxicogenomics data. Computational and Structural Biotechnology Journal, 2022, 20, 1413-1426.	1.9	5
22844	The polysaccharide-peptide complex from mushroom <i>Cordyceps militaris</i> ameliorates atherosclerosis by modulating the lncRNA-miRNA-mRNA axis. Food and Function, 2022, 13, 3185-3197.	2.1	11
22845	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. Horticulture Research, 2022, 9, .	2.9	1
22846	WikiPathways: Integrating Pathway Knowledge with Clinical Data. , 2022, , 1457-1466.		2
22847	Long-Term Nickel Contamination Increased Soil Fungal Diversity and Altered Fungal Community Structure and Co-Occurrence Patterns in Agricultural Soils. SSRN Electronic Journal, 0, , .	0.4	0
22849	Measuring Intercellular Interface Area in Plant Tissues Using Quantitative 3D Image Analysis. Methods in Molecular Biology, 2022, 2457, 457-464.	0.4	0
22850	Negative Impacts of Sea-Level Rise on Soil Microbial Involvement in Carbon Metabolisms. SSRN Electronic Journal, 0, , .	0.4	0
22851	Investigating miRNA-mRNA Interactions and Gene Regulatory Networks From VTA Dopaminergic Neurons Following Perinatal Nicotine and Alcohol Exposure Using Bayesian Network Analysis. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3550-3555.	3.9	0
22852	Computational Methods to Identify Cell-Fate Determinants, Identity Transcription Factors, and Niche-Induced Signaling Pathways for Stem Cell Research. Methods in Molecular Biology, 2022, 2471, 83-109.	0.4	2
22853	Proteomic Profiling and Protein-Protein Interaction Network Reveal the Molecular Mechanisms of Susceptibility to Drought Stress in Canola ( <i>Brassica napus</i> L.). Phyton, 2022, 91, 1403-1417.	0.4	1
22854	Virtual screening of phytochemicals from Indian medicinal plants against the endonuclease domain of SFTS virus L polymerase. RSC Advances, 2022, 12, 6234-6247.	1.7	10
22855	MicroRNAs in Differentiation of Embryoid Bodies and the Teratoma Subtype of Testicular Cancer. Cancer Genomics and Proteomics, 2022, 19, 178-193.	1.0	5
22856	A new mass spectral library for high-coverage and reproducible analysis of the <i>Plasmodium falciparum</i> infected red blood cell proteome. GigaScience, 2022, 11, .	3.3	14
22857	LINC01094 Predicts Poor Prognosis in Patients With Gastric Cancer and is Correlated With EMT and Macrophage Infiltration. Technology in Cancer Research and Treatment, 2022, 21, 153303382210809.	0.8	18



#	ARTICLE	IF	CITATIONS
22858	Identifying Potential Therapeutic Targets for Ischemic Stroke Through Immune Infiltration Analysis and Construction of a Programmed Cell Death-Related ceRNA Network. SSRN Electronic Journal, 0, , .	0.4	0
22859	An Interoperability Framework for Multicentric Breath Metabolomic Studies. SSRN Electronic Journal, 0, , .	0.4	0
22860	RCXâ€”an R package adapting the Cytoscape Exchange format for biological networks. Bioinformatics Advances, 2022, 2, .	0.9	1
22861	Computational identification of Shenshao Ningxin Yin as an effective treatment for novel coronavirus infection (COVID-19) with myocarditis. Mathematical Biosciences and Engineering, 2022, 19, 5772-5792.	1.0	1
22862	Effect of Different Exercise Training Modalities on Fasting Levels of Oxylipins and Endocannabinoids in Middle-Aged Sedentary Adults: A Randomized Controlled Trial. International Journal of Sport Nutrition and Exercise Metabolism, 2022, 32, 275-284.	1.0	2
22863	The improvement effect of astaxanthin-loaded emulsions on obesity is better than that of astaxanthin in the oil phase. Food and Function, 2022, 13, 3720-3731.	2.1	1
22864	Probing Protein Solubility Patterns with Proteomics for Insight into Network Dynamics. Methods in Molecular Biology, 2022, 2428, 261-275.	0.4	0
22865	Genome-wide analysis reflects novel 5-hydroxymethylcytosines implicated in diabetic nephropathy and the biomarker potential. , 0, , .		0
22866	Almond Consumption for 8 Weeks Altered Host and Microbial Metabolism in Comparison to a Control Snack in Young Adults. , 2023, 42, 242-254.		2
22867	Weighted correlation network analysis revealed novel long non-coding RNAs for colorectal cancer. Scientific Reports, 2022, 12, 2990.	1.6	11
22868	Multilocation proteins in organelle communication: Based on proteinâ€”protein interactions. Plant Direct, 2022, 6, e386.	0.8	5
22869	Rootstockâ€”scion exchanging mRNAs participate in the pathways of amino acid and fatty acid metabolism in cucumber under early chilling stress. Horticulture Research, 2022, 9, .	2.9	8
22870	Transcriptome analysis of pod mutant reveals plant hormones are important regulators in controlling pod size in peanut ( <i>Arachis hypogaea</i> L.). PeerJ, 2022, 10, e12965.	0.9	8
22872	Inhibition of miR-128 Enhances Vocal Sequence Organization in Juvenile Songbirds. Frontiers in Behavioral Neuroscience, 2022, 16, 833383.	1.0	0
22873	Identification of differentially expressed genes and pathways in kidney of ANCA-associated vasculitis by integrated bioinformatics analysis. Renal Failure, 2022, 44, 204-216.	0.8	6
22874	Prognostic tools and candidate drugs based on plasma proteomics of patients with severe COVID-19 complications. Nature Communications, 2022, 13, 946.	5.8	30
22875	Novel protein from larval sponge cells, ilborin, is related to energy turnover and calcium binding and is conserved among marine invertebrates. Open Biology, 2022, 12, 210336.	1.5	0
22876	Metabolomic response to collegiate football participation: Pre- and Post-season analysis. Scientific Reports, 2022, 12, 3091.	1.6	4

#	ARTICLE	IF	CITATIONS
22877	Transcriptional Landscape of Cotton Fiber Development and Its Alliance With Fiber-Associated Traits. <i>Frontiers in Plant Science</i> , 2022, 13, 811655.	1.7	5
22878	Transcriptomic and functional analysis provides molecular insights into multicellular trichome development. <i>Plant Physiology</i> , 2022, 189, 301-314.	2.3	19
22879	An Integrative Pharmacology Model for Decoding the Underlying Therapeutic Mechanisms of Ermiao Powder for Rheumatoid Arthritis. <i>Frontiers in Pharmacology</i> , 2022, 13, 801350.	1.6	3
22880	Genome-Wide Analysis of the Banana WRKY Transcription Factor Gene Family Closely Related to Fruit Ripening and Stress. <i>Plants</i> , 2022, 11, 662.	1.6	14
22882	c-Met and EPHA7 Receptor Tyrosine Kinases Are Related to Prognosis in Clear Cell Renal Cell Carcinoma: Focusing on the Association with Myoferlin Expression. <i>Cancers</i> , 2022, 14, 1095.	1.7	2
22883	Expanding the Biological Role of Lipo-Chitooligosaccharides and Chitooligosaccharides in <i>Laccaria bicolor</i> Growth and Development. <i>Frontiers in Fungal Biology</i> , 2022, 3, .	0.9	4
22884	Deciphering Novel Transcriptional Regulators of Soybean Hypocotyl Elongation Based on Gene Co-expression Network Analysis. <i>Frontiers in Plant Science</i> , 2022, 13, 837130.	1.7	2
22885	Genome-Wide Characterization of Serine/Arginine-Rich Gene Family and Its Genetic Effects on Agronomic Traits of <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 829668.	1.7	7
22886	Low Temperature Affects Fatty Acids Profiling and Key Synthesis Genes Expression Patterns in <i>Zanthoxylum bungeanum</i> Maxim. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2319.	1.8	13
22887	Response of bacterial community structure to different ecological niches and their functions in Korean pine forests. <i>PeerJ</i> , 2022, 10, e12978.	0.9	3
22888	Olfactory receptors contribute to progression of kidney fibrosis. <i>Npj Systems Biology and Applications</i> , 2022, 8, 8.	1.4	4
22889	Overexpression of MUC1 Induces Non-Canonical TGF- $\beta$ 2 Signaling in Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 821875.	1.8	8
22890	Expression Characteristics and Significant Diagnostic and Prognostic Values of ANLN in Human Cancers. <i>International Journal of General Medicine</i> , 0, Volume 15, 1957-1972.	0.8	0
22892	Sex-Specific Cell Types and Molecular Pathways Indicate Fibro-Calcific Aortic Valve Stenosis. <i>Frontiers in Immunology</i> , 2022, 13, 747714.	2.2	3
22893	Rare actinobacteria isolated from the hypersaline Ojo de Liebre Lagoon as a source of novel bioactive compounds with biotechnological potential. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	7
22894	Using Network Pharmacology to Systematically Decipher the Potential Mechanisms of JisuiKang in the Treatment of Spinal Cord Injury. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	1
22896	Comprehensive bioinformatics analysis of functional molecules in colorectal cancer. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 231-245.	0.6	6
22897	Single-Cell Transcriptome and Network Analyses Unveil Key Transcription Factors Regulating Mesophyll Cell Development in Maize. <i>Genes</i> , 2022, 13, 374.	1.0	13

#	ARTICLE	IF	CITATIONS
22898	Prothymosin Alpha: A Novel Contributor to Estradiol Receptor Alpha <sup>+</sup> -Mediated CD8 <sup>+</sup> T-Cell Pathogenic Responses and Recognition of Type 1 Collagen in Rheumatic Heart Valve Disease. <i>Circulation</i> , 2022, 145, 531-548.	1.6	12
22899	Global Genomic and Proteomic Analysis Identified Critical Pathways Modulated by Proto-Oncogene PELP1 in TNBC. <i>Cancers</i> , 2022, 14, 930.	1.7	5
22900	Inducible Regulatory T Cell Predicts Efficacy of PD-1 Blockade Therapy in Melanoma. <i>Advanced Therapeutics</i> , 2022, 5, .	1.6	2
22901	Quantitative Proteomics Analysis Expands the Roles of Lysine $\beta$ -Hydroxybutyrylation Pathway in Response to Environmental $\beta$ -Hydroxybutyrate. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	1.9	7
22903	Nigericin and Geldanamycin Are Phytotoxic Specialized Metabolites Produced by the Plant Pathogen <i>Streptomyces</i> sp. 11-1-2. <i>Microbiology Spectrum</i> , 2022, 10, e0231421.	1.2	11
22904	Identification of CXCL10 as a Prognostic Biomarker for Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2022, 12, 857619.	1.3	5
22905	Identifying Environmental Endocrine Disruptors Associated With the Age at Menarche by Integrating a Transcriptome-Wide Association Study With Chemical-Gene-Interaction Analysis. <i>Frontiers in Endocrinology</i> , 2022, 13, 836527.	1.5	1
22907	Cluster analysis of splenocyte microRNAs in the pig reveals key signal regulators of immunomodulation in the host during acute and chronic <i>Toxoplasma gondii</i> infection. <i>Parasites and Vectors</i> , 2022, 15, 58.	1.0	6
22908	Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera. <i>Ecology and Evolution</i> , 2022, 12, e8611.	0.8	3
22909	Latent Membrane Protein 1 (LMP1) from Epstein-Barr Virus (EBV) Strains M81 and B95.8 Modulate miRNA Expression When Expressed in Immortalized Human Nasopharyngeal Cells. <i>Genes</i> , 2022, 13, 353.	1.0	3
22910	Network pharmacology research indicates that Wu-Mei-Wan treats obesity by inhibiting Th17 cell differentiation and alleviating metabolic inflammation. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	1
22911	A holistic genome dataset of bacteria, archaea and viruses of the Pearl River estuary. <i>Scientific Data</i> , 2022, 9, 49.	2.4	12
22912	Ziyin Huatan Recipe, a Chinese herbal compound, inhibits migration and invasion of gastric cancer by upregulating RUNX3 expression. <i>Journal of Integrative Medicine</i> , 2022, 20, 355-364.	1.4	2
22914	Genome-wide in silico analysis indicates the involvement of OsSWEET transporters in abiotic and heavy metal (loid) stress responses in rice. <i>Biologia (Poland)</i> , 0, , 1.	0.8	1
22915	Ecological Processes Shaping Microbiomes of Extremely Low Birthweight Infants. <i>Frontiers in Microbiology</i> , 2022, 13, 812136.	1.5	5
22916	Gene expression profiling reveals candidate biomarkers and probable molecular mechanisms in chronic stress. <i>Bioengineered</i> , 2022, 13, 6048-6060.	1.4	3
22917	Network cartographs for interpretable visualizations. <i>Nature Computational Science</i> , 2022, 2, 84-89.	3.8	3
22918	Efficient link prediction in the protein-protein interaction network using topological information in a generative adversarial network machine learning model. <i>BMC Bioinformatics</i> , 2022, 23, 78.	1.2	12

#	ARTICLE	IF	CITATIONS
22919	Alleviation of Hepatic Steatosis: Dithizone-Related Gut Microbiome Restoration During Paneth Cell Dysfunction. <i>Frontiers in Microbiology</i> , 2022, 13, 813783.	1.5	6
22920	Identification of differentially expressed and methylated genes and construction of a co-expression network in age-related macular degeneration. <i>Annals of Translational Medicine</i> , 2022, 10, 223-223.	0.7	5
22921	Novel insight into pancreatic adenocarcinoma pathogenesis using liquid association analysis. <i>BMC Medical Genomics</i> , 2022, 15, 30.	0.7	2
22922	Construction of a Lactate-Related Prognostic Signature for Predicting Prognosis, Tumor Microenvironment, and Immune Response in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Immunology</i> , 2022, 13, 818984.	2.2	32
22923	Comparative Transcriptome Analysis Reveals Differential Regulation of Flavonoids Biosynthesis Between Kernels of Two Pecan Cultivars. <i>Frontiers in Plant Science</i> , 2022, 13, 804968.	1.7	3
22924	Comprehensive screening for drugs that modify radiation-induced immune responses. <i>British Journal of Cancer</i> , 2022, , .	2.9	2
22925	Deciphering the Effect of Lysine Acetylation on the Misfolding and Aggregation of Human Tau Fragment 171IPAKTPPAPK180 Using Molecular Dynamic Simulation and the Markov State Model. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2399.	1.8	5
22928	Integrating lncRNAs and mRNAs Expression Profiles in Penicillin-Induced Persistent Chlamydial Infection in HeLa Cells. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 744901.	1.6	0
22929	Identification of Potential Genes Encoding Protein Transporters in <i>Arabidopsis thaliana</i> Glucosinolate (GSL) Metabolism. <i>Life</i> , 2022, 12, 326.	1.1	2
22930	Understanding the biomass conversion processes of bovine gut microbiota through community-wide metabolic interaction network. <i>Bioresource Technology Reports</i> , 2022, 17, 100989.	1.5	0
22931	Network Pharmacology Study to Reveal the Potentiality of a Methanol Extract of <i>Caesalpinia sappan</i> L. Wood against Type-2 Diabetes Mellitus. <i>Life</i> , 2022, 12, 277.	1.1	12
22932	Machine Learning analysis of high-grade serous ovarian cancer proteomic dataset reveals novel candidate biomarkers. <i>Scientific Reports</i> , 2022, 12, 3041.	1.6	9
22933	Characterization of the pVHL Interactome in Human Testis Using High-Throughput Library Screening. <i>Cancers</i> , 2022, 14, 1009.	1.7	1
22934	Time-resolved and multi-tissue RNAseq provides new insights on the immune responses of European eels following infection with <i>Aeromonas hydrophila</i> . , 2022, 1, 100003.		3
22936	Proximity proteomics of C9orf72 dipeptide repeat proteins identifies molecular chaperones as modifiers of poly-GA aggregation. <i>Acta Neuropathologica Communications</i> , 2022, 10, 22.	2.4	22
22937	A Bacterial Genome and Culture Collection of Gut Microbial in Weanling Piglet. <i>Microbiology Spectrum</i> , 2022, 10, e0241721.	1.2	3
22938	Network-Assisted Systems Biology Analysis of the Mitochondrial Proteome in a Pre-Clinical Model of Ischemia, Revascularization and Post-Conditioning. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2087.	1.8	7
22939	Network Analysis Reveals Different Cellulose Degradation Strategies Across <i>Trichoderma harzianum</i> Strains Associated With XYR1 and CRE1. <i>Frontiers in Genetics</i> , 2022, 13, 807243.	1.1	8

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22941	Integrated bioinformatics analysis identifies established and novel TGF $\beta$ 1-regulated genes modulated by anti-fibrotic drugs. <i>Scientific Reports</i> , 2022, 12, 3080.	1.6	5
22942	Polymyxin Induces Significant Transcriptomic Perturbations of Cellular Signalling Networks in Human Lung Epithelial Cells. <i>Antibiotics</i> , 2022, 11, 307.	1.5	0
22943	Genome-Wide Characterization and Anthocyanin-Related Expression Analysis of the B-BOX Gene Family in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2022, 13, 847328.	1.1	6
22944	Ecological Networks in Urban Forest Fragments Reveal Species Associations between Native and Invasive Plant Communities. <i>Plants</i> , 2022, 11, 541.	1.6	5
22945	Plasma Oxylipin Profile Discriminates Ethnicities in Subjects with Non-Alcoholic Steatohepatitis: An Exploratory Analysis. <i>Metabolites</i> , 2022, 12, 192.	1.3	3
22946	Deciphering the Interactions of SARS-CoV-2 Proteins with Human Ion Channels Using Machine-Learning-Based Methods. <i>Pathogens</i> , 2022, 11, 259.	1.2	3
22947	Mechanism of action of <i>Tripterygium wilfordii</i> for treatment of idiopathic membranous nephropathy based on network pharmacology. <i>Renal Failure</i> , 2022, 44, 116-125.	0.8	4
22948	Discovery of actinomycin L, a new member of the actinomycin family of antibiotics. <i>Scientific Reports</i> , 2022, 12, 2813.	1.6	15
22949	Long-term sod-based rotation promotes beneficial root microbiomes and increases crop productivity. <i>Biology and Fertility of Soils</i> , 2022, 58, 403-419.	2.3	9
22950	Olfactomedin-4 improves cutaneous wound healing by promoting skin cell proliferation and migration through POU5F1/OCT4 and ESR1 signalling cascades. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 157.	2.4	6
22951	Time-course RNA-seq analysis reveals stage-specific and melatonin-triggered gene expression patterns during the hair follicle growth cycle in <i>Capra hircus</i> . <i>BMC Genomics</i> , 2022, 23, 140.	1.2	10
22952	Global Identification and Characterization of C2 Domain-Containing Proteins Associated with Abiotic Stress Response in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 2221.	1.8	1
22953	Sperm Transcripts Associated With Odorant Binding and Olfactory Transduction Pathways Are Altered in Breeding Bulls Producing Poor-Quality Semen. <i>Frontiers in Veterinary Science</i> , 2022, 9, 799386.	0.9	2
22954	Inferring the Contribution of Microbial Taxa and Organic Matter Molecular Formulas to Ecological Assembly. <i>Frontiers in Microbiology</i> , 2022, 13, 803420.	1.5	5
22955	Genomic and Transcriptomic Landscape and Evolutionary Dynamics of Heat Shock Proteins in Spotted Sea Bass ( <i>Lateolabrax maculatus</i> ) under Salinity Change and Alkalinity Stress. <i>Biology</i> , 2022, 11, 353.	1.3	8
22956	An epigenomic shift in amygdala marks the transition to maternal behaviors in alloparenting virgin female mice. <i>PLoS ONE</i> , 2022, 17, e0263632.	1.1	2
22957	Systematic analysis of putative phage-phage interactions on minimum-sized phage cocktails. <i>Scientific Reports</i> , 2022, 12, 2458.	1.6	15
22958	Chemerin Impact on Alternative mRNA Transcription in the Porcine Luteal Cells. <i>Cells</i> , 2022, 11, 715.	1.8	7

#	ARTICLE	IF	CITATIONS
22959	Comprehensively dissecting the hub regulation of PkaC on highâ€­productivity and pellet macromorphology in citric acid producing <i>Aspergillus niger</i> . <i>Microbial Biotechnology</i> , 2022, 15, 1867-1882.	2.0	16
22960	Circulating Long Non-Coding RNAs LINC00324 and LOC100507053 as Potential Liquid Biopsy Markers for Esophageal Squamous Cell Carcinoma: A Pilot Study. <i>Frontiers in Oncology</i> , 2022, 12, 823953.	1.3	9
22961	LKB1 drives stasis and C/EBP-mediated reprogramming to an alveolar type II fate in lung cancer. <i>Nature Communications</i> , 2022, 13, 1090.	5.8	5
22962	Novel Molecular Networks and Regulatory MicroRNAs in Type 2 Diabetes Mellitus: Multiomics Integration and Interactomics Study. <i>JMIR Bioinformatics and Biotechnology</i> , 2022, 3, e32437.	0.4	4
22963	Network-Based Pharmacology Study Reveals Protein Targets for Medical Benefits and Harms of Cannabinoids in Humans. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 2205.	1.3	1
22964	Liver Transcriptome Response to Heat Stress in Beijing You Chickens and Guang Ming Broilers. <i>Genes</i> , 2022, 13, 416.	1.0	9
22965	Ibrutinib reverses IL-6-induced osimertinib resistance through inhibition of Laminin $\beta$ 5/FAK signaling. <i>Communications Biology</i> , 2022, 5, 155.	2.0	12
22966	An Integrated Pharmacology-Based Strategy to Investigate the Potential Mechanism of Xiebai San in Treating Pediatric Pneumonia. <i>Frontiers in Pharmacology</i> , 2022, 13, 784729.	1.6	5
22967	Integrated Analysis of miR-7-5p-Related ceRNA Network Reveals Potential Biomarkers for the Clinical Outcome of Gastric Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	0
22968	The Efficacy Mechanism of Epigallocatechin Gallate against Pre-Eclampsia based on Network Pharmacology and Molecular Docking. <i>Reproductive Sciences</i> , 2022, 29, 1859-1873.	1.1	3
22969	Association of SPI1 Haplotypes with Altered SPI1 Gene Expression and Alzheimerâ€™s Disease Risk. <i>Journal of Alzheimer's Disease</i> , 2022, 86, 1861-1873.	1.2	10
22970	Combination of GC-MS Molecular Networking and Larvicidal Effect against <i>Aedes aegypti</i> for the Discovery of Bioactive Substances in Commercial Essential Oils. <i>Molecules</i> , 2022, 27, 1588.	1.7	7
22971	Transcriptomic Analysis of Rat Cerebral Cortex Reveals the Potential Mechanism of Electroacupuncture Opening Blood Brain Barrier. <i>Frontiers in Neuroscience</i> , 2022, 16, 834683.	1.4	2
22972	Derivation, Comprehensive Analysis, and Assay Validation of a Pyroptosis-Related lncRNA Prognostic Signature in Patients With Ovarian Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 780950.	1.3	15
22974	Salivary Glands after Prolonged Aluminum Exposure: Proteomic Approach Underlying Biochemical and Morphological Impairments in Rats. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2251.	1.8	5
22975	New Cytotoxic Secondary Metabolites from Two Deepâ€­Seaâ€­Derived Fungi and the Coâ€­Culture Impact on the Secondary Metabolic Patterns. <i>Chemistry and Biodiversity</i> , 2022, 19, e202200055.	1.0	2
22976	Impacts of the Biocontrol Strain <i>Pseudomonas simiae</i> PICF7 on the Banana Holobiont: Alteration of Root Microbial Co-occurrence Networks and Effect on Host Defense Responses. <i>Frontiers in Microbiology</i> , 2022, 13, 809126.	1.5	5
22978	Analysing miRNA-Target Gene Networks in Inflammatory Bowel Disease and Other Complex Diseases Using Transcriptomic Data. <i>Genes</i> , 2022, 13, 370.	1.0	4



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22979	DNA Methylation Markers and Prediction Model for Depression and Their Contribution for Breast Cancer Risk. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 845212.	1.4	0
22980	Non-Coding Transcriptome Provides Novel Insights into the Escherichia coli F17 Susceptibility of Sheep Lamb. <i>Biology</i> , 2022, 11, 348.	1.3	6
22981	Identification of Nifurtimox and Chrysin as Anti-Influenza Virus Agents by Clinical Transcriptome Signature Reversion. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2372.	1.8	3
22982	Comprehensive analysis of negatively correlated miRNA-mRNA regulatory pairs associated with microsatellite instability in colorectal cancer. <i>Cancer Biomarkers</i> , 2022, , 1-13.	0.8	0
22983	Reuterin in the healthy gut microbiome suppresses colorectal cancer growth through altering redox balance. <i>Cancer Cell</i> , 2022, 40, 185-200.e6.	7.7	97
22984	Identification of phenotype-specific networks from paired gene expression and cell shape imaging data. <i>Genome Research</i> , 2022, 32, 750-765.	2.4	5
22985	Enterobacteria impair host p53 tumor suppressor activity through mRNA destabilization. <i>Oncogene</i> , 2022, 41, 2173-2186.	2.6	4
22986	A novel prognostic model for hepatocellular carcinoma based on 5 microRNAs related to vascular invasion. <i>BMC Medical Genomics</i> , 2022, 15, 34.	0.7	6
22987	In Vitro Analysis of TGF- $\beta$ 2 Signaling Modulation of Porcine Alveolar Macrophages in Porcine Circovirus Type 2b Infection. <i>Veterinary Sciences</i> , 2022, 9, 101.	0.6	3
22988	Study of Dimorphism Transition Mechanism of <i>Tremella fuciformis</i> Based on Comparative Proteomics. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 242.	1.5	1
22989	Impacts of UV-C Irradiation on Marine Biofilm Community Succession. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0229821.	1.4	3
22990	Identification and regulatory network analysis of SPL family transcription factors in <i>Populus euphratica</i> Oliv. heteromorphic leaves. <i>Scientific Reports</i> , 2022, 12, 2856.	1.6	7
22991	Lower Levels of GABAergic Function Markers in Corticotropin-Releasing Hormone-Expressing Neurons in the sgACC of Human Subjects With Depression. <i>Frontiers in Psychiatry</i> , 2022, 13, 827972.	1.3	3
22992	HAUS5 Is A Potential Prognostic Biomarker With Functional Significance in Breast Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 829777.	1.3	6
22993	Transcriptome analysis reveals the potential roles of long non-coding RNAs in feed efficiency of chicken. <i>Scientific Reports</i> , 2022, 12, 2558.	1.6	6
22994	Identification and Functional Analysis of lncRNA by CRISPR/Cas9 During the Cotton Response to Sap-Sucking Insect Infestation. <i>Frontiers in Plant Science</i> , 2022, 13, 784511.	1.7	12
22995	Network modeling predicts personalized gene expression and drug responses in valve myofibroblasts cultured with patient sera. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
22996	Translational profiling of mouse dopaminergic neurons reveals region-specific gene expression, exon usage, and striatal prostaglandin E2 modulatory effects. <i>Molecular Psychiatry</i> , 2022, 27, 2068-2079.	4.1	12

#	ARTICLE	IF	CITATIONS
22997	In-Depth Serum Proteomics by DIA-MS with <i>In Silico</i> Spectral Libraries Reveals Dynamics during the Active Phase of Systemic Juvenile Idiopathic Arthritis. <i>ACS Omega</i> , 2022, 7, 7012-7023.	1.6	7
22998	Deciphering the Host-Pathogen Interactome of the Wheat Common Bunt System: A Step towards Enhanced Resilience in Next Generation Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2589.	1.8	7
23000	SiteMotif: A graph-based algorithm for deriving structural motifs in Protein Ligand binding sites. <i>PLoS Computational Biology</i> , 2022, 18, e1009901.	1.5	7
23001	IL7R Is Correlated With Immune Cell Infiltration in the Tumor Microenvironment of Lung Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2022, 13, 857289.	1.6	10
23002	Identification of Potential Key Biomarkers and Immune Infiltration in Oral Lichen Planus. <i>Disease Markers</i> , 2022, 2022, 1-20.	0.6	4
23003	Cytochromes P450 of <i>Caenorhabditis elegans</i> : Implication in Biological Functions and Metabolism of Xenobiotics. <i>Biomolecules</i> , 2022, 12, 342.	1.8	19
23004	Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365.	1.6	11
23005	Proteomic Profiling and <i>In Silico</i> Characterization of the Secretome of <i>Anisakis simplex</i> Sensu Stricto L3 Larvae. <i>Pathogens</i> , 2022, 11, 246.	1.2	8
23006	DJExpress: An Integrated Application for Differential Splicing Analysis and Visualization. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	5
23007	Genome-Wide Association Study-Guided Exome Rare Variant Burden Analysis Identifies IL1R1 and CD3E as Potential Autoimmunity Risk Genes for Celiac Disease. <i>Frontiers in Pediatrics</i> , 2022, 10, 837957.	0.9	6
23009	Soil Microbiomes in Apple Orchards Are Influenced by the Type of Agricultural Management but Never Match the Complexity and Connectivity of a Semi-natural Benchmark. <i>Frontiers in Microbiology</i> , 2022, 13, 830668.	1.5	2
23010	Commensal <i>Pseudomonas</i> strains facilitate protective response against pathogens in the host plant. <i>Nature Ecology and Evolution</i> , 2022, 6, 383-396.	3.4	44
23011	Gene expression associated with human brain activations in facial expression recognition. <i>Brain Imaging and Behavior</i> , 2022, 16, 1657-1670.	1.1	2
23012	Network Pharmacology-Based Strategy to Investigate the Anti-Breast Cancer Mechanisms of <i>Spatholobus suberectus</i> Dunn. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210778.	0.2	1
23013	Unraveling of interacting protein network of chaperonin TCP1 gamma subunit of <i>Leishmania donovani</i> . <i>Cell Stress and Chaperones</i> , 2022, 27, 205-222.	1.2	1
23015	Diversity of <i>Pseudomonas aeruginosa</i> Temperate Phages. <i>MSphere</i> , 2022, 7, e0101521.	1.3	16
23016	Genome-Wide Comparative Analysis of the R2R3-MYB Gene Family in Five Solanaceae Species and Identification of Members Regulating Carotenoid Biosynthesis in Wolfberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2259.	1.8	19
23017	Top-down stepwise refinement identifies coding and noncoding RNA-associated epigenetic regulatory maps in malignant glioma. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 2230-2250.	1.6	2

#	ARTICLE	IF	CITATIONS
23018	Ecosystem restoration and belowground multifunctionality: A network view. <i>Ecological Applications</i> , 2022, 32, e2575.	1.8	11
23019	Prognostic and immune-related value of STK17B in skin cutaneous melanoma. <i>PLoS ONE</i> , 2022, 17, e0263311.	1.1	3
23020	Vitamins D2 and D3 Have Overlapping But Different Effects on the Human Immune System Revealed Through Analysis of the Blood Transcriptome. <i>Frontiers in Immunology</i> , 2022, 13, 790444.	2.2	20
23021	The Impact of the hAPP695SW Transgene and Associated Amyloid- $\beta^2$ Accumulation on Murine Hippocampal Biochemical Pathways. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 1601-1619.	1.2	12
23022	A productive immunocompetent mouse model of cryptosporidiosis with long oocyst shedding duration for immunological studies. <i>Journal of Infection</i> , 2022, 84, 710-721.	1.7	7
23024	Integrative Analyses of Genes Associated With Otologic Disorders in Turner Syndrome. <i>Frontiers in Genetics</i> , 2022, 13, 799783.	1.1	0
23026	FVIII regulates the molecular profile of endothelial cells: functional impact on the blood barrier and macrophage behavior. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 145.	2.4	3
23027	Modular Screening Reveals Driver Induced Additive Mechanisms of Baicalin and Jasminoidin on Cerebral Ischemia Therapy. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 813983.	1.1	2
23028	Mechanisms of magnoliae cortex on treating sarcopenia explored by GEO gene sequencing data combined with network pharmacology and molecular docking. <i>BMC Genomic Data</i> , 2022, 23, 15.	0.7	1
23029	Plastics degradation by hydrolytic enzymes: The <sc>plastics&active</sc> enzymes database&sc>PAZY</sc>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1443-1456.	1.5	78
23030	Phyllidiidae (Nudibranchia, Heterobranchia, Gastropoda): an integrative taxonomic approach including chemical analyses. <i>Organisms Diversity and Evolution</i> , 0, , 1.	0.7	3
23031	Paediatric Behçet's Disease: A Comprehensive Review with an Emphasis on Monogenic Mimics. <i>Journal of Clinical Medicine</i> , 2022, 11, 1278.	1.0	7
23032	TMAO-Activated Hepatocyte-Derived Exosomes Are Widely Distributed in Mice with Different Patterns and Promote Vascular Inflammation. <i>Cardiology Research and Practice</i> , 2022, 2022, 1-9.	0.5	2
23033	Genome-Wide Identification and Expression Profiling of CONSTANS-Like Genes in Pepper ( <i>Capsicum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo Plant Science, 2022, 13, 828209.	1.7	3
23034	Comprehensive Time-Course Transcriptome and Co-expression Network Analyses Identify Salt Stress Responding Mechanisms in <i>Chlamydomonas reinhardtii</i> Strain GY-D55. <i>Frontiers in Plant Science</i> , 2022, 13, 828321.	1.7	0
23035	BTG2 Serves as a Potential Prognostic Marker and Correlates with Immune Infiltration in Lung Adenocarcinoma. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2727-2745.	0.8	7
23036	Differences Between Sorafenib and Lenvatinib Treatment from Genetic and Clinical Perspectives for Patients with Hepatocellular Carcinoma. <i>Medical Science Monitor</i> , 2022, 28, e934936.	0.5	2
23037	Multi-omics analyses provide novel biological insights to distinguish lobular ductal types of invasive breast cancers. <i>Breast Cancer Research and Treatment</i> , 2022, 193, 361-379.	1.1	9

#	ARTICLE	IF	CITATIONS
23039	Identification of cell type specific ACE2 modifiers by CRISPR screening. <i>PLoS Pathogens</i> , 2022, 18, e1010377.	2.1	9
23040	Temporal changes in plant-soil feedback effects on microbial networks, leaf metabolomics and plant-insect interactions. <i>Journal of Ecology</i> , 2022, 110, 1328-1343.	1.9	5
23041	Strategies for conducting Scientific Initiation in times of a pandemic: mitigating losses. <i>Research, Society and Development</i> , 2022, 11, e0711425923.	0.0	0
23042	The ecology of human behavior: A network perspective. <i>Methodological Innovations</i> , 0, , 205979912210779.	0.5	1
23043	ADH1C inhibits progression of colorectal cancer through the ADH1C/PHGDH /PSAT1/serine metabolic pathway. <i>Acta Pharmacologica Sinica</i> , 2022, 43, 2709-2722.	2.8	14
23044	Transcriptome and Metabolome Analyses Reveal Molecular Responses of Two Pepper ( <i>Capsicum</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc	1.7	12
23045	Mechanistic insights into the amelioration effects of lipopolysaccharide-induced acute lung injury by baicalein: An integrated systems pharmacology study and experimental validation. <i>Pulmonary Pharmacology and Therapeutics</i> , 2022, 73-74, 102121.	1.1	4
23046	Genome-Wide Identification and Expression Analysis of the R2R3-MYB Transcription Factor Family Revealed Their Potential Roles in the Flowering Process in Longan ( <i>Dimocarpus longan</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 820439.	1.7	8
23047	Identification, Characterization, and Synthesis of Natural Parasitic Cysteine Protease Inhibitors: Pentacitidins Are More Potent Falcitidin Analogues. <i>ACS Chemical Biology</i> , 2022, 17, 576-589.	1.6	3
23049	Gut microbiota from Mexican patients with metabolic syndrome and HIV infection: An inflammatory profile. <i>Journal of Applied Microbiology</i> , 2022, 132, 3839-3852.	1.4	6
23050	Pharmacological Perturbation of Mechanical Contractility Enables Robust Transdifferentiation of Human Fibroblasts into Neurons. <i>Advanced Science</i> , 2022, 9, e2104682.	5.6	7
23051	From Causal Networks to Adverse Outcome Pathways: A Developmental Neurotoxicity Case Study. <i>Frontiers in Toxicology</i> , 2022, 4, 815754.	1.6	5
23052	Expression characterization and cross-species complementation uncover the functional conservation of YABBY genes for leaf abaxial polarity and carpel polarity establishment in <i>Saccharum spontaneum</i> . <i>BMC Plant Biology</i> , 2022, 22, 124.	1.6	7
23053	Pulmonary Inflammatory Response in Lethal COVID-19 Reveals Potential Therapeutic Targets and Drugs in Phases III/IV Clinical Trials. <i>Frontiers in Pharmacology</i> , 2022, 13, 833174.	1.6	6
23054	PCBP2 maintains antiviral signaling homeostasis by regulating cGAS enzymatic activity via antagonizing its condensation. <i>Nature Communications</i> , 2022, 13, 1564.	5.8	15
23055	Distinct early life stage gene expression effects of hybridization among European and North American farmed and wild Atlantic salmon populations. <i>Molecular Ecology</i> , 2022, 31, 2712-2729.	2.0	2
23056	Lichen Secondary Metabolites Inhibit the Wnt/ $\beta$ -Catenin Pathway in Glioblastoma Cells and Improve the Anticancer Effects of Temozolomide. <i>Cells</i> , 2022, 11, 1084.	1.8	17
23058	Identification of circRNA Biomarker for Gastric Cancer through Integrated Analysis. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 857320.	1.6	7

#	ARTICLE	IF	CITATIONS
23059	Extensive metagenomic analysis of the porcine gut resistome to identify indicators reflecting antimicrobial resistance. <i>Microbiome</i> , 2022, 10, 39.	4.9	19
23060	5-Methylcytosine Related LncRNAs Reveal Immune Characteristics, Predict Prognosis and Oncology Treatment Outcome in Lower-Grade Gliomas. <i>Frontiers in Immunology</i> , 2022, 13, 844778.	2.2	15
23061	Identification of gene biomarkers with expression profiles in patients with allergic rhinitis. <i>Allergy, Asthma and Clinical Immunology</i> , 2022, 18, 20.	0.9	10
23062	A Bioinformatics Approach Toward Unravelling the Synaptic Molecular Crosstalk Between Alzheimer's Disease and Diabetes. <i>Journal of Alzheimer's Disease</i> , 2022, , 1-17.	1.2	3
23064	Seed Exchange Networks of Native Maize, Beans, and Squash in San Juan Ixtenco and San Luis Huamantla, Tlaxcala, Mexico. <i>Sustainability</i> , 2022, 14, 3779.	1.6	2
23065	Serum miRNAs as biomarkers for the rare types of muscular dystrophy. <i>Neuromuscular Disorders</i> , 2022, 32, 332-346.	0.3	5
23066	Neem and Turmeric in the management of Covid Associated Mucormycosis (CAM) derived through network pharmacology. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 3281-3294.	2.0	4
23067	Mass Spectrometric Behavior and Molecular Mechanisms of Fermented Deoxyanthocyanidins to Alleviate Ulcerative Colitis Based on Network Pharmacology. <i>International Journal of Analytical Chemistry</i> , 2022, 2022, 1-12.	0.4	1
23068	Integrated Analysis of the miRNA-mRNA Regulatory Network Involved in HIV-Associated Neurocognitive Disorder. <i>Pathogens</i> , 2022, 11, 407.	1.2	1
23069	Direct interaction of TrkA/CD44v3 is essential for NGF-promoted aggressiveness of breast cancer cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 110.	3.5	7
23070	Exploring the pharmacological components and effective mechanism of Mori Folium against periodontitis using network pharmacology and molecular docking. <i>Archives of Oral Biology</i> , 2022, 139, 105391.	0.8	5
23072	A Comprehensive Network Integrating Signature Microbes and Crucial Soil Properties During Early Biological Soil Crust Formation on Tropical Reef Islands. <i>Frontiers in Microbiology</i> , 2022, 13, 831710.	1.5	3
23074	Syndromic male subfertility: A network view of genome-phenome associations. <i>Andrology</i> , 2022, 10, 720-732.	1.9	5
23075	Identification of Potential Core Genes for the Rupture of Intracranial Aneurysms by a Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 875007.	1.1	3
23076	Dynamic miRNA Landscape Links Mammary Gland Development to the Regulation of Milk Protein Expression in Mice. <i>Animals</i> , 2022, 12, 727.	1.0	4
23077	Morel Production Associated with Soil Nitrogen-Fixing and Nitrifying Microorganisms. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 299.	1.5	24
23078	Nuclear HMGB1 protects from nonalcoholic fatty liver disease through negative regulation of liver X receptor. <i>Science Advances</i> , 2022, 8, eabg9055.	4.7	7
23079	RNA-seq and integrated network analysis reveals the hub genes and key pathway of paclitaxel inhibition on Adriamycin resistant diffuse large B cell lymphoma cells. <i>Bioengineered</i> , 2022, 13, 7607-7621.	1.4	3

#	ARTICLE	IF	CITATIONS
23080	Bioinformatical analysis identifies PDLIM3 as a potential biomarker associated with immune infiltration in patients with endometriosis. <i>PeerJ</i> , 2022, 10, e13218.	0.9	3
23081	Novel canine high-quality metagenome-assembled genomes, prophages and host-associated plasmids provided by long-read metagenomics together with Hi-C proximity ligation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
23082	IFITM3 Interacts with the HBV/HDV Receptor NTCP and Modulates Virus Entry and Infection. <i>Viruses</i> , 2022, 14, 727.	1.5	11
23083	Assessment of the targeted effect of Sijunzi decoction on the colorectal cancer microenvironment via the ESTIMATE algorithm. <i>PLoS ONE</i> , 2022, 17, e0264720.	1.1	4
23084	Size-dependent resistance to amoebic gill disease in naïve Atlantic salmon ( <i>Salmo salar</i> ). <i>Fish and Shellfish Immunology</i> , 2022, 122, 437-445.	1.6	3
23085	The Rhizosphere Microbiomes of Five Species of Coffee Trees. <i>Microbiology Spectrum</i> , 2022, 10, e0044422.	1.2	7
23086	Parkinson's disease and multiple system atrophy patient iPSC-derived oligodendrocytes exhibit alpha-synuclein-induced changes in maturation and immune reactive properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2111405119.	3.3	22
23087	Systematic Survey of the Regulatory Networks of the Long Noncoding RNA BANCR in Cervical Cancer Cells. <i>Journal of Proteome Research</i> , 2022, 21, 1137-1152.	1.8	5
23088	Differential ubiquitome analysis of <i>Cordyceps militaris</i> lysine-ubiquitinated proteins affected by blue light. , 0, , 1.		1
23089	Cell activation is associated with high-grade serous ovarian cancer survival. <i>Journal of Obstetrics and Gynaecology Research</i> , 2022, 48, 2189-2197.	0.6	6
23090	Network Pharmacology Identifies Therapeutic Targets and the Mechanisms of Glutathione Action in Ferroptosis Occurring in Oral Cancer. <i>Frontiers in Pharmacology</i> , 2022, 13, 851540.	1.6	12
23091	Integrative Analysis of Biomarkers and Mechanisms in Adamantinomatous Craniopharyngioma. <i>Frontiers in Genetics</i> , 2022, 13, 830793.	1.1	6
23092	Promoter Hypomethylation of TGFBR3 as a Risk Factor of Alzheimer's Disease: An Integrated Epigenomic-Transcriptomic Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 825729.	1.8	6
23093	Bioaugmentation of Anammox Activated Sludge with a Nitrifying Bacterial Community as a Way to Increase the Nitrogen Removal Efficiency. <i>Microbiology</i> , 2022, 91, 133-142.	0.5	4
23094	The Radiosensitivity Index Gene Signature Identifies Distinct Tumor Immune Microenvironment Characteristics Associated With Susceptibility to Radiation Therapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2022, 113, 635-647.	0.4	11
23095	Identification of the Key Pathways and Genes in Hypoxia Pulmonary Arterial Hypertension Following Intrauterine Growth Retardation. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 789736.	1.6	0
23096	Correlational networking guides the discovery of unclustered lanthipeptide protease-encoding genes. <i>Nature Communications</i> , 2022, 13, 1647.	5.8	12
23097	Integrative epigenomic and transcriptomic analyses reveal metabolic switching by intermittent fasting in brain. <i>GeroScience</i> , 2022, 44, 2171-2194.	2.1	10



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23098	BRCA1 mutations in high-grade serous ovarian cancer are associated with proteomic changes in DNA repair, splicing, transcription regulation and signaling. <i>Scientific Reports</i> , 2022, 12, 4445.	1.6	2
23099	Identification of key biomarkers related to epithelialâ€mesenchymal transition and immune infiltration in ameloblastoma using integrated bioinformatics analysis. <i>Oral Diseases</i> , 2023, 29, 1657-1667.	1.5	13
23100	Inhibition of bromodomain extraterminal histone readers alleviates skin fibrosis in experimental models of scleroderma. <i>JCI Insight</i> , 2022, 7, .	2.3	11
23101	A Novel and Ubiquitous Marine Methylophage Provides Insights into Viral-Host Coevolution and Possible Host-Range Expansion in Streamlined Marine Heterotrophic Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0025522.	1.4	2
23103	Investigating the Functional Role of Hypothetical Proteins From an Antarctic Bacterium <i>Pseudomonas</i> sp. Lz4W: Emphasis on Identifying Proteins Involved in Cold Adaptation. <i>Frontiers in Genetics</i> , 2022, 13, 825269.	1.1	4
23104	Celastrol Alleviates Autoimmune Hepatitis Through the PI3K/AKT Signaling Pathway Based on Network Pharmacology and Experiments. <i>Frontiers in Pharmacology</i> , 2022, 13, 816350.	1.6	7
23105	Identification and Verification of Potential Hub Genes in Amphetamine-Type Stimulant (ATS) and Opioid Dependence by Bioinformatic Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 837123.	1.1	0
23106	Microbial Community Structure and Ecological Networks during Simulation of Diatom Sinking. <i>Microorganisms</i> , 2022, 10, 639.	1.6	4
23107	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. <i>Frontiers in Psychiatry</i> , 2022, 13, 797329.	1.3	9
23108	Molecular Mechanism Underlying Effects of Wumeiwan on Steroid-Dependent Asthma: A Network Pharmacology, Molecular Docking, and Experimental Verification Study. <i>Drug Design, Development and Therapy</i> , 2022, Volume 16, 909-929.	2.0	7
23109	Identification of Key Modules and Genes Associated with Major Depressive Disorder in Adolescents. <i>Genes</i> , 2022, 13, 464.	1.0	2
23110	Reveal the Antimigraine Mechanism of Chuanxiong Rhizoma and Cyperi Rhizoma Based on the Integrated Analysis of Metabolomics and Network Pharmacology. <i>Frontiers in Pharmacology</i> , 2022, 13, 805984.	1.6	1
23111	Identification of Alternative Splicing Events Associated with Paratuberculosis in Dairy Cattle Using Multi-Tissue RNA Sequencing Data. <i>Genes</i> , 2022, 13, 497.	1.0	6
23113	The Câ€terminal end of mycobacterial HadBC regulates AcpM interaction during the FASâ€II pathway: a structural perspective. <i>FEBS Journal</i> , 2022, 289, 4963-4980.	2.2	2
23114	Analysis of Genes Associated with Both Neural Tube Defects and Neuroectodermal Tumors. <i>Medical Science Monitor</i> , 2022, 28, e936079.	0.5	0
23115	Study on the SHP2-Mediated Mechanism of Promoting Spermatogenesis Induced by Active Compounds of <i>Eucommiae Folium</i> in Mice. <i>Frontiers in Pharmacology</i> , 2022, 13, 851930.	1.6	0
23116	Changes of microbiome in response to sugars in a wilt pathogen-infested soil. <i>Soil Ecology Letters</i> , 2023, 5, 46-65.	2.4	1
23117	Identification of Immune-Related Gene Signature and Prediction of CeRNA Network in Active Ulcerative Colitis. <i>Frontiers in Immunology</i> , 2022, 13, 855645.	2.2	19

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23118	Fungal Communities of Eucalyptus grandis Leaves Are Influenced by the Insect Pest Leptocybe invasa. <i>Frontiers in Microbiology</i> , 2022, 13, 841621.	1.5	1
23119	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
23120	A genome-wide association study in autoimmune neurological syndromes with anti-GAD65 autoantibodies. <i>Brain</i> , 2023, 146, 977-990.	3.7	10
23121	Nicotinamide (niacin) supplement increases lipid metabolism and ROS-induced energy disruption in triple-negative breast cancer: potential for drug repositioning as an anti-tumor agent. <i>Molecular Oncology</i> , 2022, 16, 1795-1815.	2.1	10
23122	<i>Bacteroides ovatus</i> colonization influences the abundance of intestinal short chain fatty acids and neurotransmitters. <i>IScience</i> , 2022, 25, 104158.	1.9	41
23123	Multi-Omics Characterization of Type 2 Diabetes Mellitus-Induced Cognitive Impairment in the db/db Mouse Model. <i>Molecules</i> , 2022, 27, 1904.	1.7	6
23124	Mitigation of Gastric Damage Using <i>Cinnamomum cassia</i> Extract: Network Pharmacological Analysis of Active Compounds and Protection Effects in Rats. <i>Plants</i> , 2022, 11, 716.	1.6	13
23125	Integrative analysis of key microRNA-mRNA complexes and pathways in aortic aneurysm. <i>Annals of Translational Medicine</i> , 2022, 10, 358-358.	0.7	1
23126	CIGB-300-Regulated Proteome Reveals Common and Tailored Response Patterns of AML Cells to CK2 Inhibition. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 834814.	1.6	4
23127	Type I interferon transcriptional network regulates expression of coinhibitory receptors in human T cells. <i>Nature Immunology</i> , 2022, 23, 632-642.	7.0	54
23129	<i>TERT</i> promoter C228T mutation in neural progenitors confers growth advantage following telomere shortening <i>in vivo</i> . <i>Neuro-Oncology</i> , 2022, 24, 2063-2075.	0.6	9
23130	Gain of gene regulatory network interconnectivity at the origin of vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114802119.	3.3	9
23131	Predisposition to atrioventricular septal defects may be caused by SOX7 variants that impair interaction with GATA4. <i>Molecular Genetics and Genomics</i> , 2022, 297, 671-687.	1.0	2
23132	Metabolic Profiling of Interspecies Interactions During Sessile Bacterial Cultivation Reveals Growth and Sporulation Induction in <i>Paenibacillus amylolyticus</i> in Response to <i>Xanthomonas retroflexus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 805473.	1.8	1
23133	Structural and mechanistic basis for redox sensing by the cyanobacterial transcription regulator RexT. <i>Communications Biology</i> , 2022, 5, 275.	2.0	5
23134	Genome-wide Identification and Expression Analysis of RcMYB Genes in <i>Rhodiola crenulata</i> . <i>Frontiers in Genetics</i> , 2022, 13, 831611.	1.1	5
23135	Identification of Type 2 Diabetes Based on a Ten-Genes Biomarker Prediction Model Constructed Using a Support Vector Machine Algorithm. <i>BioMed Research International</i> , 2022, 2022, 1-15.	0.9	5
23136	Application of Feature-Based Molecular Networking for Comparative Metabolomics and Targeted Isolation of Stereoisomers from Algicolous Fungi. <i>Marine Drugs</i> , 2022, 20, 210.	2.2	3

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23137	Beyond Genes: Inclusion of Alternative Splicing and Alternative Polyadenylation to Assess the Genetic Architecture of Predisposition to Voluntary Alcohol Consumption in Brain of the HXB/BXH Recombinant Inbred Rat Panel. <i>Frontiers in Genetics</i> , 2022, 13, 821026.	1.1	2
23138	Transcriptome Analysis of Bovine Rumen Tissue in Three Developmental Stages. <i>Frontiers in Genetics</i> , 2022, 13, 821406.	1.1	4
23139	Myc pathway-guided alternative splicing events predict the overall survival of lung squamous cell carcinoma. <i>International Journal of Transgender Health</i> , 2022, 15, 270-282.	1.1	1
23140	Transcriptomic Profiling of Circular RNAs in the Goat Rumen During Fetal and Prepubertal Period. <i>Frontiers in Physiology</i> , 2022, 13, 858991.	1.3	2
23141	miRNAs Contained in Extracellular Vesicles Cargo Contribute to the Progression of Idiopathic Pulmonary Fibrosis: An In Vitro Approach. <i>Cells</i> , 2022, 11, 1112.	1.8	8
23142	Differential Expression of Zinc-Dependent HDAC Subtypes and their Involvement in Unique Pathways Associated with Carcinogenesis. <i>Asian Pacific Journal of Cancer Prevention</i> , 2022, 23, 877-883.	0.5	4
23143	Causal biological network models for reactive astrogliosis: a systems approach to neuroinflammation. <i>Scientific Reports</i> , 2022, 12, 4205.	1.6	2
23144	Cellular Interaction Analysis Characterizing Immunosuppressive Microenvironment Functions in MM Tumorigenesis From Precursor Stages. <i>Frontiers in Genetics</i> , 2022, 13, 844604.	1.1	3
23145	Long noncoding RNA Lnc-DIF inhibits bone formation by sequestering miR-489-3p. <i>iScience</i> , 2022, 25, 103949.	1.9	9
23146	A Comparative Transcriptome and Metabolome Combined Analysis Reveals the Key Genes and Their Regulatory Model Responsible for Glucoraphastin Accumulation in Radish Fleshly Taproots. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2953.	1.8	3
23147	Comprehensive Analysis and Validation of Competing Endogenous RNA Network and Tumor-infiltrating Immune Cells in Lung Adenocarcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, 2240-2254.	0.6	2
23148	Sow vaccination against virulent <i>Glaesserella parasuis</i> shapes the nasal microbiota of their offspring. <i>Scientific Reports</i> , 2022, 12, 3357.	1.6	9
23149	Adaptive divergence generates distinct plastic responses in two closely related <i>Senecio</i> species. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1229-1245.	1.1	13
23150	<i>in Silico</i> Analysis Identifies the Anti-Liver Injury Targets of Diammonium Glycyrrhizinate: Validated in Perfluorooctanoic Acid-Lesioned Mouse Model. <i>Chemistry and Biodiversity</i> , 2022, 19, .	1.0	0
23153	Label-free quantitative proteomics of maize roots from different root zones provides insight into proteins associated with enhance water uptake. <i>BMC Genomics</i> , 2022, 23, 184.	1.2	6
23154	Identification of Novel Prognostic Signatures for Clear Cell Renal Cell Carcinoma Based on ceRNA Network Construction and Immune Infiltration Analysis. <i>Disease Markers</i> , 2022, 2022, 1-28.	0.6	4
23155	Biocatalytic oxidative cross-coupling reactions for biaryl bond formation. <i>Nature</i> , 2022, 603, 79-85.	13.7	67
23156	Anti-HIV Drugs Cause Mitochondrial Dysfunction in Monocyte-Derived Macrophages. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0194121.	1.4	8

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23157	Transcriptome Analysis of <i>Plasmodium falciparum</i> Isolates From Benin Reveals Specific Gene Expression Associated With Cerebral Malaria. <i>Journal of Infectious Diseases</i> , 2022, 225, 2187-2196.	1.9	11
23158	Phyto-targeting the CEMIP expression as a strategy to prevent pancreatic cancer metastasis. <i>Current Pharmaceutical Design</i> , 2022, 28, .	0.9	4
23159	Developing an immune-related gene prognostic index associated with progression and providing new insights into the tumor immune microenvironment of prostate cancer. <i>Immunology</i> , 2022, 166, 197-209.	2.0	12
23160	Transcriptome Analysis in Hippocampus of Rats Prenatally Exposed to Valproic Acid and Effects of Intranasal Treatment of Oxytocin. <i>Frontiers in Psychiatry</i> , 2022, 13, 859198.	1.3	2
23161	Interaction of bacterial genera associated with therapeutic response to immune checkpoint PD-1 blockade in a United States cohort. <i>Genome Medicine</i> , 2022, 14, 35.	3.6	29
23162	Genome-wide landscape of ApiAP2 transcription factors reveals a heterochromatin-associated regulatory network during <i>Plasmodium falciparum</i> blood-stage development. <i>Nucleic Acids Research</i> , 2022, 50, 3413-3431.	6.5	23
23163	Potential Therapeutic Targets of Rehmannia Formulations on Diabetic Nephropathy: A Comparative Network Pharmacology Analysis. <i>Frontiers in Pharmacology</i> , 2022, 13, 794139.	1.6	8
23165	Strategies to access biosynthetic novelty in bacterial genomes for drug discovery. <i>Nature Reviews Drug Discovery</i> , 2022, 21, 359-378.	21.5	45
23166	iNAP: An integrated network analysis pipeline for microbiome studies. , 2022, 1, .		126
23167	SenseNet, a tool for analysis of protein structure networks obtained from molecular dynamics simulations. <i>PLoS ONE</i> , 2022, 17, e0265194.	1.1	2
23168	Comparative Transcriptome Analysis between Two Potato Cultivars in Tuber Induction to Reveal Associated Genes with Anthocyanin Accumulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3681.	1.8	7
23170	Comparison of proton transfer paths to the QA and QB sites of the <i>Rb. sphaeroides</i> photosynthetic reaction centers. <i>Photosynthesis Research</i> , 2022, 152, 153-165.	1.6	10
23171	Identification of Down-Regulated ADH1C is Associated With Poor Prognosis in Colorectal Cancer Using Bioinformatics Analysis. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 791249.	1.6	8
23172	Ageing induces tissue-specific transcriptomic changes in <i>Caenorhabditis elegans</i> . <i>EMBO Journal</i> , 2022, 41, e109633.	3.5	22
23173	Quantitative proteomics analysis of human vitreous in rhegmatogenous retinal detachment associated with choroidal detachment by data-independent acquisition mass spectrometry. <i>Molecular and Cellular Biochemistry</i> , 2022, , 1.	1.4	1
23174	Construction of a Pyroptosis-Related Signature for Prognostic Prediction and Characterization of Immune Microenvironment in Acute Myelogenous Leukemia. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2913-2927.	0.8	4
23175	Blocking UBE2N abrogates oncogenic immune signaling in acute myeloid leukemia. <i>Science Translational Medicine</i> , 2022, 14, eabb7695.	5.8	13
23176	Integrated Analysis of miRNA and mRNA Expression Profiles Reveals the Molecular Mechanism of Posttraumatic Stress Disorder and Therapeutic Drugs. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2669-2680.	0.8	1

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23177	Identification of the Potential Key Genes and Pathways Involved in Lens Changes of High Myopia. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2867-2875.	0.8	4
23178	Transcriptional Profiling and Deriving a Seven-Gene Signature That Discriminates Active and Latent Tuberculosis: An Integrative Bioinformatics Approach. <i>Genes</i> , 2022, 13, 616.	1.0	12
23179	Transcriptome sequencing and lncRNA-miRNA-mRNA network construction in cardiac fibrosis and heart failure. <i>Bioengineered</i> , 2022, 13, 7118-7133.	1.4	8
23180	Systematic mapping of nuclear domain-associated transcripts reveals speckles and lamina as hubs of functionally distinct retained introns. <i>Molecular Cell</i> , 2022, 82, 1035-1052.e9.	4.5	31
23181	Deciphering Haplotypic Variation and Gene Expression Dynamics Associated with Nutritional and Cooking Quality in Rice. <i>Cells</i> , 2022, 11, 1144.	1.8	1
23182	Outstanding prognostic value of novel ferroptosis-related genes in chemoresistance osteosarcoma patients. <i>Scientific Reports</i> , 2022, 12, 5029.	1.6	11
23183	Identification of the shared gene signatures and pathways between sarcopenia and type 2 diabetes mellitus. <i>PLoS ONE</i> , 2022, 17, e0265221.	1.1	17
23185	Multi-Omics Analyses Characterize the Gut Microbiome and Metabolome Signatures of Soldiers Under Sustained Military Training. <i>Frontiers in Microbiology</i> , 2022, 13, 827071.	1.5	2
23186	<sc>Data-mining-based</sc> of ancient traditional Chinese medicine records from 475 BC to 1949 to potentially treat COVID-19. <i>Anatomical Record</i> , 2023, 306, 2984-2996.	0.8	5
23188	Transcriptome analysis of <i>Porphyridium purpureum</i> under salinities of 0 and 68. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	0
23189	Functional and Biochemical Characterization of the MazEF6 Toxin-Antitoxin System of <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2022, 204, e0005822.	1.0	8
23190	MD2 Is a Potential Biomarker Associated with Immune Cell Infiltration in Gliomas. <i>Frontiers in Oncology</i> , 2022, 12, 854598.	1.3	3
23191	Assessment of Greenhouse Tomato Anthesis Rate Through Metabolomics Using LASSO Regularized Linear Regression Model. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 839051.	1.6	0
23192	Comprehensive characterization of the bacterial community structure and metabolite composition of food waste fermentation products via microbiome and metabolome analyses. <i>PLoS ONE</i> , 2022, 17, e0264234.	1.1	1
23193	Identification of Novel Key Molecular Signatures in the Pathogenesis of Experimental Diabetic Kidney Disease. <i>Frontiers in Endocrinology</i> , 2022, 13, 843721.	1.5	7
23194	Construction of a Quantitative Genomic Map, Identification and Expression Analysis of Candidate Genes for Agronomic and Disease-Related Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 862363.	1.7	7
23195	Identification of Biomarkers Related to Regulatory T Cell Infiltration in Oral Squamous Cell Carcinoma Based on Integrated Bioinformatics Analysis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2361-2376.	0.8	3
23196	MicroRNA-mediated post-transcriptional regulation of <i>Pinus pinaster</i> response and resistance to pinewood nematode. <i>Scientific Reports</i> , 2022, 12, 5160.	1.6	7

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23197	Stress vulnerability shapes disruption of motor cortical neuroplasticity. <i>Translational Psychiatry</i> , 2022, 12, 91.	2.4	11
23198	Amplified Drought and Seasonal Cycle Modulate <i>Quercus pubescens</i> Leaf Metabolome. <i>Metabolites</i> , 2022, 12, 307.	1.3	7
23199	Reduction of Metastasis via Epigenetic Modulation in a Murine Model of Metastatic Triple Negative Breast Cancer (TNBC). <i>Cancers</i> , 2022, 14, 1753.	1.7	7
23200	Integration of Transcriptome and Metabolome Provides New Insights to Flavonoids Biosynthesis in <i>Dendrobium huoshanense</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 850090.	1.7	12
23201	Construction of ceRNA networks with different types of IDH1 mutation status in low-grade glioma patients. <i>Annals of Translational Medicine</i> , 2022, 10, 254-254.	0.7	1
23202	Application of an iPSCâ€Derived Organoid Model for Localized Scleroderma Therapy. <i>Advanced Science</i> , 2022, 9, e2106075.	5.6	10
23203	Population Diversity of Antibiotic Resistant Enterobacterales in Samples From Wildlife Origin in Senegal: Identification of a Multidrug Resistance Transposon Carrying blaCTXâ€Mâ€15 in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 838392.	1.5	5
23204	Hsa_circ_0031608: A Potential Modulator of VSMC Phenotype in the Rupture of Intracranial Aneurysms. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 842865.	1.4	5
23205	Proteome-centric cross-omics characterization and integrated network analyses of triple-negative breast cancer. <i>Cell Reports</i> , 2022, 38, 110460.	2.9	13
23206	Computed Tomography Imaging-Based Radiogenomics Analysis Reveals Hypoxia Patterns and Immunological Characteristics in Ovarian Cancer. <i>Frontiers in Immunology</i> , 2022, 13, 868067.	2.2	31
23207	Peripheral blood mononuclear cell gene expression and cytokine profiling in patients with intermittent claudication who exhibit exercise induced acute renal injury. <i>PLoS ONE</i> , 2022, 17, e0265393.	1.1	0
23208	Identification of proteomic markers for prediction of the response to 5-Fluorouracil based neoadjuvant chemoradiotherapy in locally advanced rectal cancer patients. <i>Cancer Cell International</i> , 2022, 22, 117.	1.8	3
23209	GSDMs are potential therapeutic targets and prognostic biomarkers in clear cell renal cell carcinoma. <i>Aging</i> , 2022, 14, 2758-2774.	1.4	12
23210	Chemical modulation of the metabolism of an endophytic fungal strain of <i>Cophinforma mamane</i> using epigenetic modifiers and amino-acids. <i>Fungal Biology</i> , 2022, 126, 385-394.	1.1	5
23212	Identification of Key microRNAs and Genes in Infantile Hemangiomas. <i>Frontiers in Genetics</i> , 2022, 13, 766561.	1.1	1
23213	Enhanced Bioremediation Potential of <i>Shewanella decolorationis</i> RNA Polymerase Mutants and Evidence for Novel Azo Dye Biodegradation Pathways. <i>Frontiers in Microbiology</i> , 2022, 13, 843807.	1.5	0
23214	GeneCup: mining PubMed and GWAS catalog for geneâ€keyword relationships. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	8
23216	Comparison of the Endophytic Bacterial Microbiota of Asymptomatic andâ€Symptomatic Ginger Rhizomes During the Activation of Adventitious Bud Development. <i>Plant Disease</i> , 2022, 106, 2470-2479.	0.7	3



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23217	A BioID-Derived Proximity Interactome for SARS-CoV-2 Proteins. <i>Viruses</i> , 2022, 14, 611.	1.5	25
23218	AutoCoEvâ€”A High-Throughput In Silico Pipeline for Predicting Inter-Protein Coevolution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3351.	1.8	1
23220	A nonredundant role for TÂcell-derived interleukin 22 in antibacterial defense of colonic crypts. <i>Immunity</i> , 2022, 55, 494-511.e11.	6.6	15
23221	Identification of Guaifenesinâ€”Andrographolide as a Novel Combinatorial Drug Therapy for Epilepsy Using Network Virtual Screening and Experimental Validation. <i>ACS Chemical Neuroscience</i> , 2022, 13, 978-986.	1.7	1
23222	Salicylic acid alleviates selenium stress and promotes selenium uptake of grapevine. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 625-635.	1.4	20
23224	Unveiling Potential Mechanisms of Spatholobi Caulis against Lung Metastasis of Malignant Tumor by Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	3
23225	Chicken Peripheral Blood Mononuclear Cells Response to Avian Leukosis Virus Subgroup J Infection Assessed by Single-Cell RNA Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, 800618.	1.5	8
23226	Clr-f expression regulates kidney immune and metabolic homeostasis. <i>Scientific Reports</i> , 2022, 12, 4834.	1.6	1
23227	The Key Genes Underlying Pathophysiology Correlation Between the Acute Myocardial Infarction and COVID-19. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2479-2490.	0.8	6
23228	Effects of Si on N and P stoichiometry in degraded grassland of northern China. <i>Land Degradation and Development</i> , 2022, 33, 960-973.	1.8	4
23231	Aryl Hydrocarbon Receptor-Dependent and -Independent Pathways Mediate Curcumin Anti-Aging Effects. <i>Antioxidants</i> , 2022, 11, 613.	2.2	2
23232	Functional Similarities of Protein-Coding Genes in Topologically Associating Domains and Spatially-Proximate Genomic Regions. <i>Genes</i> , 2022, 13, 480.	1.0	0
23233	Genome-Wide Association Analyses Reveal Candidate Genes Controlling Harvest Index and Related Agronomic Traits in Brassica napus L.. <i>Agronomy</i> , 2022, 12, 814.	1.3	2
23234	Maintenance of mitochondrial integrity in midbrain dopaminergic neurons governed by a conserved developmental transcription factor. <i>Nature Communications</i> , 2022, 13, 1426.	5.8	11
23235	Circulating <sc>miRNAs</sc> in girls with abdominal obesity: <sc>miR</sc> â€”221â€”3p as a biomarker of response to weight loss interventions. <i>Pediatric Obesity</i> , 2022, , e12910.	1.4	11
23236	Systematic understanding of anti-tumor mechanisms of Tamarixetin through network and experimental analyses. <i>Scientific Reports</i> , 2022, 12, 3966.	1.6	3
23237	Relationships between Indicators of Lower Extremity Artery Disease and miRNA Expression in Peripheral Blood Mononuclear Cells. <i>Journal of Clinical Medicine</i> , 2022, 11, 1619.	1.0	1
23238	Transcriptome Analysis Revealed the Molecular Response Mechanism of Non-heading Chinese Cabbage to Iron Deficiency Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 848424.	1.7	5

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23239	Sputum Bacterial Metacomunities in Distinguishing Heterogeneity in Respiratory Health and Disease. <i>Frontiers in Microbiology</i> , 2022, 13, 719541.	1.5	2
23240	Multitarget-Based Virtual Screening for Identification of Herbal Substances toward Potential Osteoclastic Targets. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 2621.	1.3	0
23241	Monomodular <i>Pseudomonas aeruginosa</i> phage JG004 lysozyme (Pae87) contains a bacterial surface-active antimicrobial peptide-like region and a possible substrate-binding subdomain. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 435-454.	1.1	7
23242	Correlation Analysis of the Microbiome and Immune Function in the Lung-Gut Axis of Critically Ill Patients in the ICU. <i>Frontiers in Medicine</i> , 2022, 9, 808302.	1.2	4
23243	Comprehensive analysis of tumor immune microenvironment and prognosis of m6A-related lncRNAs in gastric cancer. <i>BMC Cancer</i> , 2022, 22, 316.	1.1	10
23244	Identifying Active Substances and the Pharmacological Mechanism of <i>Houttuynia cordata</i> Thunb. in Treating Radiation-Induced Lung Injury Based on Network Pharmacology and Molecular Docking Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	5
23246	DNA- and RNA-based bacterial communities and geochemical zonation under changing sediment porewater dynamics on the Aldabra Atoll. <i>Scientific Reports</i> , 2022, 12, 4257.	1.6	4
23247	Transcriptome Analysis Reveal Candidate Genes and Pathways Responses to Lactate Dehydrogenase Inhibition (Oxamate) in Hyperglycemic Human Renal Proximal Epithelial Tubular Cells. <i>Frontiers in Endocrinology</i> , 2022, 13, 785605.	1.5	2
23248	Temperature Affects Antagonism Among Coral-Associated Bacteria. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
23249	NLRP6-Dependent Pyroptosis-Related lncRNAs Predict the Prognosis of Hepatocellular Carcinoma. <i>Frontiers in Medicine</i> , 2022, 9, 760722.	1.2	5
23250	Identification of key genes associated with head and neck squamous cell carcinoma in the microenvironment. <i>Minerva Biotechnology and Biomolecular Research</i> , 2022, 34, .	0.3	0
23251	Antifungals influence the immune-related transcriptomic landscape of human monocytes after <i>Aspergillus fumigatus</i> infection. <i>Scientific Reports</i> , 2022, 12, 4581.	1.6	1
23252	The Analyses of Cetacean Virus-Responsive Genes Reveal Evolutionary Marks in Mucosal Immunity-Associated Genes. <i>Biochemical Genetics</i> , 2022, , 1.	0.8	2
23253	Degree of Freedom of Gene Expression in <i>Saccharomyces cerevisiae</i> . <i>Microbiology Spectrum</i> , 2022, , e0083821.	1.2	0
23254	Iduronate-2-sulfatase interactome: validation by yeast two-hybrid assay. <i>Heliyon</i> , 2022, 8, e09031.	1.4	0
23255	Interpreting the Pharmacological Mechanisms of Sho-saiko-to on Thyroid Carcinoma through Combining Network Pharmacology and Experimental Evaluation. <i>ACS Omega</i> , 2022, 7, 11166-11176.	1.6	2
23256	In Silico Analysis of Ion Channels and Their Correlation with Epithelial to Mesenchymal Transition in Breast Cancer. <i>Cancers</i> , 2022, 14, 1444.	1.7	6
23257	Mechanistic basis of choline import involved in teichoic acids and lipopolysaccharide modification. <i>Science Advances</i> , 2022, 8, eabm1122.	4.7	11

#	ARTICLE	IF	CITATIONS
23258	RACK1 Associates with RNA-Binding Proteins Vigilin and SERBP1 to Facilitate Dengue Virus Replication. <i>Journal of Virology</i> , 2022, , e0196221.	1.5	13
23259	Tissue-Specific Methylation Biosignatures for Monitoring Diseases: An In Silico Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2959.	1.8	6
23260	Analyzing Prognostic Hub Genes in the Microenvironment of Cutaneous Melanoma by Computer Integrated Bioinformatics. <i>Computational Intelligence and Neuroscience</i> , 2022, 2022, 1-14.	1.1	0
23261	Mechanism of Pilose Antler in Treatment of Osteoporosis Based on Network Pharmacology. <i>Journal of Healthcare Engineering</i> , 2022, 2022, 1-7.	1.1	2
23262	Computational Inference of Synaptic Polarities in Neuronal Networks. <i>Advanced Science</i> , 2022, , 2104906.	5.6	5
23263	Comprehensive analysis of competitive endogenous RNAs network: Identification and validation of prediction model composed of mRNA signature and miRNA signature in gastric cancer. <i>Oncology Letters</i> , 2022, 23, 150.	0.8	3
23264	The Shared Mechanism and Candidate Drugs of Multiple Sclerosis and Sjögren's Syndrome Analyzed by Bioinformatics Based on GWAS and Transcriptome Data. <i>Frontiers in Immunology</i> , 2022, 13, 857014.	2.2	8
23265	Rapid evolution fuels transcriptional plasticity to ocean acidification. <i>Global Change Biology</i> , 2022, 28, 3007-3022.	4.2	23
23267	Genomic Survey and Cold-Induced Expression Patterns of bHLH Transcription Factors in <i>Liriodendron chinense</i> (Hemsl) Sarg.. <i>Forests</i> , 2022, 13, 518.	0.9	10
23268	Genomic evolution and adaptation of arthropod-associated <i>Rickettsia</i> . <i>Scientific Reports</i> , 2022, 12, 3807.	1.6	25
23269	Molecular Dynamics of Cytokine Interactions and Signalling of Mesenchymal Stem Cells Undergoing Directed Neural-like Differentiation. <i>Life</i> , 2022, 12, 392.	1.1	4
23270	Exploring the Mechanism of Yiqi Qingre Ziyin Method in Regulating Neuropeptide Expression for the Treatment of Atrophic Rhinitis. <i>Disease Markers</i> , 2022, 2022, 1-12.	0.6	10
23271	Validation of an online application to identify potential immune-related adverse events associated with immune checkpoint inhibitors based on the patient's symptoms. <i>PLoS ONE</i> , 2022, 17, e0265230.	1.1	0
23272	The microbiome and resistome of apple fruits alter in the post-harvest period. <i>Environmental Microbiomes</i> , 2022, 17, 10.	2.2	11
23274	TREM2 and CD163 Ameliorate Microglia-Mediated Inflammatory Environment in the Aging Brain. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 1075-1084.	1.1	5
23275	Proteomic Signatures of Microbial Adaptation to the Highest Ultraviolet-Irradiation on Earth: Lessons From a Soil Actinobacterium. <i>Frontiers in Microbiology</i> , 2022, 13, 791714.	1.5	1
23276	SINAPs: A Software Tool for Analysis and Visualization of Interaction Networks of Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1425-1436.	2.5	4
23277	A Nrf-2 Stimulatory Hydroxylated Cannabidiol Derivative from Hemp ( <i>Cannabis sativa</i> ). <i>Journal of Natural Products</i> , 2022, 85, 1089-1097.	1.5	9

#	ARTICLE	IF	CITATIONS
23278	Preliminary identification and analysis of differential RNA editing between higher and lower backfat thickness pigs using DNA-seq and RNA-seq data. <i>Animal Genetics</i> , 2022, 53, 327-339.	0.6	4
23280	A 70â€ˆRNA model based on SVR and RFE for predicting the pancreatic cancer clinical prognosis. <i>Methods</i> , 2022, 204, 278-285.	1.9	4
23281	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	1.7	8
23282	Interacting Effects of Sea Louse ( <i>Lepeophtheirus salmonis</i> ) Infection and Formalin-Killed <i>Aeromonas salmonicida</i> on Atlantic Salmon Skin Transcriptome. <i>Frontiers in Immunology</i> , 2022, 13, 804987.	2.2	4
23284	ADAP1 promotes latent HIV-1 reactivation by selectively tuning KRASâ€ˆERKâ€ˆAP-1 T cell signaling-transcriptional axis. <i>Nature Communications</i> , 2022, 13, 1109.	5.8	2
23285	Fanconi Anemia Pathway in Colorectal Cancer: A Novel Opportunity for Diagnosis, Prognosis and Therapy. <i>Journal of Personalized Medicine</i> , 2022, 12, 396.	1.1	8
23286	Study on Mechanism of Yiqi Yangyin Jiedu Recipe Inhibiting Triple Negative Breast Cancer Growth: A Network Pharmacology and In Vitro Verification. <i>Journal of Oncology</i> , 2022, 2022, 1-11.	0.6	3
23287	In silico discovery of 3 novel quercetin derivatives against papain-like protease, spike protein, and 3C-like protease of SARS-CoV-2. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 43.	1.5	10
23288	Single-Cell RNA-Seq Reveals the Cellular Diversity and Developmental Characteristics of the Retinas of an Infant and a Young Child. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 803466.	1.8	3
23289	Global MicroRNAs Expression Profile Analysis Reveals Possible Regulatory Mechanisms of Brain Injury Induced by <i>Toxoplasma gondii</i> Infection. <i>Frontiers in Neuroscience</i> , 2022, 16, 827570.	1.4	7
23290	Identification of antimicrobial peptides from the human gut microbiome using deep learning. <i>Nature Biotechnology</i> , 2022, 40, 921-931.	9.4	142
23291	Integrated multi-omic data and analyses reveal the pathways underlying key ornamental traits in carnation flowers. <i>Plant Biotechnology Journal</i> , 2022, 20, 1182-1196.	4.1	21
23292	Evolutionarily conservative and non-conservative regulatory networks during primate interneuron development revealed by single-cell RNA and ATAC sequencing. <i>Cell Research</i> , 2022, 32, 425-436.	5.7	25
23293	BridgeDb and Wikidata: a powerful combination generating interoperable open research (BridgeDb). <i>Research Ideas and Outcomes</i> , 0, 8, .	1.0	1
23294	Production of Epoxyketone Peptide-Based Proteasome Inhibitors by <i>Streptomyces</i> sp. BRA-346: Regulation and Biosynthesis. <i>Frontiers in Microbiology</i> , 2022, 13, 786008.	1.5	0
23295	Partners to survive: <i>Hoffmannseggia doellii</i> root-associated microbiome at the Atacama Desert. <i>New Phytologist</i> , 2022, 234, 2126-2139.	3.5	10
23296	Systematic Analysis of the Expression Profile and Prognostic Significance of the IGF2BP Family in Lung Adenocarcinoma. <i>Current Cancer Drug Targets</i> , 2022, 22, 340-350.	0.8	6
23297	Network Preservation Analysis Reveals Dysregulated Synaptic Modules and Regulatory Hubs Shared Between Alzheimerâ€™s Disease and Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , 2022, 13, 821343.	1.1	7

#	ARTICLE	IF	CITATIONS
23298	Integrated Analysis of Competitive Endogenous RNA Networks in Acute Ischemic Stroke. <i>Frontiers in Genetics</i> , 2022, 13, 833545.	1.1	6
23299	Identification of a poly-cyclopropylglycine-containing peptide via bioinformatic mapping of radical S-adenosylmethionine enzymes. <i>Journal of Biological Chemistry</i> , 2022, 298, 101881.	1.6	8
23301	BAP1-Related ceRNA (NEAT1/miR-10a-5p/SERPINE1) Promotes Proliferation and Migration of Kidney Cancer Cells. <i>Frontiers in Oncology</i> , 2022, 12, 852515.	1.3	7
23302	Long non-coding RNA LINC00680 functions as a ceRNA to promote esophageal squamous cell carcinoma progression through the miR-423-5p/PAK6 axis. <i>Molecular Cancer</i> , 2022, 21, 69.	7.9	51
23303	Intrahabitat Differences in Bacterial Communities Associated with <i>Corbicula fluminea</i> in the Large Shallow Eutrophic Lake Taihu. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0232821.	1.4	6
23304	A Case Study of the Glycoside Hydrolase Enzyme Mechanism Using an Automated QM-Cluster Model Building Toolkit. <i>Frontiers in Chemistry</i> , 2022, 10, 854318.	1.8	2
23307	Sphingolipid Metabolism as a New Predictive Target Correlated with Aging and AD: A Transcriptomic Analysis. <i>Medicina (Lithuania)</i> , 2022, 58, 493.	0.8	4
23309	Transcriptome profiling of the nonlactating mammary glands of dairy goats reveals the molecular genetic mechanism of mammary cell remodeling. <i>Journal of Dairy Science</i> , 2022, 105, 5238-5260.	1.4	6
23310	Integrated LC-MS/MS and Transcriptome Sequencing Analysis Reveals the Mechanism of Color Formation During Prickly Ash Fruit Ripening. <i>Frontiers in Nutrition</i> , 2022, 9, 847823.	1.6	2
23311	Circular RNA Profiles in Viremia and ART Suppression Predict Competing circRNA-miRNA-mRNA Networks Exclusive to HIV-1 Viremic Patients. <i>Viruses</i> , 2022, 14, 683.	1.5	3
23312	CDK Inhibition Reverses Acquired 5-Fluorouracil Resistance in Hepatocellular Carcinoma Cells. <i>Disease Markers</i> , 2022, 2022, 1-9.	0.6	3
23313	Genetic Signatures from Adaptation of Bacteria to Lytic Phage Identify Potential Agents To Aid Phage Killing of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Journal of Bacteriology</i> , 2022, 204, jb0059321.	1.0	5
23314	Transcriptome Analysis of <i>Populus euphratica</i> under Salt Treatment and PeERF1 Gene Enhances Salt Tolerance in Transgenic <i>Populus alba</i> – <i>Populus glandulosa</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3727.	1.8	6
23315	Patterns of Differentially Expressed circRNAs in Human Thymocytes. <i>Non-coding RNA</i> , 2022, 8, 26.	1.3	0
23316	Solasonine Induces Apoptosis and Inhibits Proliferation of Bladder Cancer Cells by Suppressing NRP1 Expression. <i>Journal of Oncology</i> , 2022, 2022, 1-15.	0.6	11
23317	Molecular Characterization, Tumor Microenvironment Association, and Drug Susceptibility of DNA Methylation-Driven Genes in Renal Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 837919.	1.8	4
23318	<i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i> Isolated From Urine of Healthy Bovine Have Potential as Emerging Human and Bovine Pathogens. <i>Frontiers in Microbiology</i> , 2022, 13, 764760.	1.5	3
23319	Dynamic Changes in the Proteome of Early Bovine Embryos Developed In Vivo. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 863700.	1.8	5

#	ARTICLE	IF	CITATIONS
23320	A FBXO7/EYA2-SCFFBXW7 axis promotes AXL-mediated maintenance of mesenchymal and immune evasion phenotypes of cancer cells. <i>Molecular Cell</i> , 2022, 82, 1123-1139.e8.	4.5	18
23321	Groundnut Bud Necrosis Virus Modulates the Expression of Innate Immune, Endocytosis, and Cuticle Development-Associated Genes to Circulate and Propagate in Its Vector, Thrips palmi. <i>Frontiers in Microbiology</i> , 2022, 13, 773238.	1.5	12
23322	Gene Regulatory Networks of Epidermal and Neural Fate Choice in a Chordate. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
23323	Fe(II) Addition Drives Soil Bacterial Co-Occurrence Patterns and Functions Mediated by Anaerobic and Chemoautotrophic Taxa. <i>Microorganisms</i> , 2022, 10, 547.	1.6	6
23324	Co-Occurrence of <i>L. monocytogenes</i> with Other Bacterial Genera and Bacterial Diversity on Cleaned Conveyor Surfaces in a Swine Slaughterhouse. <i>Microorganisms</i> , 2022, 10, 613.	1.6	4
23325	Genome-Wide Identification, Evolution and Expression Analysis of the Glutathione S-Transferase Supergene Family in Euphorbiaceae. <i>Frontiers in Plant Science</i> , 2022, 13, 808279.	1.7	3
23326	Exploring the mechanisms of action of <i>Cordyceps sinensis</i> for the treatment of depression using network pharmacology and molecular docking. <i>Annals of Translational Medicine</i> , 2022, 10, 282-282.	0.7	7
23328	Network Pharmacology Integrated with Transcriptomics Deciphered the Potential Mechanism of <i>Codonopsis pilosula</i> against Hepatocellular Carcinoma. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-10.	0.5	6
23329	The structure of microbial communities of activated sludge of large-scale wastewater treatment plants in the city of Moscow. <i>Scientific Reports</i> , 2022, 12, 3458.	1.6	38
23330	Temporal and spatial cellular and molecular pathological alterations with single-cell resolution in the adult spinal cord after injury. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 65.	7.1	49
23331	Based on the Network Pharmacology to Investigate the Mechanism of Qingjie Fuzheng Granules against Colorectal Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	0
23332	The genetic and phenotypic landscapes of Usher syndrome: from disease mechanisms to a new classification. <i>Human Genetics</i> , 2022, 141, 709-735.	1.8	33
23333	MAdCAM-1 Costimulates T Cells through Integrin $\alpha 4 \beta 7$ to Cause Gene Expression Events Resembling Costimulation through CD28. <i>ImmunoHorizons</i> , 2022, 6, 211-223.	0.8	4
23335	Chemical Composition of Leaves, Stem, and Roots of <i>Peperomia pellucida</i> (L.) Kunth. <i>Molecules</i> , 2022, 27, 1847.	1.7	6
23337	Randomized Clinical Trial: Probiotics Alleviated Oral-Gut Microbiota Dysbiosis and Thyroid Hormone Withdrawal-Related Complications in Thyroid Cancer Patients Before Radioiodine Therapy Following Thyroidectomy. <i>Frontiers in Endocrinology</i> , 2022, 13, 834674.	1.5	18
23338	Repurposing Multiple-Molecule Drugs for COVID-19-Associated Acute Respiratory Distress Syndrome and Non-Viral Acute Respiratory Distress Syndrome via a Systems Biology Approach and a DNN-DTI Model Based on Five Drug Design Specifications. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3649.	1.8	5
23339	Network pharmacology analysis reveals neuroprotection of <i>Gynostemma pentaphyllum</i> (Thunb.) Makino in Alzheimer's™ disease. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 57.	1.2	4
23340	Identification and verification of potential core genes in pediatric septic shock. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	2



#	ARTICLE	IF	CITATIONS
23341	Connections and Biases in Health Equity and Culture Research: A Semantic Network Analysis. <i>Frontiers in Public Health</i> , 2022, 10, 834172.	1.3	3
23342	Global gene expression responses of Atlantic salmon skin to <i>Moritella viscosa</i> . <i>Scientific Reports</i> , 2022, 12, 4622.	1.6	7
23343	Distinct Roles of Honeybee Gut Bacteria on Host Metabolism and Neurological Processes. <i>Microbiology Spectrum</i> , 2022, 10, e0243821.	1.2	19
23344	Integrated In Silico Analyses Identify PUF60 and SF3A3 as New Spliceosome-Related Breast Cancer RNA-Binding Proteins. <i>Biology</i> , 2022, 11, 481.	1.3	3
23345	GENOMES UNCOUPLED1 plays a key role during the de-etiolation process in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2022, 235, 188-203.	3.5	5
23346	ACDB: An Antibiotic Combination DataBase. <i>Frontiers in Pharmacology</i> , 2022, 13, 869983.	1.6	4
23347	Gene expression study in monocytes: evidence of inflammatory dysregulation in early-onset obsessive-compulsive disorder. <i>Translational Psychiatry</i> , 2022, 12, 134.	2.4	1
23348	Chronic intermittent hypoxia induces gut microbial dysbiosis and infers metabolic dysfunction in mice. <i>Sleep Medicine</i> , 2022, 91, 84-92.	0.8	10
23349	In-silico analysis reveals the core targets and mechanisms of CA028, a new derivative of calycosin, in the treatment of colorectal cancer. <i>Intelligent Medicine</i> , 2022, 2, 127-133.	1.6	1
23351	Identification of Potential Biomarkers and Small Molecule Drugs for Cutaneous Melanoma Using Integrated Bioinformatic Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 858633.	1.8	3
23352	Revealing key lncRNAs in cytogenetically normal acute myeloid leukemia by reconstruction of the lncRNA-miRNA-mRNA network. <i>Scientific Reports</i> , 2022, 12, 4973.	1.6	3
23356	Evaluation of Ion Mobility Spectrometry for Improving Constitutional Assignment in Natural Product Mixtures. <i>Journal of Natural Products</i> , 2022, 85, 519-529.	1.5	6
23357	CENPF as an independent prognostic and metastasis biomarker corresponding to CD4+ memory T cells in cutaneous melanoma. <i>Cancer Science</i> , 2022, 113, 1220-1234.	1.7	11
23358	Notch-mediated Ephrin signaling disrupts islet architecture and $\beta^2$ cell function. <i>JCI Insight</i> , 2022, 7, .	2.3	5
23359	Integrative applications of network pharmacology and molecular docking: An herbal formula ameliorates H9c2 cells injury through pyroptosis. <i>Journal of Ginseng Research</i> , 2023, 47, 228-236.	3.0	3
23360	Integrative Functional Transcriptomic Analyses Implicate Shared Molecular Circuits in Sensorineural Hearing Loss. <i>Frontiers in Cellular Neuroscience</i> , 2022, 16, 857344.	1.8	3
23361	Long noncoding RNA signatures involved in the genomic instability of papillary thyroid carcinoma. <i>International Journal of Transgender Health</i> , 2022, 15, 358-370.	1.1	0
23362	Identification of autophagy-related long non-coding RNAs in endometrial cancer via comprehensive bioinformatics analysis. <i>BMC Women's Health</i> , 2022, 22, 85.	0.8	9

#	ARTICLE	IF	CITATIONS
23363	IDENTIFICATION OF FGFR INHIBITOR AS ST2 RECEPTOR/INTERLEUKIN-1 RECEPTOR-LIKE 1 INHIBITOR IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE DUE TO EXPOSURE TO E-CIGARETTES BY NETWORK PHARMACOLOGY AND MOLECULAR DOCKING PREDICTION. International Journal of Applied Pharmaceutics, 0, , 256-266.	0.3	2
23364	A comprehensive WGS-based pipeline for the identification of new candidate genes in inherited retinal dystrophies. Npj Genomic Medicine, 2022, 7, 17.	1.7	7
23365	Tet-mediated DNA demethylation regulates specification of hematopoietic stem and progenitor cells during mammalian embryogenesis. Science Advances, 2022, 8, eabm3470.	4.7	13
23366	Cinnamomi Ramulus inhibits the growth of colon cancer cells via Akt/ERK signaling pathways. Chinese Medicine, 2022, 17, 36.	1.6	6
23367	Manifold valued data analysis of samples of networks, with applications in corpus linguistics. Annals of Applied Statistics, 2022, 16, .	0.5	0
23368	Overexpression of Ribosomal Protein S6 Kinase A4 (RPS6KA4) Predicts a Poor Prognosis in Hepatocellular Carcinoma Patients: A Study Based on TCGA Samples. Combinatorial Chemistry and High Throughput Screening, 2022, 25, 2165-2179.	0.6	2
23369	Discovering Novel Biomarkers Associated with the Pathogenesis of Psoriasis: Evidence from Bioinformatic Analysis. International Journal of General Medicine, 2022, Volume 15, 2817-2833.	0.8	3
23371	Programmed Cell Death May Be Involved in the Seedless Phenotype Formation of Oil Palm. Frontiers in Plant Science, 2022, 13, 832017.	1.7	2
23372	Increased DNA methylation, cellular senescence and premature epigenetic aging in guinea pigs and humans with tuberculosis. Aging, 2022, 14, 2174-2193.	1.4	15
23373	Heat Shock Procedure Affects Cell Division-Associated Genes in Gynogenetic Manipulation. Marine Biotechnology, 2022, 24, 354.	1.1	2
23374	Comparative gene expression profile in circulating PBMCs of <i>Bos indicus</i> and crossbred cattle to understand disease tolerance mechanism. Animal Biotechnology, 2023, 34, 1594-1602.	0.7	0
23375	A Quartet Network Analysis Identifying Mechanically Responsive Long Noncoding RNAs in Bone Remodeling. Frontiers in Bioengineering and Biotechnology, 2022, 10, 780211.	2.0	2
23376	Adult mouse fibroblasts retain organ-specific transcriptomic identity. ELife, 2022, 11, .	2.8	14
23378	Microbiome function predicts amphibian chytridiomycosis disease dynamics. Microbiome, 2022, 10, 44.	4.9	12
23379	The Prognostic Significance and Gene Expression Characteristics of Gastric Signet-Ring Cell Carcinoma: A Study Based on the SEER and TCGA Databases. Frontiers in Surgery, 2022, 9, 819018.	0.6	5
23380	Circular RNA Profiling Identifies Novel circPPARA that Promotes Intramuscular Fat Deposition in Pigs. Journal of Agricultural and Food Chemistry, 2022, 70, 4123-4137.	2.4	22
23381	Network medicine in ovarian cancer: topological properties to drug discovery. Briefings in Bioinformatics, 2022, 23, .	3.2	7
23382	OVOL2 impairs RHO GTPase signaling to restrain mitosis and aggressiveness of Anaplastic Thyroid Cancer. Journal of Experimental and Clinical Cancer Research, 2022, 41, 108.	3.5	6

#	ARTICLE	IF	CITATIONS
23383	Proteomic-Based Machine Learning Analysis Reveals PYGB as a Novel Immunohistochemical Biomarker to Distinguish Inverted Urothelial Papilloma From Low-Grade Papillary Urothelial Carcinoma With Inverted Growth. <i>Frontiers in Oncology</i> , 2022, 12, 841398.	1.3	3
23385	Identification of lncRNA/circRNA-miRNA-mRNA ceRNA Network as Biomarkers for Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2022, 13, 838869.	1.1	24
23386	Causal association evaluation of diabetes with Alzheimer's disease and genetic analysis of antidiabetic drugs against Alzheimer's disease. <i>Cell and Bioscience</i> , 2022, 12, 28.	2.1	12
23387	Long noncoding RNAs regulated spermatogenesis in varicocele-induced spermatogenic dysfunction. <i>Cell Proliferation</i> , 2022, 55, e13220.	2.4	5
23388	A Computational Text Mining-Guided Meta-Analysis Approach to Identify Potential Xerostomia Drug Targets. <i>Journal of Clinical Medicine</i> , 2022, 11, 1442.	1.0	4
23389	Record-Breaking Rain Event Altered Estuarine Viral Assemblages. <i>Microorganisms</i> , 2022, 10, 729.	1.6	5
23390	Transcription factor protein interactomes reveal genetic determinants in heart disease. <i>Cell</i> , 2022, 185, 794-814.e30.	13.5	39
23391	Crucial Roles of microRNA-16-5p and microRNA-27b-3p in Ameloblast Differentiation Through Regulation of Genes Associated With Amelogenesis Imperfecta. <i>Frontiers in Genetics</i> , 2022, 13, 788259.	1.1	5
23392	Contribution of Host miRNA-223-3p to SARS-CoV-Induced Lung Inflammatory Pathology. <i>MBio</i> , 2022, 13, e0313521.	1.8	22
23393	Insights into the Chemical Diversity of Selected Fungi from the Tza Itz'Äi Cenote of the Yucatan Peninsula. <i>ACS Omega</i> , 2022, 7, 12171-12185.	1.6	5
23394	Development and Validation of Ischemic Events Related Signature After Carotid Endarterectomy. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 794608.	1.8	5
23395	Scale Development-Related Genes Identified by Transcriptome Analysis. <i>Fishes</i> , 2022, 7, 64.	0.7	3
23396	Anti-tumor metabolites from <i>Synadenium grantii</i> Hook F.. <i>Medicinal Chemistry Research</i> , 2022, 31, 666-673.	1.1	1
23397	The Human Myelin Proteome and Sub-Metalloproteome Interaction Map: Relevance to Myelin-Related Neurological Diseases. <i>Brain Sciences</i> , 2022, 12, 434.	1.1	2
23399	Exploration of the Potential Relationship Between Gut Microbiota Remodeling Under the Influence of High-Protein Diet and Crohn's Disease. <i>Frontiers in Microbiology</i> , 2022, 13, 831176.	1.5	6
23400	Identification of a Twelve Epithelial-Mesenchymal Transition-Related lncRNA Prognostic Signature in Kidney Clear Cell Carcinoma. <i>Disease Markers</i> , 2022, 2022, 1-18.	0.6	6
23401	Genetic evidence for facial variation being a composite phenotype of cranial variation and facial soft tissue thickness. <i>Journal of Genetics and Genomics</i> , 2022, , .	1.7	2
23402	Darling: A Web Application for Detecting Disease-Related Biomedical Entity Associations with Literature Mining. <i>Biomolecules</i> , 2022, 12, 520.	1.8	9

#	ARTICLE	IF	CITATIONS
23403	Exploration of the Mechanism of the Control of Coccidiosis in Chickens Based on Network Pharmacology and Molecular Docking With the Addition of Modified Gegen Qinlian Decoction. <i>Frontiers in Veterinary Science</i> , 2022, 9, 849518.	0.9	3
23404	Non-obligate pairwise metabolite cross-feeding suggests ammensalic interactions between <i>Bacillus amyloliquefaciens</i> and <i>Aspergillus oryzae</i> . <i>Communications Biology</i> , 2022, 5, 232.	2.0	3
23405	Multi-Omics Characterization of Early- and Adult-Onset Major Depressive Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 412.	1.1	7
23406	Investigation of the Effect of Curcumin on Protein Targets in NAFLD Using Bioinformatic Analysis. <i>Nutrients</i> , 2022, 14, 1331.	1.7	11
23407	Endoplasmic reticulum chaperone genes encode effectors of long-term memory. <i>Science Advances</i> , 2022, 8, eabm6063.	4.7	16
23408	Circulating Immune Bioenergetic, Metabolic, and Genetic Signatures Predict Melanoma Patients' Response to Anti-PD-1 Immune Checkpoint Blockade. <i>Clinical Cancer Research</i> , 2022, 28, 1192-1202.	3.2	24
23410	Systematic analysis of olfactory protein-protein interactions network of fruitfly, <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 110, e21882.	0.6	0
23411	Single-cell metabolite detection and genomics reveals uncultivated talented producer. , 2022, 1, .		15
23412	Reinvention of hermaphroditism via activation of a RADIALIS-like gene in hexaploid persimmon. <i>Nature Plants</i> , 2022, 8, 217-224.	4.7	21
23413	Distinct Epileptogenic Mechanisms Associated with Seizures in Wolf-Hirschhorn Syndrome. <i>Molecular Neurobiology</i> , 2022, 59, 3159-3169.	1.9	2
23414	Identification of CD101 in Glioma: A Novel Prognostic Indicator Expressed on M2 Macrophages. <i>Frontiers in Immunology</i> , 2022, 13, 845223.	2.2	6
23416	The AlkB Family: Potential Prognostic Biomarkers and Therapeutic Targets in Glioblastoma. <i>Frontiers in Oncology</i> , 2022, 12, 847821.	1.3	1
23417	Transcriptome Analysis Reveals the Alternative Splicing Changes in the Immune-Related Genes of the Giant Panda ( <i>Ailuropoda melanoleuca</i> ), in Response to the Canine Distemper Vaccine. <i>Zoological Science</i> , 2022, 39, .	0.3	3
23418	Integrative bioinformatics analysis of potential therapeutic targets and immune infiltration characteristics in dilated cardiomyopathy. <i>Annals of Translational Medicine</i> , 2022, 10, 348-348.	0.7	5
23419	Troloxerutin-Mediated Complement Pathway Inhibition is a Disease-Modifying Treatment for Inflammatory Arthritis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 845457.	1.8	0
23421	First trimester plasma microRNAs levels predict Matsuda Index-estimated insulin sensitivity between 24th and 29th week of pregnancy. <i>BMJ Open Diabetes Research and Care</i> , 2022, 10, e002703.	1.2	6
23423	A network biology approach to identify crucial host targets for COVID-19. <i>Methods</i> , 2022, 203, 108-115.	1.9	6
23424	Role of mobile genetic elements in the global dissemination of the carbapenem resistance gene bla <sub>NDM</sub> . <i>Nature Communications</i> , 2022, 13, 1131.	5.8	72

#	ARTICLE	IF	CITATIONS
23425	Collagen Family and Other Matrix Remodeling Proteins Identified by Bioinformatics Analysis as Hub Genes Involved in Gastric Cancer Progression and Prognosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3214.	1.8	13
23426	Extrinsic KRAS Signaling Shapes the Pancreatic Microenvironment Through Fibroblast Reprogramming. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 1673-1699.	2.3	36
23427	Hepatic adropin is regulated by estrogen and contributes to adverse metabolic phenotypes in ovariectomized mice. <i>Molecular Metabolism</i> , 2022, 60, 101482.	3.0	7
23428	Network-based approaches for the investigation of microbial community structure and function using metagenomics-based data. <i>Future Microbiology</i> , 2022, 17, 621-631.	1.0	2
23429	Circulating small RNA signatures differentiate accurately the subtypes of muscular dystrophies: small-RNA next-generation sequencing analytics and functional insights. <i>RNA Biology</i> , 2022, 19, 507-518.	1.5	1
23430	Prognostic Gene Expression Signature for Age-Related Hearing Loss. <i>Frontiers in Medicine</i> , 2022, 9, 814851.	1.2	4
23431	Predicted mouse interactome and network-based interpretation of differentially expressed genes. <i>PLoS ONE</i> , 2022, 17, e0264174.	1.1	0
23432	Lower functional redundancy in narrow functions in global soil metagenomics. <i>Soil</i> , 2022, 8, 297-308.	2.2	11
23433	A Glimpse at Siderophores Production by <i>Anabaena flos-aquae</i> UTEX 1444. <i>Marine Drugs</i> , 2022, 20, 256.	2.2	5
23434	Novel Protein-Protein Interactions Highlighting the Crosstalk between Hypoplastic Left Heart Syndrome, Ciliopathies and Neurodevelopmental Delays. <i>Genes</i> , 2022, 13, 627.	1.0	1
23435	Trichoderma-Derived Pentapeptides from the Infected Nest Mycobiome of the Subterranean Termite <i>Coptotermes testaceus</i> . <i>ChemBioChem</i> , 2022, 23, .	1.3	3
23436	The Characterization of the Phloem Protein 2 Gene Family Associated with Resistance to <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3934.	1.8	4
23437	Analysis of ceRNA crosstalk in eosinophilic chronic rhinosinusitis with nasal polyps. <i>International Forum of Allergy and Rhinology</i> , 2022, , .	1.5	3
23438	Digital Spatial Profiling Reveals Functional Shift of Enterochromaffin Cell in Patients With Ulcerative Colitis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 841090.	1.8	1
23439	Time-course transcriptome and WGCNA analysis revealed the drought response mechanism of two sunflower inbred lines. <i>PLoS ONE</i> , 2022, 17, e0265447.	1.1	15
23440	Proteomic analysis reveals rattlesnake venom modulation of proteins associated with cardiac tissue damage in mouse hearts. <i>Journal of Proteomics</i> , 2022, 258, 104530.	1.2	6
23441	Dissection of valine-glutamine genes and their responses to drought stress in <i>Arachis hypogaea</i> cv. Tifrunner. <i>Functional and Integrative Genomics</i> , 2022, , 1.	1.4	3
23442	Molecular mechanisms of Huanglian jiedu decoction on ulcerative colitis based on network pharmacology and molecular docking. <i>Scientific Reports</i> , 2022, 12, 5526.	1.6	8

#	ARTICLE	IF	CITATIONS
23444	Genome-scale transcriptomic insights into the gene co-expression network of seed abortion in triploid <i>Siraitia grosvenorii</i> . <i>BMC Plant Biology</i> , 2022, 22, 173.	1.6	2
23445	Transcriptome analysis reveals key genes and pathways related to sex differentiation in the Chinese soft-shelled turtle ( <i>Pelodiscus sinensis</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100986.	0.4	4
23446	Defining the Role of Isoeugenol from <i>Ocimum tenuiflorum</i> against Diabetes Mellitus-Linked Alzheimer's Disease through Network Pharmacology and Computational Methods. <i>Molecules</i> , 2022, 27, 2398.	1.7	41
23447	In silico analysis highlighting the prevalence of BCL2L1 gene and its correlation to miRNA in human coronavirus (HCoV) genetic makeup. <i>Infection, Genetics and Evolution</i> , 2022, 99, 105260.	1.0	5
23448	Identification of Genes Linking Natural Killer Cells to Apoptosis in Acute Myocardial Infarction and Ischemic Stroke. <i>Frontiers in Immunology</i> , 2022, 13, 817377.	2.2	7
23449	Pathways Involved in the Development of Vasculogenic Mimicry in Canine Mammary Carcinoma Cell Cultures. <i>Journal of Comparative Pathology</i> , 2022, 192, 50-60.	0.1	0
23450	High-throughput translational profiling with riboPLATE-seq. <i>Scientific Reports</i> , 2022, 12, 5718.	1.6	3
23451	Secondary resistome in bacteria: a potential biomarker for future antimicrobial resistance diagnostics. <i>Future Microbiology</i> , 2022, 17, 573-576.	1.0	2
23453	Co-Expression Networks Unveiled Long Non-Coding RNAs as Molecular Targets of Drugs Used to Treat Bipolar Disorder. <i>Frontiers in Pharmacology</i> , 2022, 13, 873271.	1.6	7
23454	Comparative genomic analyses reveal cis-regulatory divergence after polyploidization in cotton. <i>Crop Journal</i> , 2022, , .	2.3	0
23456	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>iScience</i> , 2022, 25, 104137.	1.9	20
23457	A Survey of Biological Data in a Big Data Perspective. <i>Big Data</i> , 2022, 10, 279-297.	2.1	8
23458	Multi-omics data integration analysis identifies the spliceosome as a key regulator of DNA double-strand break repair. <i>NAR Cancer</i> , 2022, 4, zcac013.	1.6	5
23460	Ultrastructural and proteomic profiling of mitochondria-associated endoplasmic reticulum membranes reveal aging signatures in striated muscle. <i>Cell Death and Disease</i> , 2022, 13, 296.	2.7	13
23461	A Single Application of Compost Can Leave Lasting Impacts on Soil Microbial Community Structure and Alter Cross-Domain Interaction Networks. <i>Frontiers in Soil Science</i> , 2022, 2, .	0.8	15
23462	Bioinformatic Analysis Reveals Hub Immune-Related Genes of Diabetic Foot Ulcers. <i>Frontiers in Surgery</i> , 2022, 9, 878965.	0.6	8
23463	Genome-Wide Identification, Expression Pattern and Sequence Variation Analysis of SnRK Family Genes in Barley. <i>Plants</i> , 2022, 11, 975.	1.6	3
23464	Short prokaryotic Argonaute systems trigger cell death upon detection of invading DNA. <i>Cell</i> , 2022, 185, 1471-1486.e19.	13.5	85



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23465	PRC1 and RACGAP1 are Diagnostic Biomarkers of Early HCC and PRC1 Drives Self-Renewal of Liver Cancer Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 864051.	1.8	6
23466	The Ahr2-Dependent <i>wfikk1</i> Gene Influences Zebrafish Transcriptome, Proteome, and Behavior. <i>Toxicological Sciences</i> , 2022, 187, 325-344.	1.4	7
23467	Identification of microRNA-mRNA-TF regulatory networks in periodontitis by bioinformatics analysis. <i>BMC Oral Health</i> , 2022, 22, 118.	0.8	3
23468	Identification of rearing temperature-dependent host defense signaling against viral hemorrhagic septicemia virus infection. <i>Fish and Shellfish Immunology</i> , 2022, 123, 257-264.	1.6	1
23469	In-Silico Functional Annotation of Plasmodium falciparum Hypothetical Proteins to Identify Novel Drug Targets. <i>Frontiers in Genetics</i> , 2022, 13, 821516.	1.1	3
23470	Rab21 in enterocytes participates in intestinal epithelium maintenance. <i>Molecular Biology of the Cell</i> , 2022, 33, mbcE21030139.	0.9	4
23472	Identification of Breast Cancer Subtypes Based on Gene Expression Profiles in Breast Cancer Stroma. <i>Clinical Breast Cancer</i> , 2022, 22, 521-537.	1.1	4
23474	Application of OpenArray RT-qPCR for identification of microRNA expression signatures of lower extremity artery disease. <i>Journal of Applied Genetics</i> , 2022, 63, 497-512.	1.0	1
23476	Integrated Bioinformatics Algorithms and Experimental Validation to Explore Robust Biomarkers and Landscape of Immune Cell Infiltration in Dilated Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 809470.	1.1	6
23477	Blood miRNAs Are Linked to Frequent Asthma Exacerbations in Childhood Asthma and Adult COPD. <i>Non-coding RNA</i> , 2022, 8, 27.	1.3	3
23478	Identification of key candidate genes and biological pathways in the synovial tissue of patients with rheumatoid arthritis. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, 368.	0.8	5
23479	Bisphenol A exposure triggers the malignant transformation of prostatic hyperplasia in beagle dogs via cfa-miR-204/KRAS axis. <i>Ecotoxicology and Environmental Safety</i> , 2022, 235, 113430.	2.9	5
23480	Soil metabolomics and bacterial functional traits revealed the responses of rhizosphere soil bacterial community to long-term continuous cropping of Tibetan barley. <i>PeerJ</i> , 2022, 10, e13254.	0.9	11
23482	Network Pharmacology-Based Approach Combined with Bioinformatic Analytics to Elucidate the Potential of Curcumol against Hepatocellular Carcinoma. <i>Genes</i> , 2022, 13, 653.	1.0	10
23483	Quantitative Proteomic Analysis Reveals Important Roles of the Acetylation of ER-Resident Molecular Chaperones for Conidiation in <i>Fusarium oxysporum</i> . <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100231.	2.5	3
23484	Identification of a novel anticancer mechanism of <i>Paeoniae Radix</i> extracts based on systematic transcriptome analysis. <i>Biomedicine and Pharmacotherapy</i> , 2022, 148, 112748.	2.5	9
23485	Integrated analysis of expression profiles with meat quality traits in cattle. <i>Scientific Reports</i> , 2022, 12, 5926.	1.6	4
23487	The microbial communities in <i>Zaopeis</i> , free amino acids in raw liquor, and their correlations for <i>Wuliangye</i> flavor raw liquor production. <i>Food Science and Nutrition</i> , 0, , .	1.5	3

#	ARTICLE	IF	CITATIONS
23488	LncRNA-mediated effects of vitrification temperatures and cryoprotectant concentrations on bovine oocyte development following vitrification at the GV stage. <i>Theriogenology</i> , 2022, 186, 135-145.	0.9	1
23489	The association of clinicopathological characterizations of colorectal cancer with membrane-bound mucins genes and LncRNAs. <i>Pathology Research and Practice</i> , 2022, 233, 153883.	1.0	4
23490	Physical and functional interactome atlas of human receptor tyrosine kinases. <i>EMBO Reports</i> , 2022, 23, e54041.	2.0	18
23491	Predicted coronavirus Nsp5 protease cleavage sites in the human proteome. <i>BMC Genomic Data</i> , 2022, 23, 25.	0.7	15
23492	Soil environment reshapes microbiota of laboratory-maintained Collembola during host development. <i>Environmental Microbiomes</i> , 2022, 17, 16.	2.2	1
23493	MicroRNAs Influence the Migratory Ability of Human Umbilical Vein Endothelial Cells. <i>Genes</i> , 2022, 13, 640.	1.0	1
23494	Genomic Insights into the Distribution of Peptidases and Proteolytic Capacity among <i>Prevotella</i> and <i>Paraprevotella</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, e0218521.	1.2	10
23495	Comprehensive Analysis on Prognosis and Immune Infiltration of Lysyl Oxidase Family Members in Pancreatic Adenocarcinoma With Experimental Verification. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 778857.	1.6	2
23496	A systems biology study unveils the association between a melatonin biosynthesis gene, O-methyl transferase 1 (OMT1) and wheat ( <i>Triticum aestivum</i> L.) combined drought and salinity stress tolerance. <i>Planta</i> , 2022, 255, 99.	1.6	9
23497	Narciclasine suppresses esophageal cancer cell proliferation and migration by inhibiting the FAK signaling pathway. <i>European Journal of Pharmacology</i> , 2022, 921, 174669.	1.7	9
23498	Identification of Key Genes and Pathways in Peripheral Blood Mononuclear Cells of Type 1 Diabetes Mellitus by Integrated Bioinformatics Analysis. <i>Diabetes and Metabolism Journal</i> , 2022, 46, 451-463.	1.8	10
23499	Transcriptome Architecture of Osteoblastic Cells Infected With <i>Staphylococcus aureus</i> Reveals Strong Inflammatory Responses and Signatures of Metabolic and Epigenetic Dysregulation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 854242.	1.8	7
23500	Comparative phosphoproteomics reveal new candidates in the regulation of spermatogenesis of <i>Drosophila melanogaster</i> . <i>Insect Science</i> , 2022, 29, 1703-1720.	1.5	4
23501	Quaternary Structure and Deoxyribonucleic Acid-Binding Properties of the Heme-Dependent, CO-Sensing Transcriptional Regulator <i>PxRcoM</i> . <i>Biochemistry</i> , 2022, 61, 678-688.	1.2	3
23502	LAMB1 Promotes Nasopharyngeal Carcinoma Cell Growth and Motility. <i>International Journal of Pharmacology</i> , 2022, 18, 721-731.	0.1	0
23503	Comparative transcriptome profiling of virulent and avirulent isolates of <i>Neoparamoeba perurans</i> . <i>Scientific Reports</i> , 2022, 12, 5860.	1.6	0
23504	Autophagy Induced by BCL2-Related ceRNA Network Participates in the Occurrence of COPD. <i>International Journal of COPD</i> , 2022, Volume 17, 791-808.	0.9	4
23505	Relative contributions of sex hormones, sex chromosomes, and gonads to sex differences in tissue gene regulation. <i>Genome Research</i> , 2022, , .	2.4	23

#	ARTICLE	IF	CITATIONS
23506	Decoding herbal materials of TCM preparations with the multi-barcode sequencing approach. <i>Scientific Reports</i> , 2022, 12, 5988.	1.6	13
23507	Genome-Wide Identification of TLP Gene Family and Their Roles in <i>Carya cathayensis</i> Sarg in Response to <i>Botryosphaeria dothidea</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 849043.	1.7	2
23508	Rewiring of the Liver Transcriptome across Multiple Time-Scales Is Associated with the Weight Loss-Independent Resolution of NAFLD Following RYGB. <i>Metabolites</i> , 2022, 12, 318.	1.3	1
23509	An Integration of MicroRNA and Transcriptome Sequencing Analysis Reveal Regulatory Roles of miRNAs in Response to Chilling Stress in Wild Rice. <i>Plants</i> , 2022, 11, 977.	1.6	4
23510	NUSAP1 Could be a Potential Target for Preventing NAFLD Progression to Liver Cancer. <i>Frontiers in Pharmacology</i> , 2022, 13, 823140.	1.6	5
23511	Circulating Tregs Accumulate in Omental Tumors and Acquire Adipose-Resident Features. <i>Cancer Immunology Research</i> , 2022, 10, 641-655.	1.6	4
23512	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	6.0	124
23513	mRNA-miRNA bipartite networks reconstruction in different tissues of bladder cancer based on gene co-expression network analysis. <i>Scientific Reports</i> , 2022, 12, 5885.	1.6	6
23514	Resveratrol Prevents Cytoarchitectural and Interneuronal Alterations in the Valproic Acid Rat Model of Autism. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4075.	1.8	6
23515	A Census of Hsp70-Mediated Proteome Solubility Changes upon Recovery from Heat Stress. <i>Journal of Proteome Research</i> , 2022, 21, 1251-1261.	1.8	2
23516	Identification of potentially functional circRNAs and prediction of circRNA-miRNA-mRNA regulatory network in periodontitis: Bridging the gap between bioinformatics and clinical needs. <i>Journal of Periodontal Research</i> , 2022, 57, 594-614.	1.4	7
23517	Data mining analysis reveals key acupoints and meridians for the treatment of chemotherapy-induced peripheral neuropathy. <i>Explore: the Journal of Science and Healing</i> , 2023, 19, 71-77.	0.4	4
23518	Overexpression of REST Causes Neuronal Injury and Decreases Cofilin Phosphorylation in Mice. <i>Journal of Alzheimer's Disease</i> , 2022, 87, 873-886.	1.2	2
23520	Preclinical In Silico Evidence Indicates the Pharmacological Targets and Mechanisms of Mogroside V in Patients With Ovarian Cancer and Coronavirus Disease 2019. <i>Frontiers in Endocrinology</i> , 2022, 13, 845404.	1.5	2
23521	Bioinformatics Screening of Potential Biomarkers from mRNA Expression Profiles to Discover Drug Targets and Agents for Cervical Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3968.	1.8	13
23522	Serum cytokine profiles in phlegm-dampness constitution and damp-heat constitution using proteomic antibody microarray. <i>European Journal of Integrative Medicine</i> , 2022, 52, 102126.	0.8	2
23523	Comparative Transcriptomics Reveals the Key lncRNA and mRNA of Sunite Sheep Adrenal Gland Affecting Seasonal Reproduction. <i>Frontiers in Veterinary Science</i> , 2022, 9, 816241.	0.9	5
23524	The Mycotoxin Beauvericin Exhibits Immunostimulatory Effects on Dendritic Cells via Activating the TLR4 Signaling Pathway. <i>Frontiers in Immunology</i> , 2022, 13, 856230.	2.2	2

#	ARTICLE	IF	CITATIONS
23525	Trophectoderm Transcriptome Analysis in LIN28 Knockdown Ovine Conceptuses Suggests Diverse Roles of the LIN28-let-7 Axis in Placental and Fetal Development. <i>Cells</i> , 2022, 11, 1234.	1.8	2
23526	Single-Cell Transcriptome Analysis Reveals the Role of Pancreatic Secretome in COVID-19 Associated Multi-organ Dysfunctions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 863-878.	2.2	3
23527	Mechanistic Origin of Different Binding Affinities of SARS-CoV and SARS-CoV-2 Spike RBDs to Human ACE2. <i>Cells</i> , 2022, 11, 1274.	1.8	8
23528	Distinct CholinomiR Blood Cell Signature as a Potential Modulator of the Cholinergic System in Women with Fibromyalgia Syndrome. <i>Cells</i> , 2022, 11, 1276.	1.8	8
23529	The pro-apoptotic <i>Bax</i> gene modifies susceptibility to craniofacial dysmorphology following gastrulation-stage alcohol exposure. <i>Birth Defects Research</i> , 2022, 114, 1229-1243.	0.8	3
23530	Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes. <i>IScience</i> , 2022, 25, 104231.	1.9	6
23531	The structure of <i>Synechococcus elongatus</i> enolase reveals key aspects of phosphoenolpyruvate binding. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 177-184.	0.4	1
23532	Bioinformatics Analysis Identified the Hub Genes, mRNA-miRNA-lncRNA Axis, and Signaling Pathways Involved in Rheumatoid Arthritis Pathogenesis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3879-3893.	0.8	5
23533	SETDB1 interactions with PELP1 contributes to breast cancer endocrine therapy resistance. <i>Breast Cancer Research</i> , 2022, 24, 26.	2.2	12
23534	Chromosome-scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass ( <i>Pennisetum purpureum</i> Schum.). <i>Molecular Ecology Resources</i> , 2022, 22, 2363-2378.	2.2	11
23535	Subunits of C1Q Are Associated With the Progression of Intermittent Claudication to Chronic Limb-Threatening Ischemia. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 864461.	1.1	1
23536	Protecting effect of emodin in experimental autoimmune encephalomyelitis mice by inhibiting microglia activation and inflammation via Myd88/PI3K/Akt/NF- $\kappa$ B signalling pathway. <i>Bioengineered</i> , 2022, 13, 9322-9344.	1.4	16
23537	Transcriptome analysis in the spleen of Northern Snakehead ( <i>Channa argus</i> ) challenged with <i>Nocardia seriolae</i> . <i>Genomics</i> , 2022, 114, 110357.	1.3	5
23538	Genetic variation and intestinal cholesterol absorption in humans: A systematic review and a gene network analysis. <i>Progress in Lipid Research</i> , 2022, 86, 101164.	5.3	5
23539	RNA sequencing reveals perivascular adipose tissue plasticity in response to angiotensin II. <i>Pharmacological Research</i> , 2022, 178, 106183.	3.1	7
23540	Proteomics and Metabolomics Profiling of Platelets and Plasma Mediators of Thrombo-Inflammation in Gestational Hypertension and Preeclampsia. <i>Cells</i> , 2022, 11, 1256.	1.8	14
23541	NUP133 Controls Nuclear Pore Assembly, Transcriptome Composition, and Cytoskeleton Regulation in Podocytes. <i>Cells</i> , 2022, 11, 1259.	1.8	4
23542	Functional and structural deficiencies of Gemin5 variants associated with neurological disorders. <i>Life Science Alliance</i> , 2022, 5, e202201403.	1.3	7

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23543	Genetic effect of ischemia-reperfusion injury upon primary graft dysfunction and chronic lung allograft dysfunction in lung transplantation: evidence based on transcriptome data. <i>Transplant Immunology</i> , 2022, 71, 101556.	0.6	6
23544	Identification of genes responsible for stress resistance in fusarium oxysporum- inoculated flax seedlings using weighted gene co-expression network analysis. <i>European Journal of Plant Pathology</i> , 0, , 1.	0.8	1
23545	Multigenomic modifications in human circulating immune cells in response to consumption of polyphenol-rich extract of yerba mate ( <i>Ilex paraguariensis</i> A. St.-Hil.) are suggestive of cardiometabolic protective effects. <i>British Journal of Nutrition</i> , 2023, 129, 185-205.	1.2	1
23546	Time-series transcriptomics reveals a drought-responsive temporal network and crosstalk between drought stress and the circadian clock in foxtail millet. <i>Plant Journal</i> , 2022, 110, 1213-1228.	2.8	11
23547	Differential transcriptomic landscapes of multiple organs from SARS-CoV-2 early infected rhesus macaques. <i>Protein and Cell</i> , 2022, 13, 920-939.	4.8	9
23548	TGF- $\beta$ 2 induced reprogramming and drug resistance in triple-negative breast cells. <i>BMC Pharmacology &amp; Toxicology</i> , 2022, 23, 23.	1.0	3
23549	Correlating the above- and belowground genotype of <i>Pinus pinaster</i> trees and rhizosphere bacterial communities under drought conditions. <i>Science of the Total Environment</i> , 2022, 832, 155007.	3.9	6
23550	Protein interaction network analysis reveals genetic enrichment of immune system genes in frontotemporal dementia. <i>Neurobiology of Aging</i> , 2022, 116, 67-79.	1.5	2
23551	Causal relationships between blood calcium, iron, magnesium, zinc, selenium, phosphorus, copper, and lead levels and multisystem disease outcomes in over 400,000 Caucasian participants. <i>Clinical Nutrition</i> , 2022, 41, 1015-1024.	2.3	0
23552	Critical assessment of metabolism and related growth and quality traits in trout fed spirulina-supplemented plant-based diets. <i>Aquaculture</i> , 2022, 553, 738033.	1.7	3
23553	Identification of metastasis-associated exoDEPs in colorectal cancer using label-free proteomics. <i>Translational Oncology</i> , 2022, 19, 101389.	1.7	2
23554	A review of methods for the inference and experimental confirmation of microbial association networks in cheese. <i>International Journal of Food Microbiology</i> , 2022, 368, 109618.	2.1	12
23555	Potential efficacious materials investigation of Yi-Yi Mixture based on Metabolome-oriented network pharmacology strategy. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2022, 1197, 123199.	1.2	5
23556	Hepatocellular carcinoma and miRNAs: An in silico approach revealing potential therapeutic targets for polyphenols. <i>Phytomedicine Plus</i> , 2022, 2, 100259.	0.9	5
23557	Molecular networking-guided strategy for the pharmacokinetic study of herbal medicines: <i>Cudrania tricuspidata</i> leaf extracts. <i>Biomedicine and Pharmacotherapy</i> , 2022, 149, 112895.	2.5	5
23558	A mixed blessing of viruses in wastewater treatment plants. <i>Water Research</i> , 2022, 215, 118237.	5.3	21
23559	Exploring the potential mechanism of radix astragali against ischemic stroke based on network pharmacology and molecular docking. <i>Phytomedicine Plus</i> , 2022, 2, 100244.	0.9	1
23560	Dynamics and correlation of microbial communities and metabolic compounds in doenjang-meju, a Korean traditional soybean brick. <i>Food Research International</i> , 2022, 155, 111085.	2.9	13

#	ARTICLE	IF	CITATIONS
23561	Comparative computational RNA analysis of cardiac-derived progenitor cells and their extracellular vesicles. <i>Genomics</i> , 2022, 114, 110349.	1.3	4
23562	Bioinformatics role of the WGCNA analysis and co-expression network identifies of prognostic marker in lung cancer. <i>Saudi Journal of Biological Sciences</i> , 2022, 29, 3519-3527.	1.8	9
23563	Network pharmacology prediction and molecular docking-based strategy to explore the potential mechanism of Huanglian Jiedu Decoction against sepsis. <i>Computers in Biology and Medicine</i> , 2022, 144, 105389.	3.9	137
23564	Evolutionary and functional characterisation of glutathione peroxidases showed splicing mediated stress responses in Maize. <i>Plant Physiology and Biochemistry</i> , 2022, 178, 40-54.	2.8	6
23565	Allosteric modulation of the chemokine receptor-chemokine CXCR4-CXCL12 complex by tyrosine sulfation. <i>International Journal of Biological Macromolecules</i> , 2022, 206, 812-822.	3.6	4
23566	A system biology approach to determine therapeutic targets by identifying molecular mechanisms and key pathways for type 2 diabetes that are linked to the development of tuberculosis and rheumatoid arthritis. <i>Life Sciences</i> , 2022, 297, 120483.	2.0	10
23567	Sequencing and de novo transcriptome assembly for discovering regulators of gene expression in Jack ( <i>Artocarpus heterophyllus</i> ). <i>Genomics</i> , 2022, 114, 110356.	1.3	1
23568	Draft genome sequence of Indian mulberry ( <i>Morus indica</i> ) provides a resource for functional and translational genomics. <i>Genomics</i> , 2022, 114, 110346.	1.3	12
23569	Pathobiology of <i>Enterocytozoon hepatopenaei</i> (EHP) in shrimp: Diagnosis and interpretation from the gut bacterial community. <i>Aquaculture</i> , 2022, 554, 738169.	1.7	8
23570	Epigenetic changes induced in mice liver by methionine-supplemented and methionine-deficient diets. <i>Food and Chemical Toxicology</i> , 2022, 163, 112938.	1.8	3
23571	Statistical and machine learning methods to study human CD4+ T cell proteome profiles. <i>Immunology Letters</i> , 2022, 245, 8-17.	1.1	3
23572	Metabarcoding analysis of microbiome dynamics during a <i>Phaeocystis globosa</i> bloom in the Beibu Gulf, China. <i>Harmful Algae</i> , 2022, 114, 102217.	2.2	3
23573	Abundance of plasma proteins in response to divergent ratios of dietary $\omega$ -3 fatty acids in gestating and lactating sows using a quantitative proteomics approach. <i>Journal of Proteomics</i> , 2022, 260, 104562.	1.2	4
23574	Deficiency of autism-related <i>Scn2a</i> gene in mice disrupts sleep patterns and circadian rhythms. <i>Neurobiology of Disease</i> , 2022, 168, 105690.	2.1	14
23575	Bioinformatics and network-based approaches for determining pathways, signature molecules, and drug substances connected to genetic basis of schizophrenia etiology. <i>Brain Research</i> , 2022, 1785, 147889.	1.1	5
23576	Mechanisms underlying the therapeutic effects of Qingfei Yin in treating acute lung injury based on GEO datasets, network pharmacology and molecular docking. <i>Computers in Biology and Medicine</i> , 2022, 145, 105454.	3.9	42
23577	Pilot study in human healthy volunteers on the mechanisms underlying remote ischemic conditioning (RIC) – Targeting circulating immune cells and immune-related proteins. <i>Journal of Neuroimmunology</i> , 2022, 367, 577847.	1.1	3
23578	Identification of the upstream regulators of KDM5B in gastric cancer. <i>Life Sciences</i> , 2022, 298, 120458.	2.0	6



#	ARTICLE	IF	CITATIONS
23579	Transcriptome analysis of colorectal cancer liver metastasis: The importance of long non-coding RNAs and fusion transcripts in the disease pathogenesis. <i>Molecular and Cellular Probes</i> , 2022, 63, 101816.	0.9	1
23580	Bioinformatic investigation and functional analysis of 214 hereditary genes identified non-coding RNAs as therapeutic tool for breast cancer management. <i>Gene Reports</i> , 2022, 27, 101565.	0.4	0
23581	Prediction of the mechanisms of action of Zhibai Dihaung Granule in cisplatin-induced acute kidney injury: A network pharmacology study and experimental validation. <i>Journal of Ethnopharmacology</i> , 2022, 292, 115241.	2.0	9
23582	A network pharmacology-based study on the quality control markers of antithrombotic herbs: Using <i>Salvia miltiorrhiza</i> - <i>Ligusticum chuanxiong</i> as an example. <i>Journal of Ethnopharmacology</i> , 2022, 292, 115197.	2.0	10
23583	Cordycepin enhances anti-tumor immunity in colon cancer by inhibiting phagocytosis immune checkpoint CD47 expression. <i>International Immunopharmacology</i> , 2022, 107, 108695.	1.7	16
23584	Interleukin 2 receptor subunit beta as a novel hub gene plays a potential role in the immune microenvironment of abdominal aortic aneurysms. <i>Gene</i> , 2022, 827, 146472.	1.0	4
23585	Using bioinformatics and systems biology to discover common pathogenetic processes between sarcoidosis and COVID-19. <i>Gene Reports</i> , 2022, 27, 101597.	0.4	3
23586	Identification and validation of Osteopontin and receptor for hyaluronic acid-mediated motility (RHAMM, CD168) for potential immunotherapeutic significance of in lung squamous cell carcinoma. <i>International Immunopharmacology</i> , 2022, 107, 108715.	1.7	6
23587	How experimental competition changes ovarian gene activity in free-living birds: Implications for steroidogenesis, maternal effects, and beyond. <i>Hormones and Behavior</i> , 2022, 142, 105171.	1.0	3
23588	The large-scale spatial patterns of ecological networks between phytoplankton and zooplankton in coastal marine ecosystems. <i>Science of the Total Environment</i> , 2022, 827, 154285.	3.9	8
23589	Effects of simultaneous denitrification and desulfurization and changes of microbial community structure with corn cob solid slow-release carbon source under different S/N ratios. <i>Journal of Water Process Engineering</i> , 2022, 47, 102737.	2.6	6
23590	Identification of microRNA and gene interactions through bioinformatic integrative analysis for revealing candidate signatures in prostate cancer. <i>Gene Reports</i> , 2022, 27, 101607.	0.4	4
23591	Short-term N addition in a <i>Pinus tabulaeformis</i> plantation: Microbial community composition and interactions show different linkages with ecological stoichiometry. <i>Applied Soil Ecology</i> , 2022, 174, 104422.	2.1	10
23592	Synchronized resistance training and bioactive herbal compounds of <i>Tribulus Terrestris</i> reverse the disruptive influence of Stanozolol. <i>Steroids</i> , 2022, 182, 109000.	0.8	1
23593	Saltwater intrusion affecting NO <sub>2</sub> <sup>-</sup> accumulation in demersal fishery species by bacterially mediated N-cycling. <i>Science of the Total Environment</i> , 2022, 827, 154371.	3.9	2
23594	Gene expression and network based study of colorectal adenocarcinoma reveals tankyrase, PIK3CB and cyclin G-associated kinase as potential target candidates. <i>Gene Reports</i> , 2022, 27, 101605.	0.4	0
23595	Comparative analysis of anatomical structure, assimilate accumulation and gene expression in lignin and carbohydrate metabolism pathway during taproot thickening of taicai and pak choi. <i>Scientia Horticulturae</i> , 2022, 301, 111046.	1.7	1
23596	Shifts of lipid metabolites help decode immobilization of soil cadmium under reductive soil disinfection. <i>Science of the Total Environment</i> , 2022, 829, 154592.	3.9	2

#	ARTICLE	IF	CITATIONS
23597	Microbial compositions, ecological networks, and metabolomics in sediments of black-odour water in Dongguan, China. <i>Environmental Research</i> , 2022, 210, 112918.	3.7	9
23598	Effects of the reduction in chemical fertilizers on soil phosphatases encoding genes (phoD and phoX) under crop residue mulching. <i>Applied Soil Ecology</i> , 2022, 175, 104428.	2.1	4
23599	Deep learning approach identified a gene signature predictive of the severity of renal damage caused by chronic cadmium accumulation. <i>Journal of Hazardous Materials</i> , 2022, 433, 128795.	6.5	4
23600	Regulation of soil micro-foodwebs to root secondary metabolites in cultivated and wild licorice plants. <i>Science of the Total Environment</i> , 2022, 828, 154302.	3.9	20
23601	Transcriptome analysis alk-SMase knockout mice reveals the effect of alkaline sphingomyelinase on liver. <i>Biochemistry and Biophysics Reports</i> , 2022, 30, 101240.	0.7	0
23602	Viral diversity and biogeochemical potential revealed in different prawn-culture sediments by virus-enriched metagenome analysis. <i>Environmental Research</i> , 2022, 210, 112901.	3.7	7
23603	Metabolome and whole transcriptome analyses reveal the molecular mechanisms underlying terpenoids biosynthesis in <i>Sapindus mukorossi</i> fruits. <i>Industrial Crops and Products</i> , 2022, 181, 114810.	2.5	5
23604	Joint effects of bacterium and biochar in remediation of antibiotic-heavy metal contaminated soil and responses of resistance gene and microbial community. <i>Chemosphere</i> , 2022, 299, 134333.	4.2	27
23605	The regulators of soil organic carbon mineralization upon lime and/or phosphate addition vary with depth. <i>Science of the Total Environment</i> , 2022, 828, 154378.	3.9	4
23606	Slope-induced factors shape bacterial communities in surface soils in a forested headwater catchment. <i>Catena</i> , 2022, 214, 106253.	2.2	6
23607	Genome-wide transcriptional profiling and functional analysis reveal miR-330-MAPK15 axis involving in cellular responses to deoxynivalenol exposure. <i>Chemosphere</i> , 2022, 298, 134199.	4.2	3
23608	p53 mutants G245S and R337H associated with the Li-Fraumeni syndrome regulate distinct metabolic pathways. <i>Biochimie</i> , 2022, 198, 141-154.	1.3	3
23609	Classifying the multi-omics data of gastric cancer using a deep feature selection method. <i>Expert Systems With Applications</i> , 2022, 200, 116813.	4.4	23
23610	Transcriptome-wide identification, characterization, and expression analysis of R2R3-MYB gene family during lignin biosynthesis in Chinese cedar ( <i>Cryptomeria fortunei</i> Hooibrenk). <i>Industrial Crops and Products</i> , 2022, 182, 114883.	2.5	8
23611	Exosomes derived from differentiated human ADMSC with the Schwann cell phenotype modulate peripheral nerve-related cellular functions. <i>Bioactive Materials</i> , 2022, 14, 61-75.	8.6	26
23613	Modular signature of long non-coding RNA association networks as a prognostic biomarker in lung cancer. <i>BMC Medical Genomics</i> , 2021, 14, 290.	0.7	4
23614	A systematic review for organizing hackathons and code camps in Covid-19 like times: Literature in demand to understand online hackathons and event result continuation. , 2021, , .		27
23616	Bioinformatics study on different gene expression profiles of fibroblasts and vascular endothelial cells in keloids. <i>Medicine (United States)</i> , 2021, 100, e27777.	0.4	2

#	ARTICLE	IF	CITATIONS
23617	Analysis of the Efficacy and Pharmacological Mechanisms of Action of Zhenren Yangzang Decoction on Ulcerative Colitis Using Meta-Analysis and Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	0
23618	Decreased miR-497-5p Suppresses IL-6 Induced Atrophy in Muscle Cells. Cells, 2021, 10, 3527.	1.8	8
23620	Transcriptomic Analysis of Sex-Associated DEGs in Female and Male Flowers of Kiwifruit (Actinidia chinensis) Using RNA-Seq. Frontiers in Plant Science, 2021, 12, 689246.	1.2	0
23621	Forensic Event Reconstruction for Drones. , 2021, , .		2
23622	Comprehensive Betalain Profiling of <i>Chenopodium formosanum</i> Cultivars Using HPLC-Q-Orbitrap High-Resolution Mass Spectrometry. Journal of Agricultural and Food Chemistry, 2021, 69, 15699-15715.	2.4	6
23623	Targeting CK2 mediated signaling to impair/tackle SARS-CoV-2 infection: a computational biology approach. Molecular Medicine, 2021, 27, 161.	1.9	9
23625	Meta-Analysis and Bioinformatics Detection of Susceptibility Genes in Diabetic Nephropathy. International Journal of Molecular Sciences, 2022, 23, 20.	1.8	5
23626	Comprehensive analysis of ceRNA network of ERCC4 in colorectal cancer. PeerJ, 2021, 9, e12647.	0.9	3
23627	Novel Tyrosine Kinase-Mediated Phosphorylation With Dual Specificity Plays a Key Role in the Modulation of Streptococcus pyogenes Physiology and Virulence. Frontiers in Microbiology, 2021, 12, 689246.	1.5	4
23629	Assessment of styrene-divinylbenzene polymer (PPL) solid-phase extraction and non-targeted tandem mass spectrometry for the analysis of xenobiotics in seawater. Limnology and Oceanography: Methods, 2022, 20, 89-101.	1.0	6
23630	Omega-6 and omega-3 oxylipins as potential markers of cardiometabolic risk in young adults. Obesity, 2022, 30, 50-61.	1.5	21
23632	A Network-based Analysis of Ingredients Lists in Nutrient Profile Systems. Current Research in Nutrition and Food Science, 2021, 9, 800-811.	0.3	0
23633	Therapeutic Mechanism and Key Alkaloids of Uncaria rhynchophylla in Alzheimer's Disease From the Perspective of Pathophysiological Processes. Frontiers in Pharmacology, 2021, 12, 806984.	1.6	14
23634	The Tongue Squamous Carcinoma Cell Line Cal27 Primarily Employs Integrin $\beta$ 4-Containing Type II Hemidesmosomes for Adhesion Which Contribute to Anticancer Drug Sensitivity. Frontiers in Cell and Developmental Biology, 2021, 9, 786758.	1.8	6
23635	ANTXR1 as a potential prognostic biomarker for hepatitis B virus-related hepatocellular carcinoma identified by a weighted gene correlation network analysis. Journal of Gastrointestinal Oncology, 2021, 12, 3079-3092.	0.6	3
23636	Roles of mTOR in thoracic aortopathy understood by complex intracellular signaling interactions. PLoS Computational Biology, 2021, 17, e1009683.	1.5	16
23637	Prognostic Significance of SATB1, SMAD3, Ezrin and $\beta$ -Catenin in Patients with Pancreatic Adenocarcinoma. Applied Sciences (Switzerland), 2022, 12, 306.	1.3	0
23638	Metabolic and Transcriptional Changes across Osteogenic Differentiation of Mesenchymal Stromal Cells. Bioengineering, 2021, 8, 208.	1.6	6

#	ARTICLE	IF	CITATIONS
23639	Chemical biology-whole genome engineering datasets predict new antibacterial combinations. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
23641	An immune-associated ten-long noncoding RNA signature for predicting overall survival in cervical cancer. <i>Translational Cancer Research</i> , 2021, 10, 5295-5306.	0.4	3
23642	Antifungal Activity of N-(4-Halobenzyl)amides against <i>Candida</i> spp. and Molecular Modeling Studies. <i>International Journal of Molecular Sciences</i> , 2022, 23, 419.	1.8	9
23643	Bioinformatics and <i>in-silico</i> findings reveal medical features and pharmacological targets of biochanin A against colorectal cancer and COVID-19. <i>Bioengineered</i> , 2021, 12, 12461-12469.	1.4	6
23644	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. <i>Human Molecular Genetics</i> , 2021, , .	1.4	2
23645	Subcellular Proteomic Analysis Reveals Dysregulation in Organization of Human A549 Cells Infected with Influenza Virus H7N9. <i>Current Proteomics</i> , 2021, 19, .	0.1	0
23648	Prognostic biomarker SMARCC1 and its association with immune infiltrates in hepatocellular carcinoma. <i>Cancer Cell International</i> , 2021, 21, 701.	1.8	10
23649	Heterocellular OSM-OSMR signalling reprograms fibroblasts to promote pancreatic cancer growth and metastasis. <i>Nature Communications</i> , 2021, 12, 7336.	5.8	40
23651	Identifying a hypoxia related score to predict the prognosis of bladder cancer: a study with The Cancer Genome Atlas (TCGA) database. <i>Translational Andrology and Urology</i> , 2021, 10, 4353-4364.	0.6	1
23652	A Bioinformatics Approach to Identifying Potential Biomarkers for <i>Cryptosporidium parvum</i> : A Coccidian Parasite Associated with Fetal Diarrhea. <i>Vaccines</i> , 2021, 9, 1427.	2.1	4
23653	Unravelling Rubber Tree Growth by Integrating GWAS and Biological Network-Based Approaches. <i>Frontiers in Plant Science</i> , 2021, 12, 768589.	1.7	14
23654	Identification of key genes associated with esophageal adenocarcinoma based on bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2021, 9, 1711-1711.	0.7	4
23655	Effects of Serum Metabolites on the Pancreatic Transcriptome in Acute Acalculous Cholecystitis. <i>Gastroenterology Research and Practice</i> , 2021, 2021, 1-15.	0.7	1
23657	The gut microbiome and microbial metabolites in acute myocardial infarction. <i>Journal of Genetics and Genomics</i> , 2022, 49, 569-578.	1.7	11
23658	ceRNA Network of lncRNA/miRNA as Circulating Prognostic Biomarkers in Non-Hodgkin Lymphomas: Bioinformatic Analysis and Assessment of Their Prognostic Value in an NHL Cohort. <i>International Journal of Molecular Sciences</i> , 2022, 23, 201.	1.8	7
23660	Integrative Analyses of Biochemical Properties and Transcriptome Reveal the Dynamic Changes in Leaf Senescence of Tobacco ( <i>Nicotiana tabacum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 790167.	1.1	5
23662	Genome-wide expression of the residual lung reacting to experimental Pneumonectomy. <i>BMC Genomics</i> , 2021, 22, 881.	1.2	3
23664	Identification of Keratinocyte Differentiation-Involved Genes for Metastatic Melanoma by Gene Expression Profiles. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-9.	0.7	3

#	ARTICLE	IF	CITATIONS
23665	Structure-Function Relationships of Human Milk Oligosaccharides on the Intestinal Epithelial Transcriptome in Caco-2 Cells and a Murine Model of Necrotizing Enterocolitis. <i>Molecular Nutrition and Food Research</i> , 2022, 66, e2100893.	1.5	9
23667	Extracellular Vesicles Induce an Aggressive Phenotype in Luminal Breast Cancer Cells Via PKM2 Phosphorylation. <i>Frontiers in Oncology</i> , 2021, 11, 785450.	1.3	6
23668	Single-Cell Regulatory Network Inference and Clustering Identifies Cell-Type Specific Expression Pattern of Transcription Factors in Mouse Sciatic Nerve. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 676515.	1.8	6
23669	Exploring potential of Plasmodium RUVBL proteins as anti-malarial drug target. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 736-752.	2.0	2
23670	Comparing Ransomware using TLSH and @DisCo Analysis Frameworks. , 2021, , .		2
23672	Hotspots for mutations in the SARS-CoV-2 spike glycoprotein: a correspondence analysis. <i>Scientific Reports</i> , 2021, 11, 23622.	1.6	9
23673	Connecting the dots: The boons and banes of network modeling. <i>Patterns</i> , 2021, 2, 100374.	3.1	3
23674	Phosphoproteomic responses of TORC1 target kinases reveal discrete and convergent mechanisms that orchestrate the quiescence program in yeast. <i>Cell Reports</i> , 2021, 37, 110149.	2.9	20
23675	SARS-CoV-2 Exacerbates Beta-Amyloid Neurotoxicity, Inflammation and Oxidative Stress in Alzheimer's Disease Patients. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13603.	1.8	30
23676	Transcriptomic Analysis Reveals the Protective Effects of Empagliflozin on Lipid Metabolism in Nonalcoholic Fatty Liver Disease. <i>Frontiers in Pharmacology</i> , 2021, 12, 793586.	1.6	10
23677	Transcranial Ultrasound Stimulation of the Anterior Cingulate Cortex Reduces Neuropathic Pain in Mice. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-14.	0.5	9
23678	Comparative Metabolomics of Reproductive Organs in the Genus <i>Aesculus</i> (Sapindaceae) Reveals That Immature Fruits Are a Key Organ of Procyanidin Accumulation and Bioactivity. <i>Plants</i> , 2021, 10, 2695.	1.6	1
23679	Integrative Molecular Analyses of an Individual Transcription Factor-Based Genomic Model for Lung Cancer Prognosis. <i>Disease Markers</i> , 2021, 2021, 1-18.	0.6	2
23680	Smell Detection Agent Optimisation Framework and Systems Biology Approach to Detect Dys-Regulated Subnetwork in Cancer Data. <i>Biomolecules</i> , 2022, 12, 37.	1.8	0
23681	Toxicokinetics of Arenobufagin and its Cardiotoxicity Mechanism Exploration Based on Lipidomics and Proteomics Approaches in Rats. <i>Frontiers in Pharmacology</i> , 2021, 12, 780016.	1.6	1
23682	Immune landscape of advanced gastric cancer tumor microenvironment identifies immunotherapeutic relevant gene signature. <i>BMC Cancer</i> , 2021, 21, 1324.	1.1	8
23683	Portuguese Common Bean Natural Variation Helps to Clarify the Genetic Architecture of the Legume's Nutritional Composition and Protein Quality. <i>Plants</i> , 2022, 11, 26.	1.6	5
23684	Convergent use of phosphatidic acid for hepatitis C virus and SARS-CoV-2 replication organelle formation. <i>Nature Communications</i> , 2021, 12, 7276.	5.8	37

#	ARTICLE	IF	CITATIONS
23685	A Novel Competing Endogenous RNA Network Associated With the Pathogenesis of Gravesâ€™ Ophthalmopathy. <i>Frontiers in Genetics</i> , 2021, 12, 795546.	1.1	6
23686	Education shapes the structure of semantic memory and impacts creative thinking. <i>Npj Science of Learning</i> , 2021, 6, 35.	1.5	15
23688	Suitability of GWAS as a Tool to Discover SNPs Associated with Tick Resistance in Cattle: A Review. <i>Pathogens</i> , 2021, 10, 1604.	1.2	5
23689	The human gut symbiont <i>Ruminococcus gnavus</i> shows specificity to blood group A antigen during mucin glycan foraging: Implication for niche colonisation in the gastrointestinal tract. <i>PLoS Biology</i> , 2021, 19, e3001498.	2.6	10
23691	Integrated Analysis of Circular RNA-Associated ceRNA Network Reveals Potential circRNA Biomarkers in Human Breast Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-16.	0.7	5
23692	Shared brain transcriptomic signature in TDP-43 type A FTLN patients with or without <i>GRN</i> mutations. <i>Brain</i> , 2022, 145, 2472-2485.	3.7	6
23693	Total Flavonoids of Chuju Decrease Oxidative Stress and Cell Apoptosis in Ischemic Stroke Rats: Network and Experimental Analyses. <i>Frontiers in Neuroscience</i> , 2021, 15, 772401.	1.4	6
23694	A Molecular Analysis of Cytokine Content across Extracellular Vesicles, Secretions, and Intracellular Space from Different Site-Specific Adipose-Derived Stem Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 397.	1.8	2
23695	Revealing the Mechanism of Astragali Radix against Cancer-Related Fatigue by Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-10.	0.5	6
23699	Integrative Analysis of ceRNA Networks in human periodontal ligament stem cells under hypoxia. <i>Oral Diseases</i> , 2023, 29, 1197-1213.	1.5	4
23700	Identification of immune subtypes of Ph-neg B-ALL with ferroptosis related genes and the potential implementation of Sorafenib. <i>BMC Cancer</i> , 2021, 21, 1331.	1.1	6
23701	Transcriptome Analysis of Large to Giant Congenital Melanocytic Nevus Reveals Cell Cycle Arrest and Immune Evasion: Identifying Potential Targets for Treatment. <i>Journal of Immunology Research</i> , 2021, 2021, 1-16.	0.9	1
23702	Comparative Genomic Study of Vinyl Chloride Cluster and Description of Novel Species, <i>Mycolicibacterium vinylchloridicum</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 767895.	1.5	2
23704	In Silico Investigation of the Biological Implications of Complex DNA Damage with Emphasis in Cancer Radiotherapy through a Systems Biology Approach. <i>Molecules</i> , 2021, 26, 7602.	1.7	2
23705	Cross-Kingdom Gene Coexpression Analysis Using <i>Stemphylium botryosum</i> "Lens ervoides" System Revealed Plasticity of Intercommunication Between the Pathogen Secretome and the Host Immune Systems. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1365-1377.	1.4	1
23707	In Vitro Study of Licorice on IL-1 <sup>Î²</sup> -Induced Chondrocytes and In Silico Approach for Osteoarthritis. <i>Pharmaceuticals</i> , 2021, 14, 1337.	1.7	8
23708	Recent Duplications Dominate VQ and WRKY Gene Expansions in Six Prunus Species. <i>International Journal of Genomics</i> , 2021, 2021, 1-16.	0.8	3
23709	An Interplay between Viruses and Bacteria Associated with the White Sea Sponges Revealed by Metagenomics. <i>Life</i> , 2022, 12, 25.	1.1	3



#	ARTICLE	IF	CITATIONS
23710	Modulation of TCR signalling components occurs prior to positive selection and lineage commitment in iNKT cells. <i>Scientific Reports</i> , 2021, 11, 23650.	1.6	2
23711	Identification of Novel Biomarkers for Predicting Prognosis and Immunotherapy Response in Head and Neck Squamous Cell Carcinoma Based on ceRNA Network and Immune Infiltration Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-42.	0.9	9
23713	Single-Larva RNA Sequencing Identifies Markers of Copper Toxicity and Exposure in Early <i>Mytilus californianus</i> Larvae. <i>Frontiers in Physiology</i> , 2021, 12, 647482.	1.3	1
23714	Differentially Expressed lncRNAs Related to the Development of Abdominal Fat in Gushi Chickens and Their Interaction Regulatory Network. <i>Frontiers in Genetics</i> , 2021, 12, 802857.	1.1	5
23715	Cholesterol Depletion Modulates Drug Resistance Pathways to Sensitize Resistant Breast Cancer Cells to Tamoxifen. <i>Anticancer Research</i> , 2022, 42, 565-579.	0.5	6
23716	Roles of ERR $\alpha$ and TGF $\beta$ signaling in stemness enhancement induced by 1-M bisphenol A exposure via human neural stem cells. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 164.	0.8	4
23719	Comparative transcriptome and metabolome analysis reveal glutathione metabolic network and functional genes underlying blue and red-light mediation in maize seedling leaf. <i>BMC Plant Biology</i> , 2021, 21, 593.	1.6	8
23720	Overexpression of SKA3 correlates with poor prognosis in female early breast cancer. <i>PeerJ</i> , 2021, 9, e12506.	0.9	2
23721	An interferon-related signature characterizes the whole blood transcriptome profile of insulin-resistant individuals—the CODAM study. <i>Genes and Nutrition</i> , 2021, 16, 22.	1.2	3
23722	Diverse Single-Stranded DNA Viruses Identified in Chicken Buccal Swabs. <i>Microorganisms</i> , 2021, 9, 2602.	1.6	6
23723	Host Factor Interaction Networks Identified by Integrative Bioinformatics Analysis Reveals Therapeutic Implications in COPD Patients With COVID-19. <i>Frontiers in Pharmacology</i> , 2021, 12, 718874.	1.6	1
23724	Ternate Chinese Medicines Alleviate Joint Pain via Inhibiting Rheumatoid Arthritis Pathway. , 2021, , .		0
23725	Comparative genomic analysis of expansin superfamily gene members in zucchini and cucumber and their expression profiles under different abiotic stresses. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2739-2756.	1.4	5
23726	Single cell sequencing analysis identifies genetics-modulated ORMDL3+ cholangiocytes having higher metabolic effects on primary biliary cholangitis. <i>Journal of Nanobiotechnology</i> , 2021, 19, 406.	4.2	16
23727	Identification of Cross-Talk and Pyroptosis-Related Genes Linking Periodontitis and Rheumatoid Arthritis Revealed by Transcriptomic Analysis. <i>Disease Markers</i> , 2021, 2021, 1-29.	0.6	6
23728	Genome-wide analysis uncovers tomato leaf lncRNAs transcriptionally active upon <i>Pseudomonas syringae</i> pv. tomato challenge. <i>Scientific Reports</i> , 2021, 11, 24523.	1.6	8
23729	Genetic Basis of Follicle Development in Dazu Black Goat by Whole-Transcriptome Sequencing. <i>Animals</i> , 2021, 11, 3536.	1.0	4
23730	A regulatory miRNA-mRNA network is associated with transplantation response in acute kidney injury. <i>Human Genomics</i> , 2021, 15, 69.	1.4	4

#	ARTICLE	IF	CITATIONS
23731	Comprehensive analysis of the ceRNA network in coronary artery disease. <i>Scientific Reports</i> , 2021, 11, 24279.	1.6	7
23732	Establishment of Human Pluripotent Stem Cell-Derived Skin Organoids Enabled Pathophysiological Model of SARS-CoV-2 Infection. <i>Advanced Science</i> , 2022, 9, e2104192.	5.6	18
23733	Phylogenomic and Microsynteny Analysis Provides Evidence of Genome Arrangements of High-Affinity Nitrate Transporter Gene Families of Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13036.	1.8	6
23734	Chromatin-contact atlas reveals disorder-mediated protein interactions and moonlighting chromatin-associated RBPs. <i>Nucleic Acids Research</i> , 2021, 49, 13092-13107.	6.5	9
23735	Insights into the Host-Pathogen Interaction Pathways through RNA-Seq Analysis of <i>Lens culinaris</i> Medik. in Response to <i>Rhizoctonia bataticola</i> Infection. <i>Genes</i> , 2022, 13, 90.	1.0	18
23736	Comprehensive Analysis of the Effects of Genetic Ancestry and Genetic Characteristics on the Clinical Evolution of Oral Squamous Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 678464.	1.8	0
23737	Differentially Expressed Extracellular Vesicle, Exosome and Non-Exosome miRNA Profile in High and Low Tick-Resistant Beef Cattle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 780424.	1.8	5
23738	Improving Analysis and Annotation of Microarray Data with Protein Interactions. <i>Methods in Molecular Biology</i> , 2022, 2401, 51-68.	0.4	0
23739	Identifying functional evolution processes of cancer according to regression residuals network. , 2021, , .		0
23740	Exploration of the Potential Mechanisms of Wumei Pill for the Treatment of Ulcerative Colitis by Network Pharmacology. <i>Gastroenterology Research and Practice</i> , 2021, 2021, 1-15.	0.7	8
23741	Discovery of Novel Cyclic Ethers with Synergistic Antiplasmodial Activity in Combination with Valinomycin. <i>Molecules</i> , 2021, 26, 7494.	1.7	2
23742	Using RNA-Seq to Investigate Immune-Metabolism Features in Immunocompromised Patients With Sepsis. <i>Frontiers in Medicine</i> , 2021, 8, 747263.	1.2	6
23743	Microbial Eukaryotes Associated With Sediments in Deep-Sea Cold Seeps. <i>Frontiers in Microbiology</i> , 2021, 12, 782004.	1.5	8
23744	Synaptic Protein Phosphorylation Networks Are Associated With Electroacupuncture-Induced Circadian Control in the Suprachiasmatic Nucleus. <i>Frontiers in Genetics</i> , 2021, 12, 762557.	1.1	1
23745	Single-cell transcriptome atlas of human mesenchymal stem cells exploring cellular heterogeneity. <i>Clinical and Translational Medicine</i> , 2021, 11, e650.	1.7	49
23746	A cis-regulatory-directed pipeline for the identification of genes involved in cardiac development and disease. <i>Genome Biology</i> , 2021, 22, 335.	3.8	4
23747	Comprehensive Annotation and Functional Exploration of MicroRNAs in Lettuce. <i>Frontiers in Plant Science</i> , 2021, 12, 781836.	1.7	7
23748	The brown root rot fungus <i>Phellinus noxius</i> affects microbial communities in different root-associated niches of <i>Ficus</i> trees. <i>Environmental Microbiology</i> , 2022, 24, 276-297.	1.8	7

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23749	Whole Genome Methylation Analysis Reveals Role of DNA Methylation in Cow's Ileal and Ileal Lymph Node Responses to Mycobacterium avium subsp. paratuberculosis Infection. <i>Frontiers in Genetics</i> , 2021, 12, 797490.	1.1	3
23750	Establishment of Sunitinib-Resistant Xenograft Model of Renal Cell Carcinoma and the Identification of Drug-Resistant Hub Genes and Pathways. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 5061-5074.	2.0	8
23751	Characterization of the Role of Extracellular Vesicles Released from Chicken Tracheal Cells in the Antiviral Responses against Avian Influenza Virus. <i>Membranes</i> , 2022, 12, 53.	1.4	2
23752	Rheum tanguticum Alleviates Cognitive Impairment in APP/PS1 Mice by Regulating Drug-Responsive Bacteria and Their Corresponding Microbial Metabolites. <i>Frontiers in Pharmacology</i> , 2021, 12, 766120.	1.6	1
23753	Screening and Identification of Muscle-Specific Candidate Genes via Mouse Microarray Data Analysis. <i>Frontiers in Veterinary Science</i> , 2021, 8, 794628.	0.9	3
23754	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. <i>Plant Journal</i> , 2022, 109, 1614-1629.	2.8	4
23755	Spinal Muscular Atrophy Patient iPSC-Derived Motor Neurons Display Altered Proteomes at Early Stages of Differentiation. <i>ACS Omega</i> , 2021, 6, 35375-35388.	1.6	9
23756	A novel circRNA-miRNA-mRNA network reveals hsa-circ-0040039 as a biomarker for intervertebral disc degeneration. <i>Journal of International Medical Research</i> , 2021, 49, 030006052096098.	0.4	3
23757	Systems biology and machine learning approaches identify drug targets in diabetic nephropathy. <i>Scientific Reports</i> , 2021, 11, 23452.	1.6	6
23758	Comprehensive Analysis of the Prognostic Values of the TRIM Family in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 767644.	1.3	16
23759	Bioinformatics analysis of long non-coding RNA-associated competing endogenous RNA network in schizophrenia. <i>Scientific Reports</i> , 2021, 11, 24413.	1.6	13
23760	Transcriptome Analysis Reveals Candidate Genes Regulating the Skin and Hair Diversity of Xinji Fine-Wool Sheep and Tan Sheep. <i>Agriculture (Switzerland)</i> , 2022, 12, 15.	1.4	3
23761	Rapid Androgen-Responsive Proteome Is Involved in Prostate Cancer Progression. <i>Biomedicines</i> , 2021, 9, 1877.	1.4	3
23762	Capturing a Comprehensive Picture of Biological Events From Adverse Outcome Pathways in the Drug Exposome. <i>Frontiers in Public Health</i> , 2021, 9, 763962.	1.3	2
23764	Trophoblast glycoprotein is a new candidate gene for Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2021, 7, 110.	2.5	2
23765	Arabidopsis thaliana Plant Natriuretic Peptide Active Domain Forms Amyloid-like Fibrils in a pH-Dependent Manner. <i>Plants</i> , 2022, 11, 9.	1.6	2
23766	Identifying biomarkers for evaluating wound extent and age in the contused muscle of rats using microarray analysis: a pilot study. <i>PeerJ</i> , 2021, 9, e12709.	0.9	1
23767	The Diversity, Metabolomics Profiling, and the Pharmacological Potential of Actinomycetes Isolated from the Estremadura Spur Pockmarks (Portugal). <i>Marine Drugs</i> , 2022, 20, 21.	2.2	8

#	ARTICLE	IF	CITATIONS
23768	Proteomic Response of <i>Deinococcus radiodurans</i> to Short-Term Real Microgravity during Parabolic Flight Reveals Altered Abundance of Proteins Involved in Stress Response and Cell Envelope Functions. <i>Life</i> , 2022, 12, 23.	1.1	1
23769	Integrative Bioinformatics Analysis Revealed Mitochondrial Defects Underlying Hypoplastic Left Heart Syndrome. <i>International Journal of General Medicine</i> , 2021, Volume 14, 9747-9760.	0.8	1
23770	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. <i>Environmental Microbiomes</i> , 2021, 16, 24.	2.2	36
23771	phytanoyl-CoA dioxygenase domain-containing protein 1 plays an important role in egg shell formation of silkworm ( <i>Bombyx mori</i> ). <i>PLoS ONE</i> , 2021, 16, e0261918.	1.1	1
23772	HPV16-LINC00393 Integration Alters Local 3D Genome Architecture in Cervical Cancer Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 785169.	1.8	8
23773	The prognostic value of plasma complement factor B (CFB) in thyroid carcinoma. <i>Bioengineered</i> , 2021, 12, 12854-12866.	1.4	10
23774	New Mutations in HFE2 and TFR2 Genes Causing Non HFE-Related Hereditary Hemochromatosis. <i>Genes</i> , 2021, 12, 1980.	1.0	4
23775	Network Pharmacology-Based Investigation and Experimental Exploration of the Antiapoptotic Mechanism of Colchicine on Myocardial Ischemia Reperfusion Injury. <i>Frontiers in Pharmacology</i> , 2021, 12, 804030.	1.6	10
23776	Integrated Isoform Sequencing and Dynamic Transcriptome Analysis Reveals Diverse Transcripts Responsible for Low Temperature Stress at Anther Meiosis Stage in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 795834.	1.7	5
23777	GENPPI: standalone software for creating protein interaction networks from genomes. <i>BMC Bioinformatics</i> , 2021, 22, 596.	1.2	1
23778	Reassortment Network of Influenza A Virus. <i>Frontiers in Microbiology</i> , 2021, 12, 793500.	1.5	6
23779	Plasma Exosomal Mir-423-5p Is Involved in the Occurrence and Development of Bicuspid Aortopathy via TGF- $\beta$ 2/SMAD2 Pathway. <i>Frontiers in Physiology</i> , 2021, 12, 759035.	1.3	10
23780	Small molecules for cell reprogramming: a systems biology analysis. <i>Aging</i> , 2021, 13, 25739-25762.	1.4	8
23783	Identification of ferroptosis-related genes as potential biomarkers of tongue squamous cell carcinoma using an integrated bioinformatics approach. <i>FEBS Open Bio</i> , 2022, 12, 412-429.	1.0	4
23784	Mechanism of Elian granules in the treatment of precancerous lesions of gastric cancer in rats through the MAPK signalling pathway based on network pharmacology. <i>Pharmaceutical Biology</i> , 2022, 60, 87-95.	1.3	12
23785	CASP5 and CR1 as potential biomarkers for Kawasaki disease: an Integrated Bioinformatics-Experimental Study. <i>BMC Pediatrics</i> , 2021, 21, 566.	0.7	5
23786	The Anti-atherosclerosis Protein Regulation Network Delivered by Onion Quercetin. , 2021, , .		0
23789	Transcriptome Profiling of Atlantic Salmon ( <i>Salmo salar</i> ) Parr With Higher and Lower Pathogen Loads Following <i>Piscirickettsia salmonis</i> Infection. <i>Frontiers in Immunology</i> , 2021, 12, 789465.	2.2	11

#	ARTICLE	IF	CITATIONS
23790	Ferroptosis-Related Long Non-Coding RNA Signature Contributes to the Prediction of Prognosis Outcomes in Head and Neck Squamous Cell Carcinomas. <i>Frontiers in Genetics</i> , 2021, 12, 785839.	1.1	14
23792	BuYang-HuanWu-Tang Alleviates Rheumatoid Arthritisâ€™ Hypoxia via BNIP3 and PI3K/ATK. , 2021, , .		2
23793	Metabolic syndrome related gene signature predicts the prognosis of patients with pancreatic ductal carcinoma. A novel link between metabolic dysregulation and pancreatic ductal carcinoma. <i>Cancer Cell International</i> , 2021, 21, 698.	1.8	3
23794	SIGNORApp: a Cytoscape 3 application to access SIGNOR data. <i>Bioinformatics</i> , 2022, 38, 1764-1766.	1.8	7
23795	Salivary and Intestinal Transcriptomes Reveal Differential Gene Expression in Starving, Fed and Trypanosoma cruzi-Infected Rhodnius neglectus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 773357.	1.8	1
23796	Visualizing Phytochemical-Protein Interaction Networks: Momordica charantia and Cancer. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	0
23797	Integral Analyses of Competing Endogenous RNA Mechanisms and DNA Methylation Reveal Regulatory Mechanisms in Osteosarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 763347.	1.8	3
23798	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 736797.	1.7	1
23799	Proteogenic Dipeptides Are Characterized by Diel Fluctuations and Target of Rapamycin Complex-Signaling Dependency in the Model Plant Arabidopsis thaliana. <i>Frontiers in Plant Science</i> , 2021, 12, 758933.	1.7	3
23800	Weighted Gene Correlation Network Analysis Identifies Specific Functional Modules and Genes in Esophageal Cancer. <i>Journal of Oncology</i> , 2021, 2021, 1-13.	0.6	6
23801	Microbial diversity and function in crystalline basement beneath the Deccan Traps explored in a 3 km borehole at Koyna, western India. <i>Environmental Microbiology</i> , 2022, 24, 2837-2853.	1.8	7
23802	Protective Effects of Dexmedetomidine on Sepsis-Induced Vascular Leakage by Alleviating Ferroptosis via Regulating Metabolic Reprogramming. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 6765-6782.	1.6	26
23803	Overexpression of microRNAs miR-25-3p, miR-185-5p and miR-132-3p in Late Onset Fetal Growth Restriction, Validation of Results and Study of the Biochemical Pathways Involved. <i>International Journal of Molecular Sciences</i> , 2022, 23, 293.	1.8	2
23804	\$\$\$ext{COSNet}}_i\$\$\$: ComplexOme-Structural Network Interpreter used to study spatial enrichment in metazoan ribosomes. <i>BMC Bioinformatics</i> , 2021, 22, 605.	1.2	2
23805	Comprehensive DNA Methylation Analysis of Human Neuroblastoma Cells Treated With Haloperidol and Risperidone. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 792874.	1.4	4
23806	Epithelialâ€™Mesenchymal Transition Participates in the Formation of Vestibular Flat Epithelium. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 809878.	1.4	0
23807	Potential Anti-Obesity, Anti-Steatosis, and Anti-Inflammatory Properties of Extracts from the Microalgae Chlorella vulgaris and Chlorococcum amblyostomatis under Different Growth Conditions. <i>Marine Drugs</i> , 2022, 20, 9.	2.2	12
23808	Understanding of the Site-Specific Microbial Patterns towards Accurate Identification for Patients with Diarrhea-Predominant Irritable Bowel Syndrome. <i>Microbiology Spectrum</i> , 2021, 9, e0125521.	1.2	7

#	ARTICLE	IF	CITATIONS
23810	Metabolomic Signatures for the Effects of Weight Loss Interventions on Severe Obesity in Children and Adolescents. <i>Metabolites</i> , 2022, 12, 27.	1.3	11
23811	Key Phytochemicals and Biological Functions of Chuanxiong Rhizoma Against Ischemic Stroke: A Network Pharmacology and Experimental Assessment. <i>Frontiers in Pharmacology</i> , 2021, 12, 758049.	1.6	15
23814	Analysis of N6-Methyladenosine Methylation Modification in Fructose-Induced Non-Alcoholic Fatty Liver Disease. <i>Frontiers in Endocrinology</i> , 2021, 12, 780617.	1.5	18
23815	The establishment of a hub differential gene model to predict prognosis in stage II and III right- and left-sided colon cancer patients. <i>Annals of Translational Medicine</i> , 2021, 9, 1763-1763.	0.7	1
23817	Identification of transcriptional regulatory network associated with response of host epithelial cells to SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 23928.	1.6	2
23818	Development of a novel necroptosis-associated miRNA risk signature to evaluate the prognosis of colon cancer patients. <i>Annals of Translational Medicine</i> , 2021, 9, 1800-1800.	0.7	13
23819	Integrated Gene Expression Profiling Analysis Reveals Potential Molecular Mechanisms and Candidate Biomarkers for Early Risk Stratification and Prediction of STEMI and Post-STEMI Heart Failure Patients. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 736497.	1.1	9
23820	Transcriptomic Analysis of Human Na <sup>+</sup> -ve and Primed Pluripotent Stem Cells. <i>Methods in Molecular Biology</i> , 2022, 2416, 213-237.	0.4	3
23821	Efficient Proximal Gradient Algorithms for Joint Graphical Lasso. <i>Entropy</i> , 2021, 23, 1623.	1.1	0
23822	CD82 protects against glaucomatous axonal transport deficits via mTORC1 activation in mice. <i>Cell Death and Disease</i> , 2021, 12, 1149.	2.7	7
23823	Molecular Networking for Drug Toxicities Studies: The Case of Hydroxychloroquine in COVID-19 Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 82.	1.8	11
23824	Effects of Neck-Arm Restraint Suspension of Beef Carcasses on Meat Quality and Proteome of Different Muscles During Post-mortem Aging. <i>Frontiers in Nutrition</i> , 2021, 8, 774529.	1.6	2
23825	Genome-Wide Identification and Characterization of Melon bHLH Transcription Factors in Regulation of Fruit Development. <i>Plants</i> , 2021, 10, 2721.	1.6	11
23826	SNP-Based Analysis Reveals Authenticity and Genetic Similarity of Russian Indigenous <i>V. vinifera</i> Grape Cultivars. <i>Plants</i> , 2021, 10, 2696.	1.6	4
23827	Development of a Personalized Intestinal Fibrosis Model Using Human Intestinal Organoids Derived From Induced Pluripotent Stem Cells. <i>Inflammatory Bowel Diseases</i> , 2022, 28, 667-679.	0.9	9
23828	Impact of Qi-Invigorating Traditional Chinese Medicines on Diffuse Large B Cell Lymphoma Based on Network Pharmacology and Experimental Validation. <i>Frontiers in Pharmacology</i> , 2021, 12, 787816.	1.6	5
23829	Structural and functional characterization of fosfomycin resistance conferred by <i>FosB</i> from <i>Enterococcus faecium</i> . <i>Protein Science</i> , 2022, 31, 580-590.	3.1	5
23830	Gut Microbiome-Based Diagnostic Model to Predict Diabetes Mellitus. <i>Bioengineered</i> , 2021, 12, 12521-12534.	1.4	16



#	ARTICLE	IF	CITATIONS
23831	Network Pharmacology and Molecular Docking Analyses of Mechanisms Underlying Effects of the Cyperi Rhizoma-Chuanxiong Rhizoma Herb Pair on Depression. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	7
23832	Oral Hsp90 inhibitor SNX-5422 attenuates SARS-CoV-2 replication and dampens inflammation in airway cells. IScience, 2021, 24, 103412.	1.9	20
23833	Characterization of Changes and Driver Microbes in Gut Microbiota During Healthy Aging Using A Captive Monkey Model. Genomics, Proteomics and Bioinformatics, 2022, 20, 350-365.	3.0	17
23834	Whole genome sequencing-based copy number variations reveal novel pathways and targets in Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1846-1867.	0.4	13
23835	A comprehensive characterization of the transcriptome in enzalutamide resistance prostate cancer. Annals of Translational Medicine, 2021, 9, 1782-1782.	0.7	0
23836	Identification of potential druggable targets of cell cycle with small-molecule inhibitors in oral squamous cell carcinoma. Pharmacogenetics and Genomics, 2021, Publish Ahead of Print, .	0.7	3
23837	FvMYB79 Positively Regulates Strawberry Fruit Softening via Transcriptional Activation of FvPME38. International Journal of Molecular Sciences, 2022, 23, 101.	1.8	15
23838	Developing metabolic gene signatures to predict intrahepatic cholangiocarcinoma prognosis and mining a miRNA regulatory network. Journal of Clinical Laboratory Analysis, 2022, 36, e24107.	0.9	5
23839	Emerging roles of circRNAs in regulating thermal and hypoxic stresses in <i>Apostichopus japonicus</i> (Echinodermata: Holothuroidea). Ecotoxicology and Environmental Safety, 2021, 228, 112994.	2.9	5
23840	Bacterial and Fungal Microbiota of Guinea Grass Silage Shows Various Levels of Acetic Acid Fermentation. Fermentation, 2022, 8, 10.	1.4	5
23841	Transcriptome analysis of transgenic apple fruit overexpressing microRNA172 reveals candidate transcription factors regulating apple fruit development at early stages. PeerJ, 2021, 9, e12675.	0.9	3
23842	Long non-coding RNA-associated competing endogenous RNA axes in the olfactory epithelium in schizophrenia: a bioinformatics analysis. Scientific Reports, 2021, 11, 24497.	1.6	9
23843	Multi-omic analysis in injured humans: Patterns align with outcomes and treatment responses. Cell Reports Medicine, 2021, 2, 100478.	3.3	35
23844	Graph Theoretic Approach for the Analysis of Comprehensive Mass-Spectrometry (MS/MS) Data of Dissolved Organic Matter. , 2021, 2021, 3742-3746.		1
23845	Mobilization of vitamin B12 transporters alters competitive dynamics in a human gut microbe. Cell Reports, 2021, 37, 110164.	2.9	8
23847	Integrative Study of the Structural and Dynamical Properties of a KirBac3.1 Mutant: Functional Implication of a Highly Conserved Tryptophan in the Transmembrane Domain. International Journal of Molecular Sciences, 2022, 23, 335.	1.8	0
23848	<i>Lactobacillus lactis</i> and <i>Pediococcus pentosaceus</i> -driven reprogramming of gut microbiome and metabolome ameliorates the progression of non-alcoholic fatty liver disease. Clinical and Translational Medicine, 2021, 11, e634.	1.7	56
23849	Preventive Effect of Anemarrhenae rhizome and Phellodendri cortex on Danazol-Induced in Precocious Puberty in Female Rats and Network Pharmacological Analysis of Active Compounds. Plants, 2022, 11, 23.	1.6	2

#	ARTICLE	IF	CITATIONS
23850	18:0 Lyso PC Derived by Bioactivity-Based Molecular Networking from Lentil Mutant Lines and Its Effects on High-Fat Diet-Induced Obese Mice. <i>Molecules</i> , 2021, 26, 7547.	1.7	2
23851	Structures of Endocrine-Disrupting Chemicals Correlate with the Activation of 12 Classic Nuclear Receptors. <i>Environmental Science &amp; Technology</i> , 2021, 55, 16552-16562.	4.6	20
23852	Composition and Function of Bacterial Communities of Bryophytes and Their Underlying Sediments in the Dajiuhu Peatland, Central China. <i>Journal of Earth Science (Wuhan, China)</i> , 2023, 34, 133-144.	1.1	3
23855	miRModuleNet: Detecting miRNA-mRNA Regulatory Modules. <i>Frontiers in Genetics</i> , 2022, 13, 767455.	1.1	16
23856	Interactome of SARS-CoV-2 Modulated Host Proteins With Computationally Predicted PPIs: Insights From Translational Systems Biology Studies. <i>Frontiers in Systems Biology</i> , 2022, 2, .	0.5	6
23857	Identification of significant genes with a poor prognosis in skin cutaneous malignant melanoma based on a bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2022, 10, 448-448.	0.7	4
23858	Systems bioinformatic approach to determine the pharmacological mechanisms of radix astragali and radix angelicae sinensis in idiopathic pulmonary fibrosis. <i>Pharmacognosy Magazine</i> , 2021, 17, 708.	0.3	1
23859	Visualising Metabolic Pathways and Networks: Past, Present, Future. , 2022, , 237-267.		2
23860	Proteomic analysis of serum in workers exposed to diesel engine exhaust. <i>Environmental and Molecular Mutagenesis</i> , 2022, 63, 18-28.	0.9	4
23861	Interference With ACSL1 Gene in Bovine Adipocytes: Transcriptome Profiling of mRNA and lncRNA Related to Unsaturated Fatty Acid Synthesis. <i>Frontiers in Veterinary Science</i> , 2021, 8, 788316.	0.9	4
23862	SimPlot++: a Python application for representing sequence similarity and detecting recombination. <i>Bioinformatics</i> , 2022, 38, 3118-3120.	1.8	28
23863	Scan of the endogenous retrovirus sequences across the swine genome and survey of their copy number variation and sequence diversity among various Chinese and Western pig breeds. <i>Zoological Research</i> , 2022, 43, 423-441.	0.9	5
23864	BioUMLâ€”towards a universal research platform. <i>Nucleic Acids Research</i> , 2022, 50, W124-W131.	6.5	10
23865	Drug Repurposing for Identification of S1P1 agonists with Potential Application in Multiple Sclerosis Using in Silico Drug Design Approaches. <i>Advanced Pharmaceutical Bulletin</i> , 2022, , .	0.6	2
23866	Artificial Selection on Cis-Element of Abl Contributes Cocoon Yield Increase in Domestic Silkworm. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
23867	DEMA: a distance-bounded energy-field minimization algorithm to model and layout biomolecular networks with quantitative features. <i>Bioinformatics</i> , 2022, 38, i359-i368.	1.8	0
23868	Intestinal microbiota signatures of clinical response and immune-related adverse events in melanoma patients treated with anti-PD-1. <i>Nature Medicine</i> , 2022, 28, 545-556.	15.2	167
23869	Dan-Shen-Yin Granules Prevent Hypoxia-Induced Pulmonary Hypertension via STAT3/HIF-1 $\beta$ /VEGF and FAK/AKT Signaling Pathways. <i>Frontiers in Pharmacology</i> , 2022, 13, 844400.	1.6	9

#	ARTICLE	IF	CITATIONS
23870	MicroRNAs in Leukemias: A Clinically Annotated Compendium. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3469.	1.8	7
23871	The Mitochondrial Routing of the Kv1.3 Channel. <i>Frontiers in Oncology</i> , 2022, 12, 865686.	1.3	9
23872	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. <i>PeerJ</i> , 2022, 10, e13084.	0.9	18
23874	Identification of potentially functional circular RNAs hsa_circ_0070934 and hsa_circ_0004315 as prognostic factors of hepatocellular carcinoma by integrated bioinformatics analysis. <i>Scientific Reports</i> , 2022, 12, 4933.	1.6	6
23875	Effect of differences in light source environment on transcriptome of leaf lettuce ( <i>Lactuca sativa</i> L.) to optimize cultivation conditions. <i>PLoS ONE</i> , 2022, 17, e0265994.	1.1	11
23876	m6A Regulator-Mediated RNA Methylation Modification Patterns are Involved in the Pathogenesis and Immune Microenvironment of Depression. <i>Frontiers in Genetics</i> , 2022, 13, 865695.	1.1	1
23877	Fecal DNA Virome Is Associated with the Development of Colorectal Neoplasia in a Murine Model of Colorectal Cancer. <i>Pathogens</i> , 2022, 11, 457.	1.2	7
23878	Plant and soil responses to grazing intensity drive changes in the soil microbiome in a desert steppe. <i>Plant and Soil</i> , 2023, 491, 219-237.	1.8	11
23879	Multiomics implicate gut microbiota in altered lipid and energy metabolism in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2022, 8, 39.	2.5	12
23880	Metagenomic Approaches to Explore the Quorum Sensing-Mediated Interactions Between Algae and Bacteria in Sequence Membrane Photo-Bioreactors. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 851376.	2.0	2
23881	Shifts of SARS-CoV-2 exposure settings in the transmission clusters of 2 epidemic waves in Hong Kong. <i>International Journal of Environmental Health Research</i> , 2023, 33, 911-923.	1.3	6
23882	Androgen conspires with the CD8 <sup>+</sup> T cell exhaustion program and contributes to sex bias in cancer. <i>Science Immunology</i> , 2022, 7, .	5.6	74
23883	Modular and mechanistic changes across stages of colorectal cancer. <i>BMC Cancer</i> , 2022, 22, 436.	1.1	3
23884	Transcriptomic and Drug Discovery Analyses Reveal Natural Compounds Targeting the KDM4 Subfamily as Promising Adjuvant Treatments in Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 860924.	1.1	2
23885	Mechanism of Jujube ( <i>Ziziphus jujuba</i> Mill.) Fruit in the Appetite Regulation Based on Network Pharmacology and Molecular Docking Method. <i>Contrast Media and Molecular Imaging</i> , 2022, 2022, 1-12.	0.4	5
23886	Identification and characterization of circular RNAs in <i>Longissimus dorsi</i> muscle tissue from two goat breeds using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2022, 297, 817-831.	1.0	7
23887	Abnormal global alternative RNA splicing in COVID-19 patients. <i>PLoS Genetics</i> , 2022, 18, e1010137.	1.5	21
23888	Best practices in metabarcoding of fungi: From experimental design to results. <i>Molecular Ecology</i> , 2022, 31, 2769-2795.	2.0	87

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23889	Molecular behavior and interactions with microbes during anaerobic degradation of bio-derived DOM in waste leachate. <i>Journal of Environmental Sciences</i> , 2023, 126, 174-183.	3.2	2
23891	The Leaf Microbiome of <i>Arabidopsis</i> Displays Reproducible Dynamics and Patterns throughout the Growing Season. <i>MBio</i> , 2022, 13, e0282521.	1.8	19
23892	Human Mesenchymal Stem Cell-Derived Miniature Joint System for Disease Modeling and Drug Testing. <i>Advanced Science</i> , 2022, 9, e2105909.	5.6	22
23893	Identification and Characterization of the Biosynthetic Pathway of the Sulfonolipid Capnine. <i>Biochemistry</i> , 2022, 61, 2861-2869.	1.2	4
23895	EpCAM as a Novel Biomarker for Survivals in Prostate Cancer Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 843604.	1.8	4
23896	A novel mitochondria-related gene signature for controlling colon cancer cell mitochondrial respiration and proliferation. <i>Human Cell</i> , 2022, 35, 1126-1139.	1.2	6
23897	Molecular networking and collision cross section prediction for structural isomer and unknown compound identification in plant metabolomics: a case study applied to <i>Zanthoxylum heitzii</i> extracts. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 4103-4118.	1.9	7
23898	Serum Antigenome Profiling Reveals Diagnostic Models for Rheumatoid Arthritis. <i>Frontiers in Immunology</i> , 2022, 13, 884462.	2.2	0
23899	Long-term artificial selection of Hanwoo (Korean) cattle left genetic signatures for the breeding traits and has altered the genomic structure. <i>Scientific Reports</i> , 2022, 12, 6438.	1.6	6
23901	Transcriptomic analysis to elucidate the response of <i>Apis mellifera</i> ligustica brain tissue to fluvalinate exposure. <i>Animal Biotechnology</i> , 2023, 34, 4175-4186.	0.7	1
23902	Mutation in <i>MCL1</i> predicted loop to helix structural transition stabilizes <i>MCL1</i> -Bax binding interaction favoring cancer cell survival. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1699-1713.	1.5	0
23904	Quantitative Lipidomic Analysis of Takotsubo Syndrome Patients' Serum. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 797154.	1.1	4
23905	Research and experimental verification of the molecular mechanism of berberine in improving premature ovarian failure based on network pharmacology. <i>Bioengineered</i> , 2022, 13, 9885-9900.	1.4	9
23906	Pangenome Evolution Reconciles Robustness and Instability of Rhizobial Symbiosis. <i>MBio</i> , 2022, 13, e0007422.	1.8	13
23907	Comprehensive Analysis of miRNA-Mediated Regulatory Network and Identification of Prognosis Biomarkers in Rectal Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 792984.	1.1	3
23908	TcdB of <i>Clostridioides difficile</i> Mediates RAS-Dependent Necrosis in Epithelial Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4258.	1.8	5
23910	Cancer Relevance of Human Genes. <i>Journal of the National Cancer Institute</i> , 2022, 114, 988-995.	3.0	2
23911	Variation in Soil Bacterial and Fungal Community Composition at Different Successional Stages of a Broad-Leaved Korean Pine Forest in the Lesser Hinggan Mountains. <i>Forests</i> , 2022, 13, 625.	0.9	11

#	ARTICLE	IF	CITATIONS
23912	Potential Inhibitors of CYP51 Enzyme in Dermatophytes by Red Sea Soft Coral <i>Nephthea</i> sp.: In Silico and Molecular Networking Studies. <i>ACS Omega</i> , 2022, 7, 13808-13817.	1.6	8
23915	Discovery of Novel Drug Candidates for Alzheimer's Disease by Molecular Network Modeling. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, 850217.	1.7	4
23916	A Novel Pyroptotic and Inflammatory Gene Signature Predicts the Prognosis of Cutaneous Melanoma and the Effect of Anticancer Therapies. <i>Frontiers in Medicine</i> , 2022, 9, 841568.	1.2	10
23917	Analysis of modular gene co-expression networks reveals molecular pathways underlying Alzheimer's disease and progressive supranuclear palsy. <i>PLoS ONE</i> , 2022, 17, e0266405.	1.1	3
23918	The <i>TbD1</i> Locus Mediates a Hypoxia-Induced Copper Response in <i>Mycobacterium bovis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 817952.	1.5	4
23919	Coding and non-coding co-expression network analysis identifies key modules and driver genes associated with precursor lesions of gastric cancer. <i>Genomics</i> , 2022, 114, 110370.	1.3	2
23920	Identification of tissue-specific microbial profile of esophageal squamous cell carcinoma by full-length 16S rDNA sequencing. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3215-3229.	1.7	10
23921	Network Pharmacology with Experimental Investigation of the Mechanisms of <i>Rhizoma Polygonati</i> against Prostate Cancer with Additional Herbzymatic Activity. <i>ACS Omega</i> , 2022, 7, 14465-14477.	1.6	9
23922	Identification and validation of candidate risk genes in endocytic vesicular trafficking associated with esophageal atresia and tracheoesophageal fistulas. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100107.	1.0	2
23923	The Euler characteristic and topological phase transitions in complex systems. <i>Journal of Physics Complexity</i> , 2022, 3, 025003.	0.9	3
23927	Microbial Ecology of Sulfur Biogeochemical Cycling at a Mesothermal Hot Spring Atop Northern Himalayas, India. <i>Frontiers in Microbiology</i> , 2022, 13, 848010.	1.5	6
23928	A draft genome of <i>Drung</i> cattle reveals clues to its chromosomal fusion and environmental adaptation. <i>Communications Biology</i> , 2022, 5, 353.	2.0	1
23929	Text-Mining Approach to Identify Hub Genes of Cancer Metastasis and Potential Drug Repurposing to Target Them. <i>Journal of Clinical Medicine</i> , 2022, 11, 2130.	1.0	5
23930	Untargeted Metabolomics Sheds Light on the Diversity of Major Classes of Secondary Metabolites in the Malpighiaceae Botanical Family. <i>Frontiers in Plant Science</i> , 2022, 13, 854842.	1.7	9
23931	Single-cell RNA sequencing coupled to TCR profiling of large granular lymphocyte leukemia T cells. <i>Nature Communications</i> , 2022, 13, 1982.	5.8	23
23932	High plasmidome diversity of extended-spectrum beta-lactam-resistant <i>Escherichia coli</i> isolates collected during one year in one community hospital. <i>Genomics</i> , 2022, 114, 110368.	1.3	5
23933	Identification of Functional CircRNA-miRNA-mRNA Regulatory Network in Dorsolateral Prefrontal Cortex Neurons of Patients With Cocaine Use Disorder. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 839233.	1.4	5
23934	Transcriptome Analysis of Schwann Cells at Various Stages of Myelination Implicates Chromatin Regulator <i>Sin3A</i> in Control of Myelination Identity. <i>Neuroscience Bulletin</i> , 2022, 38, 720-740.	1.5	5

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23935	The parameters determining hyperaccumulator rhizobacteria diversity depend on the study scale. <i>Science of the Total Environment</i> , 2022, 834, 155274.	3.9	4
23936	Identifying the shared genes and KEGG pathways of Resolvin D1-targeted network and osteoarthritis using bioinformatics. <i>Bioengineered</i> , 2022, 13, 9839-9854.	1.4	3
23937	Proteomics datasets of developing rat brain: Synaptic proteome and SUMO2/3-ylome. <i>Data in Brief</i> , 2022, 42, 108151.	0.5	2
23938	CD19 and POU2AF1 are Potential Immune-Related Biomarkers Involved in the Emphysema of COPD: On Multiple Microarray Analysis. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 2491-2507.	1.6	4
23939	Systems biology approach identifies key genes and related pathways in childhood obesity. <i>Gene</i> , 2022, , 146512.	1.0	3
23940	Perseus plugin "Metis" for metabolic-pathway-centered quantitative multi-omics data analysis for static and time-series experimental designs. <i>Cell Reports Methods</i> , 2022, 2, 100198.	1.4	0
23941	From Mouth to Brain: Distinct Supragingival Plaque Microbiota Composition in Cerebral Palsy Children With Caries. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 814473.	1.8	6
23942	Systematic identification and characterization of long noncoding RNAs (lncRNAs) during <i>Aedes albopictus</i> development. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010245.	1.3	6
23944	Pancreas Whole Tissue Transcriptomics Highlights the Role of the Exocrine Pancreas in Patients With Recently Diagnosed Type 1 Diabetes. <i>Frontiers in Endocrinology</i> , 2022, 13, 861985.	1.5	0
23945	Identifying Signal-Crosstalk Mechanism in Maize Plants during Combined Salinity and Boron Stress Using Integrative Systems Biology Approaches. <i>BioMed Research International</i> , 2022, 2022, 1-17.	0.9	6
23946	An interolog-based barley interactome as an integration framework for immune signaling. <i>Genetics</i> , 2022, 221, .	1.2	3
23947	Fungal dye-decolorizing peroxidase diversity: roles in either intra- or extracellular processes. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2993-3007.	1.7	3
23948	Integrated Analysis of Ferroptosis and Immunity-Related Genes Associated with Intestinal Ischemia/Reperfusion Injury. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 2397-2411.	1.6	7
23949	Analysis of botanicals and botanical supplements by LC-MS/MS-based molecular networking: Approaches for annotating plant metabolites and authentication. <i>FA-toterap-Å-Åç</i> , 2022, 159, 105200.	1.1	8
23950	Construction of a circRNA-Mediated ceRNA Network Reveals Novel Biomarkers for Aortic Dissection. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3951-3964.	0.8	3
23951	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, W345-W351.	6.5	328
23953	The Dysregulation of SOX Family Correlates with DNA Methylation and Immune Microenvironment Characteristics to Predict Prognosis in Hepatocellular Carcinoma. <i>Disease Markers</i> , 2022, 2022, 1-21.	0.6	5
23954	MAGI-MS: multiple seed-centric module discovery. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	0



#	ARTICLE	IF	CITATIONS
23955	Development an Immune-Related MicroRNA Risk Index in Hepatocellular Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-13.	0.6	0
23956	Genomic and Chemical Decryption of the Bacteroidetes Phylum for Its Potential to Biosynthesize Natural Products. <i>Microbiology Spectrum</i> , 2022, 10, e0247921.	1.2	11
23957	Systematic trait dissection in oilseed rape provides a comprehensive view, further insight, and exact roadmap for yield determination. , 2022, 15, 38.		1
23958	Network Pharmacology and Comparative Transcriptome Reveals Biotargets and Mechanisms of Curcumol Treating Lung Adenocarcinoma Patients With COVID-19. <i>Frontiers in Nutrition</i> , 2022, 9, 870370.	1.6	13
23959	Genome-wide analysis of the VQ motif-containing gene family and expression profiles during phytohormones and abiotic stresses in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2022, 23, 292.	1.2	14
23961	Rewiring of 3D Chromatin Topology Orchestrates Transcriptional Reprogramming and the Development of Human Dilated Cardiomyopathy. <i>Circulation</i> , 2022, 145, 1663-1683.	1.6	15
23962	Global Gene Expression and Docking Profiling of COVID-19 Infection. <i>Frontiers in Genetics</i> , 2022, 13, 870836.	1.1	9
23963	Response of Plant-Associated Microbiome to Plant Root Colonization by Exogenous Bacterial Endophyte in Perennial Crops. <i>Frontiers in Microbiology</i> , 2022, 13, 863946.	1.5	6
23966	Quiescent cancer cells resist T cell attack by forming an immunosuppressive niche. <i>Cell</i> , 2022, 185, 1694-1708.e19.	13.5	100
23968	Bronchial epithelium epithelial-mesenchymal plasticity forms aberrant basaloid-like cells in vitro. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 322, L822-L841.	1.3	4
23969	A Series of Genes for Predicting Responses to Anti-Tumor Necrosis Factor $\pm$ Therapy in Crohn's Disease. <i>Frontiers in Pharmacology</i> , 2022, 13, 870796.	1.6	3
23970	Network pharmacology and in vitro testing of Theobroma cacao extract's antioxidative activity and its effects on cancer cell survival. <i>PLoS ONE</i> , 2022, 17, e0259757.	1.1	4
23972	Screening of Immune-Related Genes and Predicting the Immunotherapeutic Effects of Formononetin in Breast Cancer: A Bioinformatics Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-12.	0.5	2
23974	Molecular Characteristics of m6A Regulators and Tumor Microenvironment Infiltration in Soft Tissue Sarcoma: A Gene-Based Study. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 846812.	2.0	2
23975	Sucrose addition directionally enhances bacterial community convergence and network stability of the shrimp culture system. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 22.	2.9	15
23976	Association of heat shock protein 8 with atopic march in a murine experimental model. <i>PeerJ</i> , 2022, 10, e13247.	0.9	0
23977	Bioinformatic Analyzes of the Association Between Upregulated Expression of JUN Gene via APOBEC-Induced FLG Gene Mutation and Prognosis of Cervical Cancer. <i>Frontiers in Medicine</i> , 2022, 9, 815450.	1.2	4
23979	A novel ceRNA-immunoregulatory axis based on immune cell infiltration in ulcerative colitis-associated colorectal carcinoma by integrated weighted gene co-expression network analysis. <i>BMC Gastroenterology</i> , 2022, 22, 188.	0.8	1

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23980	Platelets fine-tune effector responses of naïve CD4+ T cells via platelet factor 4-regulated transforming growth factor $\beta$ signaling. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 247.	2.4	4
23981	Short Linear Motifs (SLiMs) in $\alpha$ -Core-RxLR Effectors of <i>Phytophthora parasitica</i> var. <i>nicotianae</i> : a Case of PpRxLR1 Effector. <i>Microbiology Spectrum</i> , 2022, 10, e0177421.	1.2	1
23982	Wastewater surveillance of SARS-CoV-2 mutational profiles at a university and its surrounding community reveals a 20G outbreak on campus. <i>PLoS ONE</i> , 2022, 17, e0266407.	1.1	9
23983	Transcriptomic Data Meta-Analysis Sheds Light on High Light Response in <i>Arabidopsis thaliana</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4455.	1.8	7
23984	Global Transcriptomic Analysis of Bacteriophage-Host Interactions between a Kayvirus Therapeutic Phage and <i>Staphylococcus aureus</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0012322.	1.2	3
23986	Algorithm for the Pruning of Synthesis Graphs. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2226-2238.	2.5	0
23987	The Reaction Pathway of miR-30c-5p Activates Lipopolysaccharide Promoting the Course of Traumatic and Hemorrhagic Shock Acute Lung Injury. <i>BioMed Research International</i> , 2022, 2022, 1-7.	0.9	2
23988	Analysis of the Molecular Mechanism of <i>Evodia rutaecarpa</i> Fruit in the Treatment of Nasopharyngeal Carcinoma Using Network Pharmacology and Molecular Docking. <i>Journal of Healthcare Engineering</i> , 2022, 2022, 1-15.	1.1	2
23989	MoSBI: Automated signature mining for molecular stratification and subtyping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118210119.	3.3	3
23990	Manifestations of Alzheimer's disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90. <i>Scientific Reports</i> , 2022, 12, 6117.	1.6	12
23992	Construction and Comprehensive Analysis of ceRNA Networks and Tumor-Infiltrating Immune Cells in Hepatocellular Carcinoma With Vascular Invasion. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	2
23993	A Tau Pathogenesis-Based Network Pharmacology Approach for Exploring the Protections of Chuanxiong Rhizoma in Alzheimer's Disease. <i>Frontiers in Pharmacology</i> , 2022, 13, 877806.	1.6	10
23994	A natural genetic variation screen identifies insulin signaling, neuronal communication, and innate immunity as modifiers of hyperglycemia in the absence of <i>Sirt1</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, . .	0.8	2
23995	Xuanfei Baidu decoction attenuates intestinal disorders by modulating NF- $\kappa$ B pathway, regulating T cell immunity and improving intestinal flora. <i>Phytomedicine</i> , 2022, 101, 154100.	2.3	16
23996	Effect of Sample Transportation on the Proteome of Human Circulating Blood Extracellular Vesicles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4515.	1.8	11
23997	Molecular Liver Fingerprint Reflects the Seasonal Physiology of the Grey Mouse Lemur ( <i>Microcebus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	1
23999	Identifying Novel Osteoarthritis-Associated Genes in Human Cartilage Using a Systematic Meta-Analysis and a Multi-Source Integrated Network. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4395.	1.8	7
24000	Responses of Soil Microbial Communities and Networks to Precipitation Change in a Typical Steppe Ecosystem of the Loess Plateau. <i>Microorganisms</i> , 2022, 10, 817.	1.6	10

#	ARTICLE	IF	CITATIONS
24001	Identification of Common Hub Genes in Human Dermal Fibroblasts Stimulated by Mechanical Stretch at Both the Early and Late Stages. <i>Frontiers in Surgery</i> , 2022, 9, 846161.	0.6	2
24002	Prostanoid Signaling in Cancers: Expression and Regulation Patterns of Enzymes and Receptors. <i>Biology</i> , 2022, 11, 590.	1.3	2
24003	Mesenteric lymph system constitutes the second route in gut-liver axis and transports metabolism-modulating gut microbial metabolites. <i>Journal of Genetics and Genomics</i> , 2022, 49, 612-623.	1.7	3
24004	Gut mycobiome dysbiosis in rats showing retinal changes indicative of diabetic retinopathy. <i>PLoS ONE</i> , 2022, 17, e0267080.	1.1	2
24005	Jasmonates and Histone deacetylase 6 activate Arabidopsis genome-wide histone acetylation and methylation during the early acute stress response. <i>BMC Biology</i> , 2022, 20, 83.	1.7	5
24006	Prediction of Prophages and Their Host Ranges in Pathogenic and Commensal <i>Neisseria</i> Species. <i>MSystems</i> , 2022, 7, e0008322.	1.7	9
24007	Application of explainable artificial intelligence in the identification of Squamous Cell Carcinoma biomarkers. <i>Computers in Biology and Medicine</i> , 2022, 146, 105505.	3.9	23
24008	<i>mucG</i> , <i>mucH</i> and <i>mucL</i> Modulate Production of Mutanocyclin and Reutericyclins in <i>Streptococcus mutans</i> B04Sm5. <i>Journal of Bacteriology</i> , 2022, 204, e0004222.	1.0	4
24009	Identification of KIF23 as a Prognostic Biomarker Associated With Progression of Clear Cell Renal Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 839821.	1.8	3
24010	Integrated Analysis of Coding and Non-coding RNAs Reveals the Molecular Mechanism Underlying Salt Stress Response in <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 891361.	1.7	4
24011	A disease-driver population within interstitial cells of human calcific aortic valves identified via single-cell and proteomic profiling. <i>Cell Reports</i> , 2022, 39, 110685.	2.9	16
24012	Noncoding RNAs endogenously rule the cancerous regulatory realm while proteins govern the normal. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1935-1945.	1.9	2
24013	Differential regulation of intramuscular fat and abdominal fat deposition in chickens. <i>BMC Genomics</i> , 2022, 23, 308.	1.2	27
24015	Transcriptome and Proteome Analysis in LUHMES Cells Overexpressing Alpha-Synuclein. <i>Frontiers in Neurology</i> , 2022, 13, 787059.	1.1	9
24016	A Comprehensive Identification and Function Analysis of Serine/Arginine-Rich (SR) Proteins in Cotton ( <i>Gossypium</i> spp.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 4566.	1.8	4
24017	Insights Into Long Non-Coding RNA and mRNA Expression in the Jejunum of Lambs Challenged With <i>Escherichia coli</i> F17. <i>Frontiers in Veterinary Science</i> , 2022, 9, 819917.	0.9	4
24018	Identification and characterization of long non-coding RNAs in juvenile and adult skeletal muscle of largemouth bass ( <i>Micropterus salmoides</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2022, 261, 110748.	0.7	0
24020	Plasma Proteomic Profile of Patients with Tick-Borne Encephalitis and Co-Infections. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4374.	1.8	3

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24021	Impaired CD4+ T cell differentiation in HIV-1 infected patients receiving early anti-retroviral therapy. <i>Genomics</i> , 2022, 114, 110367.	1.3	2
24022	Characterising the tear bacterial microbiome in young adults. <i>Experimental Eye Research</i> , 2022, 219, 109080.	1.2	1
24023	Gene-environment interaction analysis of redox-related metals and genetic variants with plasma metabolic patterns in a general population from Spain: The Hortega Study. <i>Redox Biology</i> , 2022, 52, 102314.	3.9	9
24024	Statistics and network-based approaches to identify molecular mechanisms that drive the progression of breast cancer. <i>Computers in Biology and Medicine</i> , 2022, 145, 105508.	3.9	24
24025	CCDB: A database for exploring inter-chemical correlations in metabolomics and exposomics datasets. <i>Environment International</i> , 2022, 164, 107240.	4.8	4
24026	Unipartite and bipartite mycorrhizal networks of <i>Abies religiosa</i> forests: Incorporating network theory into applied ecology of conifer species and forest management. <i>Ecological Complexity</i> , 2022, 50, 101002.	1.4	3
24027	RNA sequence analysis identified bone morphogenetic protein-2 (BMP2) as a biomarker underlying form deprivation myopia. <i>Biochemistry and Biophysics Reports</i> , 2022, 30, 101261.	0.7	1
24028	Abundant microbial communities act as more sensitive bio-indicators for ecological evaluation of copper mine contamination than rare taxa in river sediments. <i>Environmental Pollution</i> , 2022, 305, 119310.	3.7	10
24029	Spindle and Kinetochores-Associated Complex Is Associated With Poor Prognosis in Adrenocortical Carcinoma. <i>Journal of Surgical Research</i> , 2022, 277, 50-59.	0.8	5
24030	Synergistic effect of bioanode and biocathode on nitrobenzene removal: Microbial community structure and functions. <i>Science of the Total Environment</i> , 2022, 833, 155190.	3.9	6
26875	Software Tools for Systems Biology: Visualizing the Outcomes of N Experiments on M Entities. , 0, 167-195.		0
26876	Network pharmacological prediction and molecular docking analysis of the combination of <i>Atractylodes macrocephala</i> Koidz. and <i>Paeonia lactiflora</i> Pall. in the treatment of functional constipation and its verification. <i>Animal Models and Experimental Medicine</i> , 2022, 5, 120-132.	1.3	9
26877	Proteomic-, Phosphoproteomic-, and Acetylotomic-Based Mass Spectrometry to Identify Tissue-Specific Protein Complexes and Phosphorylation in Plant Gametogenesis. <i>Methods in Molecular Biology</i> , 2022, 2484, 13-22.	0.4	0
26878	Characterization of the Myometrial Transcriptome of Long Non-coding RNA Genes in Human Labor by High-Throughput RNA-seq. <i>Reproductive Sciences</i> , 2022, 29, 2885-2893.	1.1	3
26879	<i>deCS</i> : A Tool for Systematic Cell Type Annotations of Single-Cell RNA Sequencing Data Among Human Tissues. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 370-384.	3.0	11
26880	Quantitative proteomics reveals key pathways in the symbiotic interface and the likely extracellular property of soybean symbiosome. <i>Journal of Genetics and Genomics</i> , 2023, 50, 7-19.	1.7	13
26881	Expanding the Accessible Chemical Space of SIRT2 Inhibitors through Exploration of Binding Pocket Dynamics. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2571-2585.	2.5	5
26882	Brominated Carbazole with Antibiotic Adjuvant Activity Displays Pleiotropic Effects in MRSA's Transcriptome. <i>ACS Chemical Biology</i> , 2022, 17, 1239-1248.	1.6	1

#	ARTICLE	IF	CITATIONS
26883	Genome-wide CRISPR screens identify GATA6 as a proviral host factor for SARS-CoV-2 via modulation of ACE2. <i>Nature Communications</i> , 2022, 13, 2237.	5.8	27
26884	Global analysis of biosynthetic gene clusters reveals conserved and unique natural products in entomopathogenic nematode-symbiotic bacteria. <i>Nature Chemistry</i> , 2022, 14, 701-712.	6.6	42
26885	Comparative analysis of long noncoding RNA and mRNA expression provides insights into adaptation to hypoxia in Tibetan sheep. <i>Scientific Reports</i> , 2022, 12, 6597.	1.6	3
26886	Comparison of transcriptome profiles of nucleated red blood cells in cord blood between preterm and full-term neonates. <i>Hematology</i> , 2022, 27, 263-273.	0.7	2
26887	Comprehensive bioinformatics analysis reveals the hub genes and pathways associated with multiple myeloma. <i>Hematology</i> , 2022, 27, 280-292.	0.7	6
26888	Multiomics Data Integration Identifies New Molecular Signatures for Abdominal Aortic Aneurysm and Aortic Occlusive Disease: Implications for Early Diagnosis, Prognosis, and Therapeutic Targets. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 290-304.	1.0	3
26889	Dawn and dusk peaks of outer segment phagocytosis, and visual cycle function require Rab28. <i>FASEB Journal</i> , 2022, 36, e22309.	0.2	6
26890	Molecular Mechanism of Sevoflurane Preconditioning Based on Whole-transcriptome Sequencing of Lipopolysaccharide-induced Cardiac Dysfunction in Mice. <i>Journal of Cardiovascular Pharmacology</i> , 2022, 79, 846-857.	0.8	6
26891	Comprehensive analysis of microRNAs and their target genes in oral submucous fibrosis. <i>Oral Diseases</i> , 2023, 29, 1894-1904.	1.5	1
26892	FoxP3 associates with enhancer-promoter loops to regulate T-specific gene expression.. <i>Science Immunology</i> , 2022, 7, eabj9836.	5.6	12
26893	Comparative transcriptome analysis of experimental cryptorchidism: Of mice and cynomolgus monkeys. <i>Physiological Genomics</i> , 2022, , .	1.0	0
26894	Therapeutic Targeting of EZH2 and BET BRD4 in Pediatric Rhabdoid Tumors. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 715-726.	1.9	11
26895	Proteomic profiling of kidney samples in patients with pure membranous and proliferative lupus nephritis. <i>Lupus</i> , 2022, 31, 837-847.	0.8	2
26896	Effects of growth years on ginsenoside biosynthesis of wild ginseng and cultivated ginseng. <i>BMC Genomics</i> , 2022, 23, 325.	1.2	18
26897	Identification of the potential biological target molecules related to primary open-angle glaucoma. <i>BMC Ophthalmology</i> , 2022, 22, 188.	0.6	8
26898	Screening the components of <i>Saussurea involucreata</i> for novel targets for the treatment of NSCLC using network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 53.	1.2	6
26899	Integrative analysis of eQTL and GWAS summary statistics reveals transcriptomic alteration in Alzheimer brains. <i>BMC Medical Genomics</i> , 2022, 15, 93.	0.7	2
26900	Large-scale discovery of novel neurodevelopmental disorder-related genes through a unified analysis of single-nucleotide and copy number variants. <i>Genome Medicine</i> , 2022, 14, 40.	3.6	13

#	ARTICLE	IF	CITATIONS
26902	Monitoring of inflammation using novel biosensor mouse model reveals tissue- and sex-specific responses to Western diet. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	2
26903	Cytoscape tools for the web age: D3.js and Cytoscape.js exporters. <i>F1000Research</i> , 2014, 3, 143.	0.8	18
26904	Using citation network analysis to enhance scholarship in psychological science: A case study of the human aggression literature. <i>PLoS ONE</i> , 2022, 17, e0266513.	1.1	1
26905	Up-regulation of GINS1 highlighted a good diagnostic and prognostic potential of survival in three different subtypes of human cancer. <i>Brazilian Journal of Biology</i> , 2021, 84, e250575.	0.4	7
26906	Visualization of a curated L. CDPKs Protein-Protein Interaction Network CDPK-OsPPIN.. <i>MicroPublication Biology</i> , 2022, 2022, .	0.1	0
26911	Integrative systems biology visualization with MAYDAY. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	9
26912	Prediction of thioredoxin and glutaredoxin target proteins by identifying reversibly oxidized cysteinyl residues. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	6
26915	Transcriptomic and Physiological Analysis Reveals the Responses to Auxin and Abscisic Acid Accumulation During <i>Vaccinium corymbosum</i> Flower Bud and Fruit Development. <i>Frontiers in Plant Science</i> , 2022, 13, 818233.	1.7	0
26917	Identification of significant genes and pathways associated with tenascin-C in cancer progression by bioinformatics analysis. <i>Advanced Biomedical Research</i> , 2022, 11, 17.	0.2	1
26918	A bidirectional switch in the Shank3 phosphorylation state biases synapses toward up- or downscaling. <i>ELife</i> , 2022, 11, .	2.8	15
26919	Potential Candidates for Biomarkers in Bipolar Disorder: A Proteomic Approach through Systems Biology. <i>Clinical Psychopharmacology and Neuroscience</i> , 2022, 20, 211-227.	0.9	10
26920	An analysis of the characteristics of the intestinal flora in patients with Parkinson's disease complicated with constipation.. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 13710-13722.	0.0	0
26921	Identification of key candidate genes and pathways associated with colorectal aberrant crypt foci-to-adenoma-to-carcinoma progression.. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2021, 14, S41-S50.	0.6	0
26922	SPINK2 is a prognostic biomarker related to immune infiltration in acute myeloid leukemia.. <i>American Journal of Translational Research (discontinued)</i> , 2022, 14, 197-210.	0.0	0
26923	MUC20 as a novel prognostic biomarker in ccRCC correlating with tumor immune microenvironment modulation.. <i>American Journal of Cancer Research</i> , 2022, 12, 695-712.	1.4	0
26924	Genome-wide Analysis Reflects Novel 5-Hydroxymethylcytosines Implicated in Diabetic Nephropathy and the Biomarker Potential.. , 2022, 3, 49-60.		0
26925	GLIDER: function prediction from GLIDE-based neighborhoods. <i>Bioinformatics</i> , 2022, 38, 3395-3406.	1.8	3
26926	A Bioinformatics Workflow for Investigating Fungal Biosynthetic Gene Clusters. <i>Methods in Molecular Biology</i> , 2022, 2489, 1-21.	0.4	2



#	ARTICLE	IF	CITATIONS
26927	IMEx Databases: Displaying Molecular Interactions into a Single, Standards-Compliant Dataset. <i>Methods in Molecular Biology</i> , 2022, 2449, 27-42.	0.4	4
26928	OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics. <i>Nucleic Acids Research</i> , 2022, 50, W527-W533.	6.5	58
26929	Bioinformatics network analyses of growth differentiation factor 11. <i>Open Life Sciences</i> , 2022, 17, 426-437.	0.6	0
26930	Antiviral Strategies Against SARS-CoV-2: A Systems Biology Approach. <i>Methods in Molecular Biology</i> , 2022, 2452, 317-351.	0.4	1
26931	Plant metabolomics: a new era in the advancement of agricultural research. , 2022, , 139-160.		0
26932	Identification of Prognostic Biomarkers for Glioblastoma Based on Transcriptome and Proteome Association Analysis. <i>Technology in Cancer Research and Treatment</i> , 2022, 21, 153303382110352.	0.8	3
26933	Fuel source shift or cost reduction: Context-dependent adaptation strategies in closely related <i>Neodon fuscus</i> and <i>Lasiopodomys brandtii</i> against hypoxia. <i>Zoological Research</i> , 2022, 43, 497-513.	0.9	0
26934	GNB1, a novel diagnostic and prognostic potential biomarker of head and neck and liver hepatocellular carcinoma. <i>Journal of Cancer Research and Therapeutics</i> , 2022, .	0.3	0
26935	ANI analysis of poxvirus genomes reveals its potential application to viral species rank demarcation. <i>Virus Evolution</i> , 2022, 8, .	2.2	7
26936	Increased salt intake is associated with diabetes and characteristic dietary habits: a community-based cross-sectional study in Japan. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2022, 71, 143-150.	0.6	5
26937	YKL-40 and its co-expression analysis with major non-communicable diseases biomarkers. <i>AIP Conference Proceedings</i> , 2022, , .	0.3	0
26938	Insight into the potential pathogenesis of human osteoarthritis via single-cell RNA sequencing data on osteoblasts. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 6344-6361.	1.0	2
26939	Identification of potential key genes in resveratrol biosynthesis via transcriptional analyses of berry development in grapevine ( <i>Vitis</i> spp.) genotypes varying in <i>trans-resveratrol</i> content. <i>Fruit Research</i> , 2022, 2, 1-10.	0.9	2
26940	Quantitative analysis of the serum proteome during early pregnancy in mares. <i>Animal Science Journal</i> , 2022, 93, e13727.	0.6	0
26941	Establishing the mutational effect on the binding susceptibility of AMG510 to KRAS switch II binding pocket: Computational insights. <i>Informatics in Medicine Unlocked</i> , 2022, 30, 100952.	1.9	9
26942	PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases. <i>Nucleic Acids Research</i> , 2022, 50, W551-W559.	6.5	31
26943	Global Proteomic Profiling of Embryonic Stem Cells Using iTRAQ Isobaric Tags with LC-MS/MS Quantification. <i>Methods in Molecular Biology</i> , 2022, 2490, 157-177.	0.4	0
26944	GNAT toxins evolve toward narrow tRNA target specificities. <i>Nucleic Acids Research</i> , 2022, 50, 5807-5817.	6.5	2

#	ARTICLE	IF	CITATIONS
26945	Epididymis cell atlas in a patient with a sex development disorder and a novel <i>NR5A1</i> gene mutation. <i>Asian Journal of Andrology</i> , 2022, .	0.8	0
26946	Structural and Pharmacological Network Analysis of miRNAs Involved in Acute Ischemic Stroke: A Systematic Review. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4663.	1.8	6
26947	Upregulation of the Long Non-coding RNA LINC01480 Is Associated With Immune Infiltration in Coronary Artery Disease Based on an Immune-Related lncRNA-mRNA Co-expression Network. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 724262.	1.1	4
26948	CircRNA Expression Profiles in Canine Mammary Tumours. <i>Veterinary Sciences</i> , 2022, 9, 205.	0.6	1
26949	Utilizing Network Pharmacology and Molecular Docking Integrated Surface Plasmon Resonance Technology to Investigate the Potential Targets and Mechanisms of <i>Tripterygium wilfordii</i> against Pulmonary Artery Hypertension. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	3
26950	Novel MicroRNA-Regulated Transcript Networks Are Associated with Chemotherapy Response in Ovarian Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4875.	1.8	2
26951	Identification of Alzheimer's Disease Molecular Subtypes Based on Parallel Large-Scale Sequencing. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, 770136.	1.7	9
26952	Deciphering a Novel Necroptosis-Related miRNA Signature for Predicting the Prognosis of Clear Cell Renal Carcinoma. <i>Analytical Cellular Pathology</i> , 2022, 2022, 1-27.	0.7	7
26953	Specific Gain and Loss of Co-Expression Modules in Long-Lived Individuals Indicate a Role of circRNAs in Human Longevity. <i>Genes</i> , 2022, 13, 749.	1.0	3
26954	Lobophorin Producing Endophytic <i>Streptomyces olivaceus</i> JB1 Associated With <i>Maesa japonica</i> (Thunb.) Moritzi & Zoll.. <i>Frontiers in Microbiology</i> , 2022, 13, 881253.	1.5	2
26955	Genome-Wide Identification and Analysis of Lipases in Fig Wasps (Chalcidoidea, Hymenoptera). <i>Insects</i> , 2022, 13, 407.	1.0	2
26956	TRPM8-Rap1A Interaction Sites as Critical Determinants for Adhesion and Migration of Prostate and Other Epithelial Cancer Cells. <i>Cancers</i> , 2022, 14, 2261.	1.7	6
26957	Interaction of Neurovascular Signals in the Degraded Condylar Cartilage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 901749.	2.0	4
26958	Plant Hormone Response to Low-Temperature Stress in Cold-Tolerant and Cold-Sensitive Varieties of <i>Zanthoxylum bungeanum</i> Maxim. <i>Frontiers in Plant Science</i> , 2022, 13, 847202.	1.7	10
26959	Exploring Diverse Coagulation Factor XIII Subunit Expression Datasets: A Bioinformatic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4725.	1.8	5
26960	Metagenomic Analyses of the Soybean Root Mycobiome and Microbiome Reveal Signatures of the Healthy and Diseased Plants Affected by Taproot Decline. <i>Microorganisms</i> , 2022, 10, 856.	1.6	4
26961	Genome-Wide Characterization of High-Affinity Nitrate Transporter 2 (NRT2) Gene Family in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 4965.	1.8	8
26963	Comprehensive Analysis of Long Noncoding RNA Modified by m6A Methylation in Oxidative and Glycolytic Skeletal Muscles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4600.	1.8	6

#	ARTICLE	IF	CITATIONS
26964	Licoflavone A Suppresses Gastric Cancer Growth and Metastasis by Blocking the VEGFR-2 Signaling Pathway. <i>Journal of Oncology</i> , 2022, 2022, 1-19.	0.6	2
26965	Transcriptome Profiles of lncRNA and mRNA Highlight the Role of Ferroptosis in Chronic Neuropathic Pain With Memory Impairment. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 843297.	1.8	9
26966	PEG induces maturation of somatic embryos of <i>Passiflora edulis</i> Sims 'Rio Dourado'™ by differential accumulation of proteins and modulation of endogenous contents of free polyamines. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 150, 527-541.	1.2	5
26967	Role of Long Noncoding RNAs in Smoking-Induced Lung Cancer: An In Silico Study. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-20.	0.7	2
26968	Network analysis reveals dysregulated functional patterns in type II diabetic skin. <i>Scientific Reports</i> , 2022, 12, 6889.	1.6	2
26969	Comparative Proteomic Analysis of Plasma Membrane Proteins in Rice Leaves Reveals a Vesicle Trafficking Network in Plant Immunity That Is Provoked by Blast Fungi. <i>Frontiers in Plant Science</i> , 2022, 13, 853195.	1.7	2
26970	Identification of Potential Muscle Biomarkers in McArdle Disease: Insights from Muscle Proteome Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4650.	1.8	0
26971	Glucose-Dependent miR-125b Is a Negative Regulator of $\beta$ -Cell Function. <i>Diabetes</i> , 2022, 71, 1525-1545.	0.3	10
26972	Sample-Specific Perturbation of Gene Interactions Identifies Pancreatic Cancer Subtypes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4792.	1.8	2
26973	Comprehensive Target Screening and Cellular Profiling of the Cancer-Active Compound b-AP15 Indicate Abrogation of Protein Homeostasis and Organelle Dysfunction as the Primary Mechanism of Action. <i>Frontiers in Oncology</i> , 2022, 12, 852980.	1.3	2
26974	The <i>Arabidopsis</i> gene co-expression network. <i>Plant Direct</i> , 2022, 6, e396.	0.8	4
26975	Comparative Genomics of <i>Xylella fastidiosa</i> Explores Candidate Host-Specificity Determinants and Expands the Known Repertoire of Mobile Genetic Elements and Immunity Systems. <i>Microorganisms</i> , 2022, 10, 914.	1.6	8
26976	The Regulatory Network and Role of the circRNA-miRNA-mRNA ceRNA Network in the Progression and the Immune Response of Wilms Tumor Based on RNA-Seq. <i>Frontiers in Genetics</i> , 2022, 13, 849941.	1.1	5
26977	Anti-POSTN and Anti-TIMP1 Autoantibodies as Diagnostic Markers in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Genetics</i> , 2022, 13, 860611.	1.1	0
26978	Reduced adhesion of aged intestinal stem cells contributes to an accelerated clonal drift. <i>Life Science Alliance</i> , 2022, 5, e202201408.	1.3	2
26979	A Community-Driven, Openly Accessible Molecular Pathway Integrating Knowledge on Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2022, 12, 849640.	1.3	4
26980	Analysis of environmental driving factors on Core Functional Community during Daqu fermentation. <i>Food Research International</i> , 2022, 157, 111286.	2.9	30
26981	Analysis of circRNA-miRNA-mRNA Regulatory Network in Peripheral Blood of Radiation Workers. <i>Dose-Response</i> , 2022, 20, 155932582210887.	0.7	0

#	ARTICLE	IF	CITATIONS
26982	Photoperiod-Dependent Expression of MicroRNA in <i>Drosophila</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 4935.	1.8	1
26983	Characterization of the Upper Respiratory Bacterial Microbiome in Critically Ill COVID-19 Patients. <i>Biomedicines</i> , 2022, 10, 982.	1.4	8
26984	Overexpression of NDR1 leads to pathogen resistance at elevated temperatures. <i>New Phytologist</i> , 2022, 235, 1146-1162.	3.5	8
26985	Protein-Protein Interaction (PPI) Network of Zebrafish Oestrogen Receptors: A Bioinformatics Workflow. <i>Life</i> , 2022, 12, 650.	1.1	1
26986	Gene Expression Changes Implicate Specific Peripheral Immune Responses to Deep and Lobar Intracerebral Hemorrhages in Humans. <i>Brain Hemorrhages</i> , 2022, , .	0.4	1
26987	A systems genomics approach to uncover patient-specific pathogenic pathways and proteins in ulcerative colitis. <i>Nature Communications</i> , 2022, 13, 2299.	5.8	9
26988	Characterization and functional interrogation of the SARS-CoV-2 RNA interactome. <i>Cell Reports</i> , 2022, 39, 110744.	2.9	30
26989	Wuzi Yanzong pill attenuates MPTP-induced Parkinson's Disease via PI3K/Akt signaling pathway. <i>Metabolic Brain Disease</i> , 2022, 37, 1435-1450.	1.4	7
26990	Functional Analysis of Bronchopulmonary Dysplasia-Related Neuropeptides in Preterm Infants and miRNA-Based Diagnostic Model Construction. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-17.	0.7	3
26992	EGCG Alleviates Obesity-Induced Myocardial Fibrosis in Rats by Enhancing Expression of SCN5A. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 869279.	1.1	3
26993	Insight into the CBL and CIPK gene families in pecan ( <i>Carya illinoensis</i> ): identification, evolution and expression patterns in drought response. <i>BMC Plant Biology</i> , 2022, 22, 221.	1.6	13
26994	Gene Expression Meta-Analysis of Potential Shared and Unique Pathways between Autoimmune Diseases under Anti-TNF $\pm$ Therapy. <i>Genes</i> , 2022, 13, 776.	1.0	3
26995	Dissociation of nanosilicates induces downstream endochondral differentiation gene expression program. <i>Science Advances</i> , 2022, 8, eabl9404.	4.7	9
26996	The interferon-inducible GTPase MxB promotes capsid disassembly and genome release of herpesviruses. <i>ELife</i> , 2022, 11, .	2.8	16
26997	Identification of Bioactive Components of <i>Stephania epigaea</i> Lo and Their Potential Therapeutic Targets by UPLC-MS/MS and Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	1
26998	Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. <i>F1000Research</i> , 0, 11, 458.	0.8	0
26999	Deterministic Process Dominated Belowground Community Assembly When Suffering Tomato Bacterial Wilt Disease. <i>Agronomy</i> , 2022, 12, 1024.	1.3	6
27000	Identification of Novel Prognostic Biomarkers Relevant to Immune Infiltration in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 2022, 13, 863796.	1.1	0

#	ARTICLE	IF	CITATIONS
27001	Prioritizing Cancer lncRNA Modulators via Integrated lncRNA-mRNA Network and Somatic Mutation Data. <i>Current Bioinformatics</i> , 2022, 17, 723-734.	0.7	3
27002	Prognostic and Immunotherapeutic Roles of KRAS in Pan-Cancer. <i>Cells</i> , 2022, 11, 1427.	1.8	2
27003	Expression Pattern and Prognostic Significance of Chemokines in Breast cancer: An Integrated Bioinformatics Analysis. <i>Clinical Breast Cancer</i> , 2022, 22, 567-578.	1.1	26
27004	Chemical Diversity and Potential Target Network of Woody Peony Flower Essential Oil from Eleven Representative Cultivars ( <i>Paeonia suffruticosa</i> Andr.). <i>Molecules</i> , 2022, 27, 2829.	1.7	5
27005	Metabolomic Analysis of Serum and Tear Samples from Patients with Obesity and Type 2 Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4534.	1.8	10
27006	Transcriptome Analysis Indicates Immune Responses against <i>Vibrio harveyi</i> in Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Animals</i> , 2022, 12, 1144.	1.0	4
27007	Selective bromodomain and extra-terminal bromodomain inhibitor inactivates macrophages and hepatic stellate cells to inhibit liver inflammation and fibrosis. <i>Bioengineered</i> , 2022, 13, 10914-10930.	1.4	4
27008	Identification of WRKY transcription factors involved in regulating the biosynthesis of the anti-cancer drug camptothecin in <i>Ophiorrhiza pumila</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	24
27009	PCMT1 Is a Potential Prognostic Biomarker and Is Correlated with Immune Infiltrates in Breast Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-18.	0.9	7
27010	Cross Brain-Gut Analysis Highlighted Hub Genes and lncRNA Networks Differentially Modified During Leucine Consumption and Endurance Exercise in Mice with Depression-Like Behaviors. <i>Molecular Neurobiology</i> , 2022, 59, 4106-4123.	1.9	28
27011	Analytical Considerations of Large-Scale Aptamer-Based Datasets for Translational Applications. <i>Cancers</i> , 2022, 14, 2227.	1.7	3
27012	Proteomics and Computational Analysis of Cytosolic Proteome of a Thermoacidophilic Euryarchaeon <i>Picrophilus torridus</i> . <i>Current Proteomics</i> , 2022, 19, .	0.1	0
27013	Jiedu Huoxue Decoction for Cytokine Storm and Thrombosis in Severe COVID-19: A Combined Bioinformatics and Computational Chemistry Approach. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210969.	0.2	0
27014	Temporal and sex-dependent gene expression patterns in a renal ischemia-reperfusion injury and recovery pig model. <i>Scientific Reports</i> , 2022, 12, 6926.	1.6	4
27015	Identification of replication fork-associated proteins in <i>Drosophila</i> embryos and cultured cells using iPOND coupled to quantitative mass spectrometry. <i>Scientific Reports</i> , 2022, 12, 6903.	1.6	5
27016	Skeletal muscle properties show collagen organization and immune cell content are associated with resistance exercise response heterogeneity in older persons. <i>Journal of Applied Physiology</i> , 2022, 132, 1432-1447.	1.2	12
27017	AI beyond Deus ex Machina – Reimagining Intelligence in Future Cities with Urban Experts. , 2022, , .		5
27018	High Expression of DC-STAMP Gene Predicts Adverse Outcomes in AML. <i>Frontiers in Genetics</i> , 2022, 13, 876689.	1.1	3

#	ARTICLE	IF	CITATIONS
27019	Transcriptome Analysis of Monocytes and Fibroblasts Provides Insights Into the Molecular Features of Periodontal Ehlers-Danlos Syndrome. <i>Frontiers in Genetics</i> , 2022, 13, 834928.	1.1	1
27020	The potential mechanism of <i>Fructus Ligustri Lucidi</i> promoting osteogenetic differentiation of bone marrow mesenchymal stem cells based on network pharmacology, molecular docking and experimental identification. <i>Bioengineered</i> , 2022, 13, 10640-10653.	1.4	5
27021	Bioinformatics and Screening of a Circular RNA-microRNA-mRNA Regulatory Network Induced by Cocksackievirus Group B5 in Human Rhabdomyosarcoma Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4628.	1.8	3
27022	Differential Gene Expression in Cancer: An Overrated Analysis?. <i>Current Bioinformatics</i> , 2022, 17, 396-400.	0.7	0
27023	Framework for assessing and easing global COVID-19 travel restrictions. <i>Scientific Reports</i> , 2022, 12, 6985.	1.6	7
27024	Transcriptome and iTRAQ-Based Proteome Reveal the Molecular Mechanism of Intestinal Injury Induced by Weaning Ewe's Milk in Lambs. <i>Frontiers in Veterinary Science</i> , 2022, 9, 809188.	0.9	2
27025	Exploring the possible molecular targeting mechanism of <i>Saussurea involucrata</i> in the treatment of COVID-19 based on bioinformatics and network pharmacology. <i>Computers in Biology and Medicine</i> , 2022, 146, 105549.	3.9	7
27026	Comparative Transcriptome Analysis Reveals Regulatory Mechanism of Long Non-Coding RNAs during Abdominal Preadipocyte Adipogenic Differentiation in Chickens. <i>Animals</i> , 2022, 12, 1099.	1.0	1
27027	Application of Artificial Intelligence in Discovery and Development of Anticancer and Antidiabetic Therapeutic Agents. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	5
27028	Bioinformatics Study Revealed Significance of Exosome Transcriptome in Hepatocellular Carcinoma Diagnosis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 813701.	1.8	3
27029	Exploring Key Genes to Construct a Diagnosis Model of Dilated Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 865096.	1.1	4
27030	MiR-150-5p Overexpression in Triple-Negative Breast Cancer Contributes to the In Vitro Aggressiveness of This Breast Cancer Subtype. <i>Cancers</i> , 2022, 14, 2156.	1.7	12
27031	Alternative polyadenylation associated with prognosis and therapy in colorectal cancer. <i>Scientific Reports</i> , 2022, 12, 7036.	1.6	4
27032	Multi-Omic Profiling of Multi-Biosamples Reveals the Role of Amino Acid and Nucleotide Metabolism in Endometrial Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 861142.	1.3	3
27033	Comprehensive Genome-Wide Identification, Characterization, and Expression Analysis of CCHC-Type Zinc Finger Gene Family in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 892105.	1.7	6
27034	A Six-Gene Risk Model Based on the Immune Score Reveals Prognosis in Intermediate-Risk Acute Myeloid Leukemia. <i>BioMed Research International</i> , 2022, 2022, 1-9.	0.9	1
27035	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022, 434, 167603.	2.0	3
27036	Identification and Biosynthesis of Pro-Inflammatory Sulfolipids from an Opportunistic Pathogen <i>Chryseobacterium gleum</i> . <i>ACS Chemical Biology</i> , 2022, 17, 1197-1206.	1.6	12



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27039	RNA-Seq Analysis Identifies Transcription Factors Involved in Anthocyanin Biosynthesis of "Red Zaosu"™ Pear Peel and Functional Study of PpPIF8. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4798.	1.8	5
27040	lncRNA MALAT1 mediates osteogenic differentiation of bone mesenchymal stem cells by sponging miR-129-5p. <i>PeerJ</i> , 2022, 10, e13355.	0.9	10
27041	Expression and clinical significance of lncRNA BC041954 in ovarian cancer. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, .	0.8	2
27042	<i>Quercus suber</i> Transcriptome Analyses: Identification of Genes and SNPs Related to Cork Quality. , 2022, 11, .		2
27043	The Effects of <i>Helicobacter pylori</i> Infection on Gastric Microbiota in Children With Duodenal Ulcer. <i>Frontiers in Microbiology</i> , 2022, 13, 853184.	1.5	1
27044	Systematic Elaboration of the Pharmacological Targets and Potential Mechanisms of ZhiKe GanCao Decoction for Preventing and Delaying Intervertebral Disc Degeneration. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	3
27045	Identification of Potential Diagnoses Based on Immune Infiltration and Autophagy Characteristics in Major Depressive Disorder. <i>Frontiers in Genetics</i> , 2022, 13, 702366.	1.1	3
27046	Identification of new Omega-3 very long chain poly-unsaturated fatty acids in meibomian gland secretions. <i>Biochimie</i> , 2022, 203, 3-10.	1.3	2
27047	Mechanism of Ba Zhen Tang Delaying Skin Photoaging Based on Network Pharmacology and Molecular Docking. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2022, Volume 15, 763-781.	0.8	3
27048	Combined Network Pharmacology, Molecular Docking, and Experimental Verification Approach to Investigate the Potential Mechanisms of Polydatin Against COVID-19. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210953.	0.2	3
27049	Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans. <i>Cell Host and Microbe</i> , 2022, 30, 848-862.e7.	5.1	48
27050	Functional network analysis of p85 and PI3K as potential gene targets and mechanism of oleanolic acid in overcoming breast cancer resistance to tamoxifen. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 66.	1.5	3
27051	Open Search-Based Proteomics Reveals Widespread Tryptophan Modifications Associated with Hypoxia in Lung Cancer. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-18.	1.9	1
27052	Integrated computational analysis reveals HOX genes cluster as oncogenic drivers in head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2022, 12, 7952.	1.6	1
27053	Functional Redundancy in Soil Microbial Community Based on Metagenomics Across the Globe. <i>Frontiers in Microbiology</i> , 2022, 13, 878978.	1.5	15
27054	Integrative Analysis of lncRNA-miRNA-mRNA Regulatory Network Reveals the Key lncRNAs Implicated Potentially in the Differentiation of Adipocyte in Goats. <i>Frontiers in Physiology</i> , 2022, 13, .	1.3	4
27055	Thyroid Transcriptomic Profiling Reveals the Follicular Phase Differential Regulation of lncRNA and mRNA Related to Prolificacy in Small Tail Han Sheep with Two <i>FecB</i> Genotypes. <i>Genes</i> , 2022, 13, 849.	1.0	4
27057	Organizing the Global Diversity of Microviruses. <i>MBio</i> , 2022, 13, e0058822.	1.8	21

#	ARTICLE	IF	CITATIONS
27058	Identification of miRNA-mRNA-TF regulatory networks in peripheral blood mononuclear cells of type 1 diabetes. <i>BMC Endocrine Disorders</i> , 2022, 22, 119.	0.9	1
27059	The Rho guanosine nucleotide exchange factors Vav2 and Vav3 modulate epidermal stem cell function. <i>Oncogene</i> , 2022, 41, 3341-3354.	2.6	3
27060	Proteomic Analysis Reveals Differential Expression Profiles in Idiopathic Pulmonary Fibrosis Cell Lines. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5032.	1.8	2
27061	Biofluid Specificity of Long Non-Coding RNA Profile in Hypertension: Relevance of Exosomal Fraction. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5199.	1.8	1
27062	Exploring Relevant mRNAs and miRNAs in Injured Urethral Tissues of Rats with High-Throughput Sequencing. <i>Genes</i> , 2022, 13, 824.	1.0	2
27063	Molecular modeling of lactoferrin for food and nutraceutical applications: insights from <i>in silico</i> techniques. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 9074-9097.	5.4	2
27064	Short-Term Blockade of Pro-Inflammatory Alarmin S100A9 Favorably Modulates Left Ventricle Proteome and Related Signaling Pathways Involved in Post-Myocardial Infarction Recovery. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5289.	1.8	3
27065	<i>Fusobacterium nucleatum</i> promotes colon cancer progression by changing the mucosal microbiota and colon transcriptome in a mouse model. <i>World Journal of Gastroenterology</i> , 2022, 28, 1981-1995.	1.4	13
27066	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	2
27067	High-rate cotreatment of purified terephthalate and dimethyl terephthalate manufacturing wastewater by a mesophilic upflow anaerobic sludge blanket reactor and the microbial ecology relevant to aromatic compound degradation. <i>Water Research</i> , 2022, 219, 118581.	5.3	20
27068	Identification of major candidate genes for multiple abiotic stress tolerance at seedling stage by network analysis and their validation by expression profiling in rice ( <i>Oryza sativa</i> L.). <i>3 Biotech</i> , 2022, 12, 127.	1.1	5
27069	The macrophage-associated microRNA-4715-3p / Gasdermin D axis potentially indicates fibrosis progression in nonalcoholic fatty liver disease: evidence from transcriptome and biological data. <i>Bioengineered</i> , 2022, 13, 11740-11751.	1.4	2
27070	B3 Transcription Factors Determine Iron Distribution and FERRITIN Gene Expression in Embryo but Do Not Control Total Seed Iron Content. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
27071	The Construction and Exploration of a Comprehensive MicroRNA Centered Regulatory Network in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
27072	RNA-seq and Network Analysis Reveal Unique Chemokine Activity Signatures in the Synovial Tissue of Patients With Rheumatoid Arthritis. <i>Frontiers in Medicine</i> , 2022, 9, .	1.2	3
27073	Colony stimulating factor-1 producing endothelial cells and mesenchymal stromal cells maintain monocytes within a perivascular bone marrow niche. <i>Immunity</i> , 2022, 55, 862-878.e8.	6.6	24
27074	Genomic signatures underlying the oogenesis of the ectoparasitic mite <i>Varroa destructor</i> on its new host <i>Apis mellifera</i> . <i>Journal of Advanced Research</i> , 2023, 44, 1-11.	4.4	2
27075	Delineating functional mechanisms of the p53/p63/p73 family of transcription factors through identification of protein-protein interactions using interface mimicry. <i>Molecular Carcinogenesis</i> , 2022, 61, 629-642.	1.3	1

#	ARTICLE	IF	CITATIONS
27076	Comprehensive characterization of pre- and post-treatment samples of breast cancer reveal potential mechanisms of chemotherapy resistance. <i>Npj Breast Cancer</i> , 2022, 8, 60.	2.3	11
27077	Altered Lipid Profile in COVID-19 Patients and Metabolic Reprogramming. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	10
27078	Identification of Key Genes and Pathways Associated with PIEZO1 in Bone-Related Disease Based on Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5250.	1.8	2
27079	Single-cell transcriptomics identifies premature aging features of TERC-deficient mouse brain and bone marrow. <i>GeroScience</i> , 2022, , 1.	2.1	3
27080	Identification of key genes and miRNA-mRNA regulatory networks associated with bone marrow immune microenvironment regulations in multiple myeloma by integrative bioinformatics analysis. <i>Hematology</i> , 2022, 27, 506-517.	0.7	4
27082	Common and distinguishing genetic factors for substance use behavior and disorder: an integrated analysis of genomic and transcriptomic studies from both human and animal studies. <i>Addiction</i> , 2022, 117, 2515-2529.	1.7	3
27083	KATP channel dependent heart multiome atlas. <i>Scientific Reports</i> , 2022, 12, 7314.	1.6	1
27084	SDR enzymes oxidize specific lipidic alkynylcarbinols into cytotoxic protein-reactive species. <i>ELife</i> , 2022, 11, .	2.8	2
27085	Phosphoproteomics Unravel HBV Triggered Rewiring of Host Phosphosignaling Events. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5127.	1.8	0
27086	Rice LEAFY COTYLEDON1 Hinders Embryo Greening During the Seed Development. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3
27087	In-silico, interactomic based screening and identification of differentially expressed miRNAs in oral submucous fibrosis and oral squamous cell carcinoma. , 2022, 33, 201041.		1
27088	Single-Cell Analysis Reveals Transcriptomic Reprogramming in Aging Cardiovascular Endothelial Cells. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, .	1.1	7
27089	Profiling Yeast Deletion Strains Using Sample Multiplexing and Network-Based Analyses. <i>Journal of Proteome Research</i> , 2022, , .	1.8	1
27090	Correlation of NTRK1 Downregulation with Low Levels of Tumor-Infiltrating Immune Cells and Poor Prognosis of Prostate Cancer Revealed by Gene Network Analysis. <i>Genes</i> , 2022, 13, 840.	1.0	3
27091	Identification of Common Oncogenic Genes and Pathways Both in Osteosarcoma and Ewing's Sarcoma Using Bioinformatics Analysis. <i>Journal of Immunology Research</i> , 2022, 2022, 1-30.	0.9	6
27092	Genome-wide tandem repeat expansions contribute to schizophrenia risk. <i>Molecular Psychiatry</i> , 2022, 27, 3692-3698.	4.1	20
27093	MicroRNA Signature and Cellular Characterization of Undifferentiated and Differentiated House Ear Institute-Organ of Corti 1 (HEI-OC1) Cells. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2022, 23, 467-489.	0.9	4
27094	ImShot: An Open-Source Software for Probabilistic Identification of Proteins In Situ and Visualization of Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100242.	2.5	3

#	ARTICLE	IF	CITATIONS
27095	Discovery of novel targets and mechanisms of MEK inhibitor Selumetinib for LGG treatment based on molecular docking and molecular dynamics simulation. <i>Journal of Molecular Modeling</i> , 2022, 28, 138.	0.8	3
27096	Vitamin D3 reverses the transcriptional profile of offspring CD4+ T lymphocytes exposed to intrauterine inflammation. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2022, 221, 106120.	1.2	3
27097	Integrated small RNA profiling and degradome analysis of <i>Anthurium andraeanum</i> cultivars with different-colored spathes. <i>Journal of Plant Research</i> , 2022, 135, 609-626.	1.2	1
27098	Andrographolide in atherosclerosis: integrating network pharmacology and <i>in vitro</i> pharmacological evaluation. <i>Bioscience Reports</i> , 2022, 42, .	1.1	5
27099	Associations between bacterial communities and microplastics from surface seawater of the Northern Patagonian area of Chile. <i>Environmental Pollution</i> , 2022, 306, 119313.	3.7	9
27100	Downregulation of miR-122-5p Activates Glycolysis via PKM2 in Kupffer Cells of Rat and Mouse Models of Non-Alcoholic Steatohepatitis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5230.	1.8	11
27101	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. <i>Developmental Cell</i> , 2022, 57, 1177-1192.e6.	3.1	27
27102	The cytotoxic action of BCI is not dependent on its stated DUSP1 or DUSP6 targets in neuroblastoma cells. <i>FEBS Open Bio</i> , 2022, , .	1.0	4
27103	Construction of a lncRNA-associated competing endogenous RNA regulatory network after traumatic brain injury in mouse. <i>Molecular Brain</i> , 2022, 15, 40.	1.3	3
27104	Terpenoid Backbone Biosynthesis among Pig Hippocampal Pathways Impacted by Stressors. <i>Genes</i> , 2022, 13, 814.	1.0	8
27105	Duo Cadherin-Functionalized Microparticles Synergistically Induce Chondrogenesis and Cartilage Repair of Stem Cell Aggregates. <i>Advanced Healthcare Materials</i> , 2022, 11, e2200246.	3.9	4
27106	Differential expression analysis of genes and long non-coding RNAs associated with KRAS mutation in colorectal cancer cells. <i>Scientific Reports</i> , 2022, 12, 7965.	1.6	8
27107	Exploring Key Genes and Mechanisms in Respiratory Syncytial Virus-Infected BALB/c Mice via Multi-Organ Expression Profiles. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 858305.	1.8	2
27108	Persisting uropathogenic <i>Escherichia coli</i> lineages show signatures of niche-specific within-host adaptation mediated by mobile genetic elements. <i>Cell Host and Microbe</i> , 2022, 30, 1034-1047.e6.	5.1	13
27109	Differential expression of gene co-expression networks related to the mTOR signaling pathway in bipolar disorder. <i>Translational Psychiatry</i> , 2022, 12, 184.	2.4	4
27110	A Prognosis Marker Dynein Cytoplasmic 1 Heavy Chain 1 Correlates with EMT and Immune Signature in Liver Hepatocellular Carcinoma by Bioinformatics and Experimental Analysis. <i>Disease Markers</i> , 2022, 1-18.	0.6	7
27111	The ceRNA Crosstalk between mRNAs and lncRNAs in Diabetes Myocardial Infarction. <i>Disease Markers</i> , 2022, 2022, 1-12.	0.6	0
27112	Preliminary study on gene regulation and its pathways in Chinese Holstein cows with clinical mastitis caused by <i>Staphylococcus aureus</i> . <i>Journal of Veterinary Research (Poland)</i> , 2022, .	0.3	0

#	ARTICLE	IF	CITATIONS
27113	Establishment of a Novel Combined Nomogram for Predicting the Risk of Progression Related to Castration Resistance in Patients With Prostate Cancer. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4
27114	Pyroptosis-Related Gene Signature and Expression Patterns in the Deterioration of Atherosclerosis. <i>Disease Markers</i> , 2022, 2022, 1-24.	0.6	1
27115	Conservation and divergence of myelin proteome and oligodendrocyte transcriptome profiles between humans and mice. <i>ELife</i> , 2022, 11, .	2.8	24
27116	Multi-staged gene expression profiling reveals potential genes and the critical pathways in kidney cancer. <i>Scientific Reports</i> , 2022, 12, 7240.	1.6	10
27117	Nezzle: an interactive and programmable visualization of biological networks in Python. <i>Bioinformatics</i> , 2022, 38, 3310-3311.	1.8	0
27118	Discovery of Anticancer Activity of Amentoflavone on Esophageal Squamous Cell Carcinoma: Bioinformatics, Structure-based Virtual Screening, and Biological Evaluation. <i>Journal of Microbiology and Biotechnology</i> , 2022, 32, 1-10.	0.9	5
27119	Systematic comparison of the protein-protein interaction network of bacterial Universal stress protein A (UspA): an insight into its discrete functions. , 0, , .		3
27120	vRhyme enables binning of viral genomes from metagenomes. <i>Nucleic Acids Research</i> , 2022, 50, e83-e83.	6.5	30
27121	Modulation of GPCR receptors common to gut inflammatory diseases and neuronal disorders, Alzheimerâ€™s and Parkinsonâ€™s diseases as druggable targets through <i>Withania somnifera</i> bioactives: an <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 4485-4503.	2.0	5
27122	The network makeup artist (NORMA-2.0): distinguishing annotated groups in a network using innovative layout strategies. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	4
27123	Host phylogeny, habitat, and diet are main drivers of the cephalopod and mollusk gut microbiome. <i>Animal Microbiome</i> , 2022, 4, 30.	1.5	11
27124	Deciphering the Effects and Mechanisms of Yi-Fei-San-Jie-pill on Non-Small Cell Lung Cancer With Integrating Network Target Analysis and Experimental Validation. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	2
27125	Profiling of Non-Coding Regulators and Their Targets in Epicardial Fat from Patients with Coronary Artery Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5297.	1.8	5
27126	Data Mining Identifies CCN2 and THBS1 as Biomarker Candidates for Cardiac Hypertrophy. <i>Life</i> , 2022, 12, 726.	1.1	2
27127	Genome-scale metabolic models for natural and long-term drug-induced viral control in HIV infection. <i>Life Science Alliance</i> , 2022, 5, e202201405.	1.3	7
27128	A comparative transcriptomics and eQTL approach identifies <i>SlWD40</i> as a tomato fruit ripening regulator. <i>Plant Physiology</i> , 2022, 190, 250-266.	2.3	9
27129	Metabolomic and transcriptomic analyses reveal new insights into the role of abscisic acid in modulating mango fruit ripening. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
27130	Uncovering <i>in vivo</i> biochemical patterns from time-series metabolic dynamics. <i>PLoS ONE</i> , 2022, 17, e0268394.	1.1	3

#	ARTICLE	IF	CITATIONS
27131	lncRNAâ€™ mRNA Expression Patterns in Invasive Pituitary Adenomas: A Microarray Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	7
27132	Comparative 3D genome architecture in vertebrates. <i>BMC Biology</i> , 2022, 20, 99.	1.7	25
27133	A Crucial Angiogenesis-Associated Gene MEOX2 Could Be a Promising Biomarker Candidate for Breast Cancer. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	1
27135	Mycobiomes of the Ocular Surface in Bacterial Keratitis Patients. <i>Frontiers in Ophthalmology</i> , 2022, 2, .	0.2	1
27136	Genomic insights into variation in thermotolerance between hybridizing swordtail fishes. <i>Molecular Ecology</i> , 2022, , .	2.0	6
27137	Systematic characterization of gene function in the photosynthetic alga <i>Chlamydomonas reinhardtii</i> . <i>Nature Genetics</i> , 2022, 54, 705-714.	9.4	42
27138	SPINNAKER: an R-based tool to highlight key RNA interactions in complex biological networks. <i>BMC Bioinformatics</i> , 2022, 23, 166.	1.2	2
27139	Solute carrier family 2 members 1 and 2 as prognostic biomarkers in hepatocellular carcinoma associated with immune infiltration. <i>World Journal of Clinical Cases</i> , 2022, 10, 3989-4019.	0.3	6
27141	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 900-910.	1.8	9
27142	Kinetic, Inhibition, and Structural Characterization of a Malonate Semialdehyde Decarboxylase-like Protein from <i>Calothrix</i> sp. PCC 6303: A Gateway to the non-Pro1 Tautomerase Superfamily Members. <i>Biochemistry</i> , 2022, , .	1.2	2
27144	Systematic analysis of prognostic significance, functional enrichment and immune implication of STK10 in acute myeloid leukemia. <i>BMC Medical Genomics</i> , 2022, 15, 101.	0.7	3
27145	Persistent Properties of a Subpopulation of Cancer Cells Overexpressing the Hedgehog Receptor Patched. <i>Pharmaceutics</i> , 2022, 14, 988.	2.0	2
27146	Microbial and Nonvolatile Chemical Diversities of Chinese Dark Teas Are Differed by Latitude and Pile Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 5701-5714.	2.4	11
27147	Host-Associated Phages Disperse across the Extraterrestrial Analogue Antarctica. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0031522.	1.4	7
27148	Analysis of the different characteristics between omental preadipocytes and differentiated white adipocytes using bioinformatics methods. <i>Adipocyte</i> , 2022, 11, 227-238.	1.3	4
27149	Targeting Circulating lncRNA ENST00000538705.1 Relieves Acute Coronary Syndrome via Modulating ALOX15. <i>Disease Markers</i> , 2022, 2022, 1-24.	0.6	1
27150	Identification of Differential Genes of DNA Methylation Associated With Alzheimerâ€™s Disease Based on Integrated Bioinformatics and Its Diagnostic Significance. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, .	1.7	5
27151	Integrative analysis of circRNA, miRNA, and mRNA profiles to reveal ceRNA regulation in chicken muscle development from the embryonic to post-hatching periods. <i>BMC Genomics</i> , 2022, 23, 342.	1.2	8



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27152	Spatiotemporal mapping of gene expression landscapes and developmental trajectories during zebrafish embryogenesis. <i>Developmental Cell</i> , 2022, 57, 1284-1298.e5.	3.1	56
27153	Andrographolide Inhibits ER-Positive Breast Cancer Growth and Enhances Fulvestrant Efficacy via ROS-FOXM1-ER- $\beta$ Axis. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	3
27154	CircMiMi: a stand-alone software for constructing circular RNA-microRNA-mRNA interactions across species. <i>BMC Bioinformatics</i> , 2022, 23, 164.	1.2	8
27155	Single-cell transcriptome highlights a multilayer regulatory network on an invasive trajectory within colorectal cancer progression. <i>Journal of Cancer Research and Clinical Oncology</i> , 2022, , 1.	1.2	0
27156	Biomarkers and Disease Trajectories Influencing Women's Health: Results from the UK Biobank Cohort. <i>Phenomics</i> , 2022, 2, 184-193.	0.9	9
27157	Multiphoton Microscopy Reveals DAPK1-Dependent Extracellular Matrix Remodeling in a Chorioallantoic Membrane (CAM) Model. <i>Cancers</i> , 2022, 14, 2364.	1.7	5
27158	Causal Effect of Genetically Determined Blood Copper Concentrations on Multiple Diseases: A Mendelian Randomization and Phenome-Wide Association Study. <i>Phenomics</i> , 2022, 2, 242-253.	0.9	5
27160	Metabolic characterization of hypertrophic cardiomyopathy in human heart. , 2022, 1, 445-461.		8
27161	Exploring the Mechanism of Yi-Jing Decoction in Treating Polycystic Ovary Syndrome by Using Network Pharmacology. <i>Current Medicinal Chemistry</i> , 2022, 29, .	1.2	3
27162	Exploring Mechanisms by Which Danggui Buxue Decoction Regulates Inflammation and Improves Renal Anemia Based on Network Pharmacology. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210939.	0.2	0
27163	Pharmacogenomics of in vitro response of the NCI-60 cancer cell line panel to Indian natural products. <i>BMC Cancer</i> , 2022, 22, 512.	1.1	3
27164	U1RNP/lncRNA/Transcription Cycle Axis Promotes Tumorigenesis of Hepatocellular Carcinoma. <i>Diagnostics</i> , 2022, 12, 1133.	1.3	2
27165	Multiple Sclerosis Biomarker Candidates Revealed by Cell-Type-Specific Interactome Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 305-317.	1.0	2
27166	Transcriptome Analysis Reveals Candidate Lignin-Related Genes and Transcription Factors during Fruit Development in Pomelo ( <i>Citrus maxima</i> ). <i>Genes</i> , 2022, 13, 845.	1.0	6
27167	Small RNA sequencing and bioinformatics analysis of RAW264.7-derived exosomes after <i>Mycobacterium Bovis Bacillus Calmette-Guérin</i> infection. <i>BMC Genomics</i> , 2022, 23, 355.	1.2	5
27168	Intrapericardial Administration of Secretomes from Menstrual Blood-Derived Mesenchymal Stromal Cells: Effects on Immune-Related Genes in a Porcine Model of Myocardial Infarction. <i>Biomedicines</i> , 2022, 10, 1117.	1.4	3
27170	miR-29a-5p Inhibits Prenatal Hair Placode Formation Through Targeting EDAR by ceRNA Regulatory Network. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	0
27171	Oral dysbiosis and its linkage with SARS-CoV-2 infection. <i>Microbiological Research</i> , 2022, 261, 127055.	2.5	21

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27172	Network Pharmacology and Absolute Bacterial Quantification-Combined Approach to Explore the Mechanism of Tianqi Pingchan Granule Against 6-OHDA-Induced Parkinson's Disease in Rats. <i>Frontiers in Nutrition</i> , 2022, 9, .	1.6	2
27173	High-resolution 3D spatiotemporal transcriptomic maps of developing <i>Drosophila</i> embryos and larvae. <i>Developmental Cell</i> , 2022, 57, 1271-1283.e4.	3.1	58
27174	A Data Science Approach for the Identification of Molecular Signatures of Aggressive Cancers. <i>Cancers</i> , 2022, 14, 2325.	1.7	3
27175	Network pharmacology of iridoid glycosides from <i>Eucommia ulmoides</i> Oliver against osteoporosis. <i>Scientific Reports</i> , 2022, 12, 7430.	1.6	11
27176	Age-dependent modulation of oleoresin production in the stem of <i>Sindora glabra</i> . <i>Tree Physiology</i> , 2022, , .	1.4	0
27177	Enhanced Anti-Cancer Effects of Conditioned Medium from Hypoxic Human Adult Dermal Fibroblasts on Cervical Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5134.	1.8	1
27178	<i>P. aeruginosa</i> type III and type VI secretion systems modulate early response gene expression in type II pneumocytes in vitro. <i>BMC Genomics</i> , 2022, 23, 345.	1.2	4
27179	Single-Cell RNA Sequencing Profiles Identify Important Pathophysiologic Factors in the Progression of Diabetic Nephropathy. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	5
27180	Exploring the Diversity and Antibacterial Potentiality of Cultivable Actinobacteria from the Soil of the Saxaul Forest in Southern Gobi Desert in Mongolia. <i>Microorganisms</i> , 2022, 10, 989.	1.6	6
27181	Identification of Candidate Genes Associated With Tolerance to Apple Replant Disease by Genome-Wide Transcriptome Analysis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5
27182	Comparative Transcriptional Analysis of Two Contrasting Rice Genotypes in Response to Salt Stress. <i>Agronomy</i> , 2022, 12, 1163.	1.3	2
27183	High-Throughput Sequencing Reveals Transcriptome Signature of Early Liver Development in Goat Kids. <i>Genes</i> , 2022, 13, 833.	1.0	1
27184	Exploration of the System-Level Mechanisms of the Herbal Drug FDY003 for Pancreatic Cancer Treatment: A Network Pharmacological Investigation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	0
27185	Analysis of Multifactor-Driven Myopia Disease Modules to Guide Personalized Treatment and Drug Development. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-10.	0.7	2
27186	The developmental stage of the medulloblastoma cell-of-origin restricts Sonic hedgehog pathway usage and drug sensitivity. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	2
27187	Dysregulated miRNAs as Biomarkers and Therapeutic Targets in Neurodegenerative Diseases. <i>Journal of Personalized Medicine</i> , 2022, 12, 770.	1.1	21
27188	Long-term nickel contamination increased soil fungal diversity and altered fungal community structure and co-occurrence patterns in agricultural soils. <i>Journal of Hazardous Materials</i> , 2022, 436, 129113.	6.5	19
27189	Evaluation of tea ( <i>Camellia sinensis</i> L.) phytochemicals as multi-disease modulators, a multidimensional in silico strategy with the combinations of network pharmacology, pharmacophore analysis, statistics and molecular docking. <i>Molecular Diversity</i> , 2023, 27, 487-509.	2.1	4

#	ARTICLE	IF	CITATIONS
27190	STRIDER: Steric hindrance and metal coordination identifier. <i>Computational Biology and Chemistry</i> , 2022, 98, 107686.	1.1	2
27192	Magnolol alleviates hypoxia-induced pulmonary vascular remodeling through inhibition of phenotypic transformation in pulmonary arterial smooth muscle cells. <i>Biomedicine and Pharmacotherapy</i> , 2022, 150, 113060.	2.5	4
27193	Assessment of diphenhydramine toxicity â€œ Is its mode of action conserved between human and zebrafish?. <i>Environment International</i> , 2022, 164, 107263.	4.8	9
27194	Convergent lines of evidence supporting involvement of NFKB1 in schizophrenia. <i>Psychiatry Research</i> , 2022, 312, 114588.	1.7	8
27195	RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles. <i>Nucleic Acids Research</i> , 2022, 50, W651-W656.	6.5	75
27196	Analyzing single cell transcriptome data from severe COVID-19 patients. <i>STAR Protocols</i> , 2022, 3, 101379.	0.5	1
27197	Composition and spatial-temporal dynamics of phytoplankton community shaped by environmental selection and interactions in the Jiaozhou Bay. <i>Water Research</i> , 2022, 218, 118488.	5.3	34
27198	Chicory polysaccharides alleviate high-fat diet-induced non-alcoholic fatty liver disease via alteration of lipid metabolism- and inflammation-related gene expression. <i>Food Science and Human Wellness</i> , 2022, 11, 954-964.	2.2	9
27199	Interleukin-6 inhibition in ST-elevation myocardial infarction: Immune cell profile in the randomised ASSAIL-MI trial. <i>EBioMedicine</i> , 2022, 80, 104013.	2.7	22
27200	Uncovering early thyroid hormone signalling events through temperature-mediated activation of molecular memory in the cultured bullfrog tadpole tail fin. <i>General and Comparative Endocrinology</i> , 2022, 323-324, 114047.	0.8	2
27201	A snapshot of the global drinking water virome: Diversity and metabolic potential vary with residual disinfectant use. <i>Water Research</i> , 2022, 218, 118484.	5.3	14
27202	First report on delineation of differentially expressed genes and pathways in milk somatic cells of mastitic and healthy Murrah buffaloes. <i>Gene</i> , 2022, 831, 146575.	1.0	2
27203	FoodMicrobionet v4: A large, integrated, open and transparent database for food bacterial communities. <i>International Journal of Food Microbiology</i> , 2022, 372, 109696.	2.1	7
27204	An integrated network pharmacology and cell metabolomics approach to reveal the role of rhein, a novel PPAR $\alpha$ agonist, against renal fibrosis by activating the PPAR $\alpha$ -CPT1A axis. <i>Phytomedicine</i> , 2022, 102, 154147.	2.3	9
27205	Hepatic glycerolipid metabolism is critical to the egg laying rate of Guangxi Ma chickens. <i>Gene</i> , 2022, 830, 146500.	1.0	0
27206	Network for network concept offers new insights into host- SARS-CoV-2 protein interactions and potential novel targets for developing antiviral drugs. <i>Computers in Biology and Medicine</i> , 2022, 146, 105575.	3.9	12
27207	Potential mechanism of four agents decoction in the treatment of endometriosis based on network pharmacology and molecular docking. <i>South African Journal of Botany</i> , 2022, 148, 162-169.	1.2	1
27208	Meroterpenoids and sesquiterpene dimers from <i>Sarcandra glabra</i> with anti-neuroinflammatory activity. <i>Industrial Crops and Products</i> , 2022, 183, 114983.	2.5	20

#	ARTICLE	IF	CITATIONS
27209	Hearing Impairment in Mucopolysaccharidosis: A Systems Biology Approach. <i>Journal of Inborn Errors of Metabolism and Screening</i> , 0, 10, .	0.3	0
27210	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	9.4	55
27211	EGR1 Is Implicated in Right Ventricular Cardiac Remodeling Associated with Pulmonary Hypertension. <i>Biology</i> , 2022, 11, 677.	1.3	6
27212	Sorghum root epigenetic landscape during limiting phosphorus conditions. <i>Plant Direct</i> , 2022, 6, .	0.8	5
27213	Diagnosis of pulmonary tuberculosis via identification of core genes and pathways utilizing blood transcriptional signatures: a multicohort analysis. <i>Respiratory Research</i> , 2022, 23, 125.	1.4	3
27214	Characterising sex differences of autosomal DNA methylation in whole blood using the Illumina EPIC array. <i>Clinical Epigenetics</i> , 2022, 14, 62.	1.8	34
27215	Modelling liver cancer microenvironment using a novel 3D culture system. <i>Scientific Reports</i> , 2022, 12, 8003.	1.6	24
27216	An Integrated Approach Reveals DNA Damage and Proteotoxic Stress as Main Effects of Proton Radiation in <i>S. cerevisiae</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 5493.	1.8	2
27217	Identification of genes and pathways associated with sex in Non-smoking lung cancer population. <i>Gene</i> , 2022, 831, 146566.	1.0	4
27218	Pan-Cancer Single-Cell Analysis Reveals the Core Factors and Pathway in Specific Cancer Stem Cells of Upper Gastrointestinal Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, .	2.0	2
27219	The Comparative Survey of Coordinated Regulation of Steroidogenic Pathway in Japanese Flounder ( <i>Paralichthys olivaceus</i> ) and Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 5520.	1.8	5
27220	Elevated Vulnerability of Chronic Leukemia Patients to COVID-19 Infection: A Systems Biology Approach. <i>Dr Sulaiman Al Habib Medical Journal</i> , 2022, 4, 32-45.	0.3	1
27221	Development and validation of an eight-gene signature based predictive model to evaluate the prognosis of hepatocellular carcinoma patients: a bioinformatic study. <i>Annals of Translational Medicine</i> , 2022, 10, 524-524.	0.7	0
27222	ProMetheusDB: An In-Depth Analysis of the High-Quality Human Methyl-proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100243.	2.5	3
27223	In Silico Integration of Transcriptome and Interactome Predicts an ETP-ALL-Specific Transcriptional Footprint that Decodes its Developmental Propensity. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	3
27224	The Overexpression of SLC25A13 Predicts Poor Prognosis and Is Correlated with Immune Cell Infiltration in Patients with Skin Cutaneous Melanoma. <i>Disease Markers</i> , 2022, 2022, 1-15.	0.6	3
27225	Soyasapogenol C from Fermented Soybean ( <i>Glycine Max</i> ) Acting as a Novel AMPK/PPAR $\alpha$ Dual Activator Ameliorates Hepatic Steatosis: A Novel SANDA Methodology. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5468.	1.8	3
27226	Transcriptomic Analysis Reveals Endometrial Dynamics in Normoweight and Overweight/Obese Polycystic Ovary Syndrome Women. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4

#	ARTICLE	IF	CITATIONS
27227	Novel Mutations in ACP5 and SAMHD1 in a Patient With Pediatric Systemic Lupus Erythematosus. <i>Frontiers in Pediatrics</i> , 2022, 10, .	0.9	5
27228	Establishment of prognostic risk model and drug sensitivity based on prognostic related genes of esophageal cancer. <i>Scientific Reports</i> , 2022, 12, 8008.	1.6	8
27229	In-silico Identification and Analysis of Hub Proteins for Designing Novel First-line Anti-seizure Medications. <i>Letters in Drug Design and Discovery</i> , 2023, 20, 662-673.	0.4	1
27230	Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. <i>ISME Journal</i> , 2022, 16, 1980-1992.	4.4	14
27231	Role of miRNAs in Human T Cell Leukemia Virus Type 1 Induced T Cell Leukemia: A Literature Review and Bioinformatics Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5486.	1.8	5
27232	Proteome-wide prediction and analysis of the <i>Cryptosporidium parvum</i> protein-protein interaction network through integrative methods. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2322-2331.	1.9	2
27233	Protein interactome and cell-type expression analyses reveal that cytoplasmic FMR1-interacting protein 1 (CYFIP1), but not CYFIP2, associates with astrocytic focal adhesion. <i>Journal of Neurochemistry</i> , 2022, 162, 190-206.	2.1	3
27234	Characteristics of alveolar macrophages in bronchioalveolar lavage fluids from active tuberculosis patients identified by single-cell RNA sequencing. <i>Journal of Biomedical Research</i> , 2022, 36, 167.	0.7	6
27235	Single-cell analysis of transcription factor regulatory networks reveals molecular basis for subtype-specific dysregulation in acute myeloid leukemia. <i>Blood Science</i> , 2022, 4, 65-75.	0.4	4
27236	Identification and validation of an eight-lncRNA signature that predicts prognosis in patients with esophageal squamous cell carcinoma. <i>Cellular and Molecular Biology Letters</i> , 2022, 27, 39.	2.7	11
27237	Microbial Consortium Associated with Crustacean Shells Composting. <i>Microorganisms</i> , 2022, 10, 1033.	1.6	3
27238	Genome-Wide Identification and Characterization of Long Non-Coding RNAs in Longissimus dorsi Skeletal Muscle of Shandong Black Cattle and Luxi Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	3
27239	Integrative Analysis of KCNK Genes and Establishment of a Specific Prognostic Signature for Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	3
27240	The Construction and Analysis of Immune Infiltration and Competing Endogenous RNA Network in Acute Ischemic Stroke. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, .	1.7	6
27241	Metabolism-related MOGS Gene is Dysregulated After Peripheral Nerve Injury and Negatively Regulates Schwann Cell Plasticity. <i>Journal of Molecular Neuroscience</i> , 2022, , .	1.1	2
27242	A Network Pharmacology Analysis of Cytotoxic Triterpenes Isolated from <i>Euphorbia abyssinica</i> Latex Supported by Drug-likeness and ADMET Studies. <i>ACS Omega</i> , 2022, 7, 17713-17722.	1.6	9
27243	Quantitative proteomic sequencing of F1 hybrid populations reveals the function of sorbitol in apple resistance to <i>Botryosphaeria dothidea</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	6
27244	Immune-Related Biomarkers Associated with Lung Metastasis from the Colorectal Cancer Microenvironment. <i>Journal of Interferon and Cytokine Research</i> , 2022, 42, 220-234.	0.5	0

#	ARTICLE	IF	CITATIONS
27245	Distinctive functional regime of endogenous lncRNAs in dark regions of human genome. Computational and Structural Biotechnology Journal, 2022, 20, 2381-2390.	1.9	1
27246	Transcriptional competition shapes proteotoxic ER stress resolution. Nature Plants, 2022, 8, 481-490.	4.7	7
27247	Transcriptional Profiling of Hippocampus Identifies Network Alterations in Alzheimer's Disease. Applied Sciences (Switzerland), 2022, 12, 5035.	1.3	2
27248	The PagKNAT2/6b-PagBOP1/2a Regulatory Module Controls Leaf Morphogenesis in Populus. International Journal of Molecular Sciences, 2022, 23, 5581.	1.8	0
27249	Chrysosporazines Revisited: Regioisomeric Phenylpropanoid Piperazine P-Glycoprotein Inhibitors from Australian Marine Fish-Derived Fungi. Molecules, 2022, 27, 3172.	1.7	7
27250	Identification of Novel Characteristics in TP53-Mutant Hepatocellular Carcinoma Using Bioinformatics. Frontiers in Genetics, 2022, 13, .	1.1	7
27251	FAM81A identified as a stemness-related gene by screening DNA methylation sites based on machine learning-accessed stemness in pancreatic cancer. Epigenomics, 2022, 14, 569-588.	1.0	2
27252	Sleep and Late-Onset Alzheimer's Disease: Shared Genetic Risk Factors, Drug Targets, Molecular Mechanisms, and Causal Effects. Frontiers in Genetics, 2022, 13, .	1.1	5
27253	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
27254	Comprehensive Biochemical, Physiological, and Transcriptomic Analyses Provide Insights Into Floral Bud Dormancy in Rhododendron delavayi Franch. Frontiers in Genetics, 2022, 13, .	1.1	2
27255	Spatial Mapping of Plant N-Glycosylation Cellular Heterogeneity Inside Soybean Root Nodules Provided Insights Into Legume-Rhizobia Symbiosis. Frontiers in Plant Science, 2022, 13, .	1.7	7
27256	A molecular view of amyotrophic lateral sclerosis through the lens of interaction network modules. PLoS ONE, 2022, 17, e0268159.	1.1	2
27257	Transcriptome-Wide Characterization of Seed Aging in Rice: Identification of Specific Long-Lived mRNAs for Seed Longevity. Frontiers in Plant Science, 2022, 13, .	1.7	4
27258	Legacy and dispersant influence microbial community dynamics in cold seawater contaminated by crude oil water accommodated fractions. Environmental Research, 2022, 212, 113467.	3.7	4
27259	Fractionated irradiation of MCF7 breast cancer cells rewires a gene regulatory circuit towards a treatment-resistant stemness phenotype. Molecular Oncology, 2022, 16, 3410-3435.	2.1	2
27260	Insights into Prokaryotic Community and Its Potential Functions in Nitrogen Metabolism in the Bay of Bengal, a Pronounced Oxygen Minimum Zone. Microbiology Spectrum, 2022, 10, e0089221.	1.2	9
27261	Zng1 is a GTP-dependent zinc transferase needed for activation of methionine aminopeptidase. Cell Reports, 2022, 39, 110834.	2.9	20
27262	Identification of miRNA biomarkers for stomach adenocarcinoma. BMC Bioinformatics, 2022, 23, 181.	1.2	2



#	ARTICLE	IF	CITATIONS
27263	System-Wide Analysis of the GATC-Binding Nucleoid-Associated Protein Gbn and Its Impact on <i>Streptomyces</i> Development. <i>MSystems</i> , 2022, 7, e0006122.	1.7	4
27264	NEAT1 can be a diagnostic biomarker in the breast cancer and gastric cancer patients by targeting XIST, hsa-miR-612, and MTRNR2L8: integrated RNA targetome interaction and experimental expression analysis. <i>Genes and Environment</i> , 2022, 44, 16.	0.9	9
27265	Molecular mechanisms affecting the difference in salinity adaptability between juvenile and adult Hong Kong oysters. <i>Aquaculture Reports</i> , 2022, 24, 101171.	0.7	2
27266	Genetic Survey of <i>Psilocybe</i> Natural Products. <i>ChemBioChem</i> , 2022, 23, .	1.3	16
27267	Chinese Medicine Meets Conventional Medicine in Targeting COVID-19 Pathophysiology, Complications and Comorbidities. <i>Chinese Journal of Integrative Medicine</i> , 2022, , .	0.7	1
27268	The role of non-coding RNAs in neuroinflammatory process in multiple sclerosis. <i>Molecular Neurobiology</i> , 2022, 59, 4651-4668.	1.9	3
27269	Distinct gene clusters drive formation of ferrosome organelles in bacteria. <i>Nature</i> , 2022, 606, 160-164.	13.7	15
27270	Effects of interleukin $1\beta$ on long noncoding RNA and mRNA expression profiles of human synovial fluid derived mesenchymal stem cells. <i>Scientific Reports</i> , 2022, 12, 8432.	1.6	1
27271	NMR-based metabolomic profiling can differentiate follicular lymphoma from benign lymph node tissues and may be predictive of outcome. <i>Scientific Reports</i> , 2022, 12, 8294.	1.6	1
27272	Unbiased proteomic analysis detects painful systemic inflammatory profile in the serum of nerve-injured mice. <i>Pain</i> , 2023, 164, e77-e90.	2.0	6
27273	Feasibility analysis and mechanism exploration of Rhei Radix et Rhizomea Schisandrae Sphenantherae Fructus (RS) against COVID-19. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	11
27274	The <i>Brassica napus</i> seed microbiota is cultivar-specific and transmitted via paternal breeding lines. <i>Microbial Biotechnology</i> , 2022, 15, 2379-2390.	2.0	14
27275	The effect of resistance and endurance training with ursolic acid on atrophy-related biomarkers in muscle tissue of diabetic male rats induced by streptozotocin and a high-fat diet. <i>Journal of Food Biochemistry</i> , 2022, , e14202.	1.2	3
27276	A basement membrane discovery pipeline uncovers network complexity, regulators, and human disease associations. <i>Science Advances</i> , 2022, 8, eabn2265.	4.7	76
27277	Revealing the novel complexity of plant long non-coding RNA by strand-specific and whole transcriptome sequencing for evolutionarily representative plant species. <i>BMC Genomics</i> , 2022, 23, 381.	1.2	3
27278	Connecting DCX, COMT and FMR1 in social behavior and cognitive impairment. <i>Behavioral and Brain Functions</i> , 2022, 18, 7.	1.4	9
27279	New biomarker: the gene HLA-DRA associated with low-grade glioma prognosis. <i>Chinese Neurosurgical Journal</i> , 2022, 8, 12.	0.3	1
27280	Multi-omics approaches for comprehensive analysis and understanding of the immune response in the miniature pig breed. <i>PLoS ONE</i> , 2022, 17, e0263035.	1.1	1

#	ARTICLE	IF	CITATIONS
27281	Transcriptome Profiling of Cisplatin Resistance in Triple-negative Breast Cancer: New Insight into the Role of PI3k/Akt Pathway. <i>Current Molecular Medicine</i> , 2023, 23, 559-568.	0.6	0
27282	The Isolation and Characterization of Rare Mycobiome Associated With Spacecraft Assembly Cleanrooms. <i>Frontiers in Microbiology</i> , 2022, 13, 777133.	1.5	7
27283	Identification of PBK as a hub gene and potential therapeutic target for medulloblastoma. <i>Oncology Reports</i> , 2022, 48, .	1.2	2
27284	Identification of immune-related biomarkers associated with tumorigenesis and prognosis in skin cutaneous melanoma.. <i>American Journal of Cancer Research</i> , 2022, 12, 1727-1739.	1.4	0
27285	Oncogenic ACSM1 in prostate cancer is through metabolic and extracellular matrix-receptor interaction signaling pathways.. <i>American Journal of Cancer Research</i> , 2022, 12, 1824-1842.	1.4	0
27286	Identification of key gene contributing to vitiligo by immune infiltration.. <i>International Journal of Clinical and Experimental Pathology</i> , 2022, 15, 157-167.	0.5	0
27287	Potential biomarkers and molecular mechanisms in preeclampsia progression. <i>Open Life Sciences</i> , 2022, 17, 529-543.	0.6	0
27288	Single-cell landscape reveals active cell subtypes and their interaction in the tumor microenvironment of gastric cancer. <i>Theranostics</i> , 2022, 12, 3818-3833.	4.6	40
27289	3,3'-Diindolylmethane plus Eflornithine suppress DNA Replication and Cell Cycle in Esophageal Squamous Cell Carcinoma <i>in vivo</i> . <i>Journal of Cancer</i> , 2022, 13, 2607-2619.	1.2	1
27290	Integrated Network Discovery Using Multi-Proteomic Data. <i>Methods in Molecular Biology</i> , 2022, , 173-183.	0.4	1
27292	Construction of the miRNA-mRNA regulatory networks for both the cartilage formation and remodel zones in the antler tip in sika deer ( <i>Cervus nippon</i> ). <i>Animal Production Science</i> , 2022, , .	0.6	0
27293	Analysis and modeling tools of metabolic flux. , 2022, , 45-68.		0
27294	RNA interference screens discover proteases as synthetic lethal partners of PI3K inhibition in breast cancer cells. <i>Theranostics</i> , 2022, 12, 4348-4373.	4.6	3
27295	New Clues to Prognostic Biomarkers of Four Hematological Malignancies. <i>Journal of Cancer</i> , 2022, 13, 2490-2503.	1.2	2
27303	Integrative network-based approaches identified systems-level molecular signatures associated with gallbladder cancer pathogenesis from gallstone diseases. <i>Journal of Biosciences</i> , 2022, 47, .	0.5	0
27304	Constraint-Based, Score-Based and Hybrid Algorithms to Construct Bayesian Gene Networks in the Bovine Transcriptome. <i>Animals</i> , 2022, 12, 1305.	1.0	0
27305	Explore the Effect of Asthma Regulating HIF-1 Pathway on Sperm Quality Based on Rat Model. <i>BioMed Research International</i> , 2022, 2022, 1-10.	0.9	1
27307	The Four Key Genes Participated in and Maintained Atrial Fibrillation Process via Reprogramming Lipid Metabolism in AF Patients. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	8

#	ARTICLE	IF	CITATIONS
27308	Three-Dimensional Organotypic Cultures Reshape the microRNAs Transcriptional Program in Breast Cancer Cells. <i>Cancers</i> , 2022, 14, 2490.	1.7	6
27309	Immunopathogenic overlap between COVID-19 and tuberculosis identified from transcriptomic meta-analysis and human macrophage infection. <i>IScience</i> , 2022, 25, 104464.	1.9	19
27310	Transcriptomic analyses of NeuroD1-mediated astrocyte-to-neuron conversion. <i>Developmental Neurobiology</i> , 2022, 82, 375-391.	1.5	18
27311	Screening the Potential Biomarkers of COVID-19-Related Thrombosis Through Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	0
27312	A Defined Medium for Cultivation and Exometabolite Profiling of Soil Bacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	11
27313	Comprehensive analysis of placental gene-expression profiles and identification of EGFR-mediated autophagy and ferroptosis suppression in intrahepatic cholestasis of pregnancy. <i>Gene</i> , 2022, 834, 146594.	1.0	4
27314	The Downregulated Lipo-Related Gene Expression Pattern in Keloid Indicates Fat Graft Is a Potential Clinical Option for Keloid. <i>Frontiers in Medicine</i> , 2022, 9, .	1.2	1
27315	Remission of peanut allergy is associated with rewiring of allergen-driven T helper 2-related gene networks. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 0, , .	2.7	9
27316	Genome-Wide Mutant Screening in Yeast Reveals that the Cell Wall is a First Shield to Discriminate Light From Heavy Lanthanides. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	7
27317	Single-cell transcriptomes underscore genetically distinct tumor characteristics and microenvironment for hereditary kidney cancers. <i>IScience</i> , 2022, 25, 104463.	1.9	4
27318	Methanotrophy Alleviates Nitrogen Constraint of Carbon Turnover by Rice Root-Associated Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
27320	Comparative transcriptomic analysis reveals region-specific expression patterns in different beef cuts. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
27321	Prediction of the Medicinal Mechanisms of <i>Pinellia ternata</i> Breitenbach, a Traditional Medicine for Gastrointestinal Motility Disorders, through Network Pharmacology. <i>Plants</i> , 2022, 11, 1348.	1.6	2
27324	Host-genotype-dependent cecal microbes are linked to breast muscle metabolites in Chinese chickens. <i>IScience</i> , 2022, 25, 104469.	1.9	5
27325	Genome-wide identification and association analysis for virus-responsive lncRNAs in rice ( <i>Oryza sativa</i> ) Tj ETQq0 0 Q rgBT /Overlock 10 T	1.8	2
27326	Full-Length Transcriptional Analysis of the Same Soybean Genotype With Compatible and Incompatible Reactions to <i>Heterodera glycines</i> Reveals Nematode Infection Activating Plant Defense Response. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	4
27327	Large-scale chromatin reorganization reactivates placenta-specific genes that drive cellular aging. <i>Developmental Cell</i> , 2022, 57, 1347-1368.e12.	3.1	32
27328	Revealing the Organization of Catalytic Sequence-Defined Oligomers via Combined Molecular Dynamics Simulations and Network Analysis. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2761-2770.	2.5	5

#	ARTICLE	IF	CITATIONS
27330	A Conserved Biosynthetic Gene Cluster Is Regulated by Quorum Sensing in a Shipworm Symbiont. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	4
27332	Study on Mechanism of Invigorating Qi and Promoting Blood Circulation in Treatment of Angiogenesis after Myocardial Infarction Using Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	0
27333	Transcriptome Analysis of Traditional Chinese Medicine “Kechuanning Plaster”™ in the Treatment of Asthma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 778-788.	0.6	1
27334	Characterization of a small <sc><b>tRNA</b></sc> â€binding protein that interacts with the archaeal proteasome complex. <i>Molecular Microbiology</i> , 0, , .	1.2	1
27335	Transcriptome Profiling Reveals Genes Related to Sex Determination and Differentiation in Sugarcane Borer ( <i>Chilo sacchariphagus</i> Bojer). <i>Insects</i> , 2022, 13, 500.	1.0	2
27337	Integrated UPLC-Q-TOF-MS/MS and Network Pharmacology Approach to Investigating the Metabolic Profile of Marein of <i>Coreopsis tinctoria</i> Nutt.. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-15.	0.5	0
27338	Comprehensive analysis of gene expression profiles to identify differential prognostic factors of primary and metastatic breast cancer. <i>Saudi Journal of Biological Sciences</i> , 2022, 29, 103318.	1.8	3
27339	Large-scale microbiome data integration enables robust biomarker identification. <i>Nature Computational Science</i> , 2022, 2, 307-316.	3.8	30
27340	Feedback from nuclear RNA on transcription promotes robust RNA concentration homeostasis in human cells. <i>Cell Systems</i> , 2022, 13, 454-470.e15.	2.9	25
27341	Identification of Four Novel Prognostic Biomarkers and Construction of Two Nomograms in Adrenocortical Carcinoma: A Multi-Omics Data Study via Bioinformatics and Machine Learning Methods. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	1
27343	Single-Cell RNA-seq Analysis Reveals Dysregulated Cell-Cell Interactions in a Tumor Microenvironment Related to HCC Development. <i>Disease Markers</i> , 2022, 2022, 1-15.	0.6	3
27344	Identification of the Transcriptional Biomarkers Panel Linked to Pathological Remodelling of the Eye Tissues in Various HD Mouse Models. <i>Cells</i> , 2022, 11, 1675.	1.8	2
27345	Fertilization practices affect biological nitrogen fixation by modulating diazotrophic communities in an acidic soil in southern China. <i>Pedosphere</i> , 2023, 33, 301-311.	2.1	5
27346	Decoding Seven Basic Odors by Investigating Pharmacophores and Molecular Features of Odorants. <i>Current Bioinformatics</i> , 2022, 17, 759-774.	0.7	1
27347	Serum miRNA Profile in Diabetic Patients With Ischemic Heart Disease as a Promising Non-Invasive Biomarker. <i>Frontiers in Endocrinology</i> , 2022, 13, .	1.5	6
27348	Identification and Expression Analysis of Calcium-Dependent Protein Kinases Gene Family in Potato Under Drought Stress. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	8
27350	Comparing Efficiency of Lysis Buffer Solutions and Sample Preparation Methods for Liquid Chromatographyâ€Mass Spectrometry Analysis of Human Cells and Plasma. <i>Molecules</i> , 2022, 27, 3390.	1.7	5
27351	Insights into the Transcriptional Reprogramming in Tomato Response to PSTVd Variants Using Network Approaches. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5983.	1.8	5

#	ARTICLE	IF	CITATIONS
27352	Differential proteome and interactome analysis reveal the basis of pleiotropy associated with the histidine methyltransferase Hpm1p. <i>Molecular and Cellular Proteomics</i> , 2022, , 100249.	2.5	1
27353	Hemostasis and oxidative stress in chronic kidney disease in children and adolescents. <i>Canadian Journal of Physiology and Pharmacology</i> , 0, , .	0.7	0
27354	Identification and characterization of conserved miRNAs from <i>Gossypium hirsutum</i> . <i>Ecological Genetics and Genomics</i> , 2022, 24, 100125.	0.3	0
27355	Adipokines Level and Cognitive Function Disturbance in Homeostasis in Older People with Poorly Managed Hypertension: A Pilot Study. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 6467.	1.2	1
27356	A Quantitative Proteomic Approach Explores the Possible Mechanisms by Which the Small Molecule Stemazole Promotes the Survival of Human Neural Stem Cells. <i>Brain Sciences</i> , 2022, 12, 690.	1.1	2
27357	ErbB Signaling Pathway Genes Are Differentially Expressed in Monozygotic Twins Discordant for Sports-Related Concussion. <i>Twin Research and Human Genetics</i> , 0, , 1-8.	0.3	0
27358	Insights into phenol monomers in response to electron transfer capacity of humic acid during corn straw composting process. <i>Environmental Pollution</i> , 2022, 307, 119548.	3.7	11
27359	Yield-associated putative gene regulatory networks in <i>Oryza sativa</i> L. subsp. indica and their association with high-yielding genotypes. <i>Molecular Biology Reports</i> , 2022, 49, 7649-7663.	1.0	1
27360	Study of microRNA expression in <i>Salmonella Typhimurium</i> -infected porcine ileum reveals miR-194a-5p as an important regulator of the TLR4-mediated inflammatory response. <i>Veterinary Research</i> , 2022, 53, .	1.1	3
27361	Profiling of the Prognostic Role of Extracellular Matrix-Related Genes in Neuroblastoma Using Databases and Integrated Bioinformatics. <i>Onco</i> , 2022, 2, 85-112.	0.2	2
27362	Quantitative proteomics reveals the antibiotics adaptation mechanism of <i>Aeromonas hydrophila</i> under kanamycin stress. <i>Journal of Proteomics</i> , 2022, 264, 104621.	1.2	2
27363	A multi-dimensional liquid chromatography/high-resolution mass spectrometry approach combined with computational data processing for the comprehensive characterization of the multicomponents from <i>Cuscuta chinensis</i> . <i>Journal of Chromatography A</i> , 2022, 1675, 463162.	1.8	21
27364	Hydrocarbon exposure effect on energetic metabolism and immune response in <i>Crassostrea virginica</i> . <i>Marine Pollution Bulletin</i> , 2022, 180, 113738.	2.3	1
27365	Sparstolonin B inhibits pancreatic adenocarcinoma through the NF- $\kappa$ B signaling pathway. <i>Experimental Cell Research</i> , 2022, 417, 113214.	1.2	4
27366	Systematic analysis of nutrigenomic effects of polyphenols related to cardiometabolic health in humans Evidence from untargeted mRNA and miRNA studies. <i>Ageing Research Reviews</i> , 2022, 79, 101649.	5.0	11
27367	Negative impacts of sea-level rise on soil microbial involvement in carbon metabolism. <i>Science of the Total Environment</i> , 2022, 838, 156087.	3.9	7
27368	Nontargeted metabolomics coupled with multivariate modelling techniques for discrimination of <i>Cyclocarya paliurus</i> (Batal.) Ijinskaja leaves from different geographic altitudes. <i>Analytical Methods</i> , 2022, 14, 3270-3279.	1.3	2
27369	RBM15 Protects Cardiomyocytes Apoptosis Under Myocardial Infarction Through Stabilizing NAE1. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
27370	Inflammation Modulates Intercellular Adhesion and Mechanotransduction in Human Epidermis via ROCK2. SSRN Electronic Journal, 0, , .	0.4	0
27371	Single Cell Transcriptomic Analysis of the Identity and Function of Fibro/Adipogenic Progenitors in Healthy and Dystrophic Muscle. SSRN Electronic Journal, 0, , .	0.4	1
27373	DNA methylation plays an important role in iron-overloaded Tibetans. Genes and Genetic Systems, 2022, 97, 55-66.	0.2	6
27374	Decoding the byssus fabrication by spatiotemporal secretome analysis of scallop foot. Computational and Structural Biotechnology Journal, 2022, 20, 2713-2722.	1.9	2
27375	Antibiotics-Induced Transfer of Resistance Genes and Emergence of New Resistant Bacteria in Red Swamp Crayfish Guts and Culture Sediments. SSRN Electronic Journal, 0, , .	0.4	0
27376	Advanced Database Mining of Efficient Biocatalysts by Sequence and Structure Bioinformatics and Microfluidics. SSRN Electronic Journal, 0, , .	0.4	0
27377	Comparative Functional Microrna Landscape of Trophoblast Stem Cell- And Mesenchymal Stem Cell-Derived Exosomes Using Small RNA Profiling. SSRN Electronic Journal, 0, , .	0.4	0
27378	Unraveling Sulfur, Nitrogen Metabolism and Microbial Community Diversity in a High-Temperature Offshore Oilfield. SSRN Electronic Journal, 0, , .	0.4	0
27379	Adaptive Immune Receptor Repertoire (AIRR) Community Guide to Repertoire Analysis. Methods in Molecular Biology, 2022, , 297-316.	0.4	5
27380	Deep Denoising of Raw Biomedical Knowledge Graph From COVID-19 Literature, LitCovid, and Pubtator: Framework Development and Validation. Journal of Medical Internet Research, 2022, 24, e38584.	2.1	4
27381	Automatic MS/MS Data Mining Strategy for Discovering Target Natural Products: A Case of Lindenane Sesquiterpenoids. Analytical Chemistry, 2022, 94, 8514-8522.	3.2	3
27382	The Neuroprotective Effect of Shenmai Injection on Oxidative Stress Injury in PC12 Cells Based on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-13.	0.5	0
27383	Exploring the Effect and Mechanism of Si-Miao-Yong-An Decoction on Abdominal Aortic Aneurysm Based on Mice Experiment and Bioinformatics Analysis. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-15.	0.5	0
27384	High-throughput unmanned aerial vehicle-based phenotyping provides insights into the dynamic process and genetic basis of rapeseed waterlogging response in the field. Journal of Experimental Botany, 2022, 73, 5264-5278.	2.4	7
27385	A novel and diverse set of SNP markers for rangewide genetic studies in Picea abies. Conservation Genetics Resources, 2022, 14, 267-270.	0.4	1
27386	Relationship Between Particle Properties and Immunotoxicological Effects of Environmentally-Sourced Microplastics. Frontiers in Water, 2022, 4, .	1.0	4
27387	Stool microbiota show greater linkages with plasma metabolites compared to salivary microbiota in a multinational cirrhosis cohort. Liver International, 2022, 42, 2274-2282.	1.9	4
27388	Community Competition Is the Microorganism Feedback to Sedimentary Carbon Degradation Process in Aquaculture Tidal Flats. Frontiers in Marine Science, 2022, 9, .	1.2	1



#	ARTICLE	IF	CITATIONS
27389	MLBioGE: integration and interplay of machine learning and bioinformatics approach to identify the genetic effect of SARS-COV-2 on idiopathic pulmonary fibrosis patients. <i>Biology Methods and Protocols</i> , 2022, 7, .	1.0	8
27390	Computational Metabolomics Tools Reveal Metabolic Reconfigurations Underlying the Effects of Biostimulant Seaweed Extracts on Maize Plants under Drought Stress Conditions. <i>Metabolites</i> , 2022, 12, 487.	1.3	21
27391	Combining Activity Profiling with Advanced Annotation to Accelerate the Discovery of Natural Products Targeting Oncogenic Signaling in Melanoma. <i>Journal of Natural Products</i> , 2022, 85, 1540-1554.	1.5	11
27392	Silicon-substituted calcium phosphate promotes osteogenic-angiogenic coupling by activating the TLR4/PI3K/AKT signaling axis. <i>Journal of Biomaterials Applications</i> , 2022, 37, 459-473.	1.2	2
27393	Gut microbiota transplantation drives the adoptive transfer of colonic genotype-phenotype characteristics between mice lacking catestatin and their wild type counterparts. <i>Gut Microbes</i> , 2022, 14, .	4.3	2
27394	Genome-Wide Selection Signatures and Human-Mediated Introgression Events in <i>Bos taurus indicus</i> -influenced Composite Beef Cattle. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
27395	Identification of an Endoplasmic Reticulum Stress-Related Gene Signature to Evaluate the Immune Status and Predict the Prognosis of Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
27396	Hidden impacts of environmental stressors on freshwater communities could be revealed at lower concentrations by correlation of abundances network analyses: An example with herbicides glyphosate, 2, <sc>4â€D</sc>, and their mixtures. <i>Austral Ecology</i> , 2022, 47, 1144-1153.	0.7	2
27397	Identification of an Autophagy-Related Signature Based on Whole Bone Marrow Sequencing for the Prognosis and Immune Microenvironment Characterization of Multiple Myeloma. <i>Journal of Immunology Research</i> , 2022, 2022, 1-14.	0.9	1
27398	Tissue Sampling and Homogenization with NIRL Enables Spatially Resolved Cell Layer Specific Proteomic Analysis of the Murine Intestine. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6132.	1.8	3
27399	Key gene network related to primary ciliary dyskinesia in hippocampus of patients with Alzheimerâ€™s disease revealed by weighted gene co-expression network analysis. <i>BMC Neurology</i> , 2022, 22, .	0.8	1
27401	Variability in the Aerobic Fitness-Related Dependence on Respiratory Processes During Muscle Work Is Associated With the ACE-I/D Genotype. <i>Frontiers in Sports and Active Living</i> , 0, 4, .	0.9	4
27402	Identification of Core Genes and Screening of Potential Targets in Intervertebral Disc Degeneration Using Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
27403	Proteomic Analysis of Lung Cancer Typesâ€™A Pilot Study. <i>Cancers</i> , 2022, 14, 2629.	1.7	7
27404	miRNA-432 and SLC38A1 as Predictors of Hepatocellular Carcinoma Complicated with Alcoholic Steatohepatitis. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-18.	1.9	2
27405	Three Prognostic Biomarkers Correlate with Immune Checkpoint Blockade Response in Bladder Urothelial Carcinoma. <i>International Journal of Genomics</i> , 2022, 2022, 1-35.	0.8	1
27406	Autoreactive CD8+ T cells are restrained by an exhaustion-like program that is maintained by LAG3. <i>Nature Immunology</i> , 2022, 23, 868-877.	7.0	32
27407	Identification and Regulatory Network Analysis of Genes Related to Reproductive Performance in the Hypothalamus and Pituitary of Angus Cattle. <i>Genes</i> , 2022, 13, 965.	1.0	1

#	ARTICLE	IF	CITATIONS
27408	Identification of Metabolic Pathways Differentially Regulated in Somatic and Zygotic Embryos of Maritime Pine. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	8
27409	Bioinformatics prediction of potential mechanisms and biomarkers underlying dilated cardiomyopathy. <i>World Journal of Cardiology</i> , 2022, 14, 282-296.	0.5	3
27410	Multi-omics analysis reveals the mechanism of seed coat color formation in <i>Brassica rapa</i> L.. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2083-2099.	1.8	7
27411	<i>Drosophila</i> gustatory projections are segregated by taste modality and connectivity. <i>ELife</i> , 0, 11, .	2.8	9
27412	Identification of Potential Biomarkers for Pan-Cancer Diagnosis and Prognosis Through the Integration of Large-Scale Transcriptomic Data. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
27413	Interaction Between Cecal Metabolites and Liver Lipid Metabolism Pathways During Induced Molting in Laying Hens. <i>Frontiers in Physiology</i> , 2022, 13, .	1.3	3
27415	ASPM and TROAP gene expression as potential malignant tumor markers. <i>Annals of Translational Medicine</i> , 2022, 10, 586-586.	0.7	4
27416	Genome-Wide Identification, In Silico Characterization of AtCOP1-Targeting Regulatory Proteins Network and their Expression Profiling in The COP1 Downregulated <i>Arabidopsis thaliana</i> . <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
27417	Analysis of Age-Dependent Transcriptomic Changes in Response to Intracerebral Hemorrhage in Mice. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, .	1.4	0
27418	XIST loss impairs mammary stem cell differentiation and increases tumorigenicity through Mediator hyperactivation. <i>Cell</i> , 2022, 185, 2164-2183.e25.	13.5	22
27419	Effects of different ratios of omega-6:omega-3 fatty acids in the diet of sows on the proteome of milk-derived extracellular vesicles. <i>Journal of Proteomics</i> , 2022, 264, 104632.	1.2	2
27420	Overexpression of cytoplasmic dynamin 2 is associated with worse outcomes in patients with clear cell renal cell carcinoma. <i>Cancer Biomarkers</i> , 2022, 35, 27-45.	0.8	4
27421	Identification of potential therapeutic targets associated with diagnosis and prognosis of colorectal cancer patients based on integrated bioinformatics analysis. <i>Computers in Biology and Medicine</i> , 2022, 146, 105688.	3.9	14
27422	Computational investigation of benzalacetophenone derivatives against SARS-CoV-2 as potential multi-target bioactive compounds. <i>Computers in Biology and Medicine</i> , 2022, 146, 105668.	3.9	20
27424	SifR is an Rrf2-family quinone sensor associated with catechol iron uptake in <i>Streptococcus pneumoniae</i> D39. <i>Journal of Biological Chemistry</i> , 2022, , 102046.	1.6	9
27425	Transcriptomic profiling and differential analysis revealed the neurodevelopmental toxicity mechanisms of zebrafish ( <i>Danio rerio</i> ) larvae in response to tetrabromobisphenol A bis(2-hydroxyethyl) ether (TBBPA-DHEE) exposure. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> . 2022. 259. 109382.	1.3	7
27426	Expression Profile and Diagnostic Significance of MicroRNAs in Papillary Thyroid Cancer. <i>Cancers</i> , 2022, 14, 2679.	1.7	7
27427	Molecular Mechanism of the Effect of Zhizhu Pill on Gastroesophageal Reflux Disease Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	4

#	ARTICLE	IF	CITATIONS
27429	Deciphering miR-520c-3p as a probable target for immunometabolism in non-small cell lung cancer using systems biology approach. <i>Oncotarget</i> , 2022, 13, 725-746.	0.8	4
27430	Evolutionary association of receptor-wide amino acids with G protein-coupling selectivity in aminergic GPCRs. <i>Life Science Alliance</i> , 2022, 5, e202201439.	1.3	4
27431	A network analysis to identify lung cancer comorbid diseases. <i>Applied Network Science</i> , 2022, 7, .	0.8	6
27432	Clozapine Long-Term Treatment Might Reduce Epigenetic Age Through Hypomethylation of Longevity Regulatory Pathways Genes. <i>Frontiers in Psychiatry</i> , 2022, 13, .	1.3	1
27433	Comprehensive Analysis of the Immune Cell Infiltration Landscape and Immune-Related Methylation in Retinoblastoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
27434	Gene co-expression network based on part mutual information for gene-to-gene relationship and gene-cancer correlation analysis. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
27435	The impact of different feeds on DNA methylation, glycolysis/gluconeogenesis signaling pathway, and gene expression of sheep muscle. <i>PeerJ</i> , 0, 10, e13455.	0.9	0
27436	Tissue-Specific Analysis of Alternative Splicing Events and Differential Isoform Expression in Large Yellow Croaker ( <i>Larimichthys crocea</i> ) After <i>Cryptocaryon irritans</i> Infection. <i>Marine Biotechnology</i> , 2022, 24, 640-654.	1.1	3
27437	Vineyard establishment under exacerbated summer stress: effects of mycorrhization on rootstock agronomical parameters, leaf element composition and root-associated bacterial microbiota. <i>Plant and Soil</i> , 2022, 478, 613-634.	1.8	3
27438	Identifying Candidate Flavonoids for Non-Alcoholic Fatty Liver Disease by Network-Based Strategy. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
27439	Comparative Transcriptomic Immune Responses of Mullet ( <i>Mugil cephalus</i> ) Infected by Planktonic and Biofilm <i>Lactococcus Garvieae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
27440	Bioinformatics Study Identified EGF as a Crucial Gene in Papillary Renal Cell Cancer. <i>Disease Markers</i> , 2022, 2022, 1-19.	0.6	0
27442	Metabolome and Transcriptome Analysis Reveals the Transcriptional Regulatory Mechanism of Triterpenoid Saponin Biosynthesis in Soapberry ( <i>Sapindus mukorossi</i> Gaertn.). <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 7095-7109.	2.4	10
27443	Metabolic control of arginine and ornithine levels paces the progression of leaf senescence. <i>Plant Physiology</i> , 2022, 189, 1943-1960.	2.3	15
27444	Host-dependent impairment of parasite development and reproduction in the acanthocephalan model. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	3
27446	Seasonal co-occurrence patterns of bacteria and eukaryotic phytoplankton and the ecological response in urban aquatic ecosystem. <i>Journal of Oceanology and Limnology</i> , 2022, 40, 1508-1529.	0.6	2
27447	Transcriptional profiling of human V1 T cells reveals a pathogen-driven adaptive differentiation program. <i>Cell Reports</i> , 2022, 39, 110858.	2.9	13
27448	A Photo-Crosslinking Approach to Identify Class II SUMO-1 Binders. <i>Frontiers in Chemistry</i> , 2022, 10, .	1.8	3

#	ARTICLE	IF	CITATIONS
27449	Anti-inflammatory effects of recreational marijuana in virally suppressed youth with HIV-1 are reversed by use of tobacco products in combination with marijuana. <i>Retrovirology</i> , 2022, 19, .	0.9	9
27450	Further insights into the association of the protein phosphatase gene <i>ABI1</i> with drought and salinity stress responses in Brassica species. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2023, 32, 106-120.	0.9	3
27451	The combined use of acetazolamide and <i>Rhodiola</i> in the prevention and treatment of altitude sickness. <i>Annals of Translational Medicine</i> , 2022, 10, 541-541.	0.7	4
27452	Transcriptome Analysis of Response to Aluminum Stress in <i>Pinus massoniana</i> . <i>Forests</i> , 2022, 13, 837.	0.9	5
27454	Exploring the metabolic landscape of pancreatic ductal adenocarcinoma cells using genome-scale metabolic modeling. <i>IScience</i> , 2022, 25, 104483.	1.9	4
27456	Differential <i>Etv2</i> threshold requirement for endothelial and erythropoietic development. <i>Cell Reports</i> , 2022, 39, 110881.	2.9	9
27457	Asthma and the Missing Heritability Problem: Necessity for Multiomics Approaches in Determining Accurate Risk Profiles. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	5
27458	A Random Forest-Based Genome-Wide Scan Reveals Fertility-Related Candidate Genes and Potential Inter-Chromosomal Epistatic Regions Associated With Age at First Calving in Nellore Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
27459	Integrated bioinformatics and statistical approaches to explore molecular biomarkers for breast cancer diagnosis, prognosis and therapies. <i>PLoS ONE</i> , 2022, 17, e0268967.	1.1	16
27460	Identification of Hub Genes Associated with Nonspecific Orbital Inflammation by Weighted Gene Coexpression Network Analysis. <i>Disease Markers</i> , 2022, 2022, 1-9.	0.6	1
27461	Somatostatin signalling promotes the differentiation of rod photoreceptors in human pluripotent stem cell-derived retinal organoid. <i>Cell Proliferation</i> , 2022, 55, .	2.4	6
27462	Activation of <i>Nlx2.5</i> transcriptional program is required for adult myocardial repair. <i>Nature Communications</i> , 2022, 13, .	5.8	7
27463	Identification of the Active Compound of Liu Wei Di Huang Wan for Treatment of Gestational Diabetes Mellitus via Network Pharmacology and Molecular Docking. <i>Journal of Diabetes Research</i> , 2022, 2022, 1-13.	1.0	3
27467	Biomedical Analytics of Four Chinese Medicinals in Treatment of Insomnia Based on Network Pharmacology. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	0
27468	Transcriptome Sequencing Analysis Reveals Dynamic Changes in Major Biological Functions during the Early Development of Clearhead Icefish, <i>Protosalanx chinensis</i> . <i>Fishes</i> , 2022, 7, 115.	0.7	2
27469	Identification of Key Prognostic Genes of Triple Negative Breast Cancer by LASSO-Based Machine Learning and Bioinformatics Analysis. <i>Genes</i> , 2022, 13, 902.	1.0	14
27471	Amentoflavone derivatives significantly act towards the main protease (3CLPRO/MPRO) of SARS-CoV-2: in silico admet profiling, molecular docking, molecular dynamics simulation, network pharmacology. <i>Molecular Diversity</i> , 2023, 27, 857-871.	2.1	26
27472	An Integrated Metabolome and Transcriptome Analysis Reveal the Regulation Mechanisms of Flavonoid Biosynthesis in a Purple Tea Plant Cultivar. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	8

#	ARTICLE	IF	CITATIONS
27473	Cross-Species Analysis Reveals Co-Expressed Genes Regulating Antler Development in Cervidae. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
27474	Trained Immunity in Perivascular Adipose Tissue of Abdominal Aortic Aneurysm—A Novel Concept for a Still Elusive Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	7
27476	Prognostic implications of PPL expression in ovarian cancer. <i>Discover Oncology</i> , 2022, 13, .	0.8	3
27478	Promising <i>Acinetobacter baumannii</i> Vaccine Candidates and Drug Targets in Recent Years. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
27480	Expression Profiles and Characteristics of Apple lncRNAs in Roots, Phloem, Leaves, Flowers, and Fruit. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5931.	1.8	4
27481	Identification of Peripheral Blood miRNA Biomarkers in First-Episode Drug-Free Schizophrenia Patients Using Bioinformatics Strategy. <i>Molecular Neurobiology</i> , 2022, 59, 4730-4746.	1.9	9
27482	Single-cell transcriptomics reveals lineage trajectory of human scalp hair follicle and informs mechanisms of hair graying. <i>Cell Discovery</i> , 2022, 8, .	3.1	11
27483	Sustainability of the rice-crayfish co-culture aquaculture model: microbiome profiles based on multi-kingdom analyses. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	7
27484	Peripheral Blood Microbiome Analysis via Noninvasive Prenatal Testing Reveals the Complexity of Circulating Microbial Cell-Free DNA. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
27485	Genome-wide identification of Aux/IAA and ARF gene families in bread wheat ( <i>Triticum aestivum</i> L.). <i>Protoplasma</i> , 2023, 260, 257-270.	1.0	7
27486	Spatial region-resolved proteome map reveals mechanism of COVID-19-associated heart injury. <i>Cell Reports</i> , 2022, 39, 110955.	2.9	16
27487	A network-based pharmacological study on the mechanism of action of muscone in breast cancer. <i>Translational Cancer Research</i> , 2022, 11, 1195-1206.	0.4	1
27488	Development of a Prognostic Model Based on Pyroptosis-Related Genes in Pancreatic Adenocarcinoma. <i>Disease Markers</i> , 2022, 2022, 1-28.	0.6	4
27489	Regulatory T Cell-Related Gene Indicators in Pulmonary Hypertension. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
27490	Analysis of multiple databases identifies crucial genes correlated with prognosis of hepatocellular carcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
27491	ARID Regulates <i>P. falciparum</i> Malaria Parasite Male Gametogenesis and Female Fertility and Is Critical for Parasite Transmission to the Mosquito Vector. <i>MBio</i> , 2022, 13, .	1.8	8
27492	Effects of ACTH-Induced Long-Term Hypercortisolism on the Transcriptome of Canine Visceral Adipose Tissue. <i>Veterinary Sciences</i> , 2022, 9, 250.	0.6	1
27493	Glenthmycins—M: Macrocyclic Spirotetronate Polyketide Antibacterials from the Australian Pasture Plant-Derived <i>Streptomyces</i> sp. CMB-PB041. <i>Journal of Natural Products</i> , 2022, 85, 1641-1657.	1.5	3

#	ARTICLE	IF	CITATIONS
27494	A Prognostic Signature for Clear Cell Renal Cell Carcinoma Based on Ferroptosis-Related lncRNAs and Immune Checkpoints. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	8
27495	Deep vertical rotary tillage increases the diversity of bacterial communities and alters the bacterial network structure in soil planted to corn. <i>Canadian Journal of Soil Science</i> , 0, , .	0.5	0
27496	Integrated Analysis of Glutathione Metabolic Pathway in Pancreatic Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
27497	Two differentially methylated region networks in nonalcoholic fatty liver disease, viral hepatitis, and hepatocellular carcinoma. <i>BMC Gastroenterology</i> , 2022, 22, .	0.8	3
27498	Transcriptome analysis reveals the spinal expression profiles of non-coding RNAs involved in anorectal malformations in rat fetuses. <i>Journal of Pediatric Surgery</i> , 2022, , .	0.8	0
27499	Applications of Omics Technology for Livestock Selection and Improvement. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	10
27500	Circulating lncRNA- and miRNA-Associated ceRNA Network as a Potential Prognostic Biomarker for Non-Hodgkin Lymphoma: A Bioinformatics Analysis and a Pilot Study. <i>Biomedicines</i> , 2022, 10, 1322.	1.4	2
27501	Bioinformatics-Led Discovery of Osteoarthritis Biomarkers and Inflammatory Infiltrates. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	31
27502	Insights gained from Single-Cell analysis of immune cells on Cyclosporine A treatment in autoimmune uveitis. <i>Biochemical Pharmacology</i> , 2022, 202, 115116.	2.0	3
27503	Analysis of microarray-identified genes and MicroRNAs associated with Trifluridine resistance in colorectal cancer. <i>International Journal of Transgender Health</i> , 2022, 15, 636-648.	1.1	0
27504	Comparative transcriptomics in the hypothalamic-pituitary-gonad axis of mammals and poultry. <i>Genomics</i> , 2022, 114, 110396.	1.3	9
27505	Recapitulated Crosstalk between Cerebral Metastatic Lung Cancer Cells and Brain Perivascular Tumor Microenvironment in a Microfluidic Co-culture Chip. <i>Advanced Science</i> , 2022, 9, .	5.6	12
27506	A Standardized Framework for Better Understanding of Phenotypic Differences within Bacterial Phyla Based on Protein Domain. <i>Journal of Bacteriology</i> , 0, , .	1.0	0
27507	MeWRKY Ilas, Subfamily Genes of WRKY Transcription Factors From Cassava, Play an Important Role in Disease Resistance. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3
27508	Identification of candidate biomarkers and pathways associated with type 1 diabetes mellitus using bioinformatics analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
27509	Targeted Assessment of Mucosal Immune Gene Expression Predicts Clinical Outcomes in Children with Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1735-1750.	0.6	2
27510	Gastrointestinal symbiont diversity in wild gorilla: A comparison of bacterial and strongylid communities across multiple localities. <i>Molecular Ecology</i> , 2022, 31, 4127-4145.	2.0	2
27512	Genome-Wide Identification and Analysis of Ariadne Gene Family Reveal Its Genetic Effects on Agronomic Traits of <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6265.	1.8	3



#	ARTICLE	IF	CITATIONS
27513	Role of Nucleolin in Endometrial Precancerous Hyperplasia and Carcinogenesis: Ex Vivo and In Silico Study. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6228.	1.8	3
27514	A comparative meta-proteomic pipeline for the identification of plasmodesmata proteins and regulatory conditions in diverse plant species. <i>BMC Biology</i> , 2022, 20, .	1.7	9
27515	Characterisation of a nucleo-adhesome. <i>Nature Communications</i> , 2022, 13, .	5.8	4
27516	ASCL2 Affects the Efficacy of Immunotherapy in Colon Adenocarcinoma Based on Single-Cell RNA Sequencing Analysis. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	1
27517	Identification of biomarkers, immune infiltration landscape, and treatment targets of ischemiaâ€“reperfusion acute kidney injury at an early stage by bioinformatics methods. <i>Hereditas</i> , 2022, 159, .	0.5	6
27518	Deregulation of ceRNA Networks in Frontal Cortex and Choroid Plexus of Brain during SARSâ€“CoVâ€“2 Infection Aggravates Neurological Manifestations: An Insight from Bulk and Singleâ€“Cell Transcriptomic Analyses. <i>Advanced Biology</i> , 2022, 6, .	1.4	2
27519	Mechanisms of <i>Gynostemma pentaphyllum</i> against nonâ€“alcoholic fibre liver disease based on network pharmacology and molecular docking. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 3760-3771.	1.6	5
27520	A Network Pharmacological Elucidation of the Systematic Treatment Activities and Mechanisms of the Herbal Drug FDY003 Against Esophageal Cancer. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211053.	0.2	0
27521	Leveraging transcriptome and epigenome landscapes to infer regulatory networks during the onset of sexual maturation. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
27522	Alterations of Gut Microbiome and Metabolite Profiles Associated With Anabolic Lipid Dysmetabolism in Thyroid Cancer. <i>Frontiers in Endocrinology</i> , 2022, 13, .	1.5	15
27523	Exploring the Potential Mechanisms of <i>Melilotus officinalis</i> (L.) Pall. in Chronic Muscle Repair Patterns Using Single Cell Receptor-Ligand Marker Analysis and Molecular Dynamics Simulations. <i>Disease Markers</i> , 2022, 2022, 1-11.	0.6	7
27524	Differential Gene Expression and Weighted Correlation Network Dynamics in High-Throughput Datasets of Prostate Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	11
27525	A gene prognostic index from cellular senescence predicting metastasis and radioresistance for prostate cancer. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	19
27526	Bioinformatics and System Biology Approach to Reveal the Interaction Network and the Therapeutic Implications for Non-Small Cell Lung Cancer Patients With COVID-19. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	4
27527	Genome-Wide Identification of Long Noncoding RNA and Their Potential Interactors in ISWI Mutants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6247.	1.8	2
27528	Synthetic negative genome screen of the GPN-loop GTPase NPA3 in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2022, 68, 343-360.	0.8	3
27529	Integrated metabolomic and transcriptomic analyses of two peanut ( <i>Arachis hypogaea</i> L.) cultivars differing in amino acid metabolism of the seeds. <i>Plant Physiology and Biochemistry</i> , 2022, 185, 132-143.	2.8	5
27530	Liver transcriptome analysis reveals biological pathways and transcription factors in response to high ammonia exposure. <i>Inhalation Toxicology</i> , 2022, 34, 219-229.	0.8	2

#	ARTICLE	IF	CITATIONS
27531	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. <i>Science Advances</i> , 2022, 8, .	4.7	14
27532	Comparative proteomics analysis of <i>Arabidopsis thaliana</i> response to light-emitting diode of narrow wavelength 450Ånm, 595Ånm, and 650Ånm. <i>Journal of Proteomics</i> , 2022, 265, 104635.	1.2	2
27533	Differentially Expressed miRNAs in Ulcerative Colitis and Crohn's Disease. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	15
27534	Novel targets in rectal cancer by considering lncRNA-miRNA-mRNA network in response to <i>Lactobacillus acidophilus</i> consumption: a randomized clinical trial. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
27535	Profiling the Tumor-Infiltrating Lymphocytes in Gastric Cancer Reveals Its Implication in the Prognosis. <i>Genes</i> , 2022, 13, 1017.	1.0	2
27536	Identification of hub pathways and drug candidates in gastric cancer through systems biology. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
27537	Whole-Blood Transcriptional Profiles Enable Early Prediction of the Presence of Coronary Atherosclerosis and High-Risk Plaque Features at Coronary CT Angiography. <i>Biomedicines</i> , 2022, 10, 1309.	1.4	4
27538	Combined LC-MS/MS and Molecular Networking Approach Reveals Antioxidant and Antimicrobial Compounds from <i>Erismadelphus exsul</i> Bark. <i>Plants</i> , 2022, 11, 1505.	1.6	5
27539	Synthesis of Coumarin and Homoisoflavonoid Derivatives and Analogs: The Search for New Antifungal Agents. <i>Pharmaceuticals</i> , 2022, 15, 712.	1.7	11
27540	Whole-Transcriptome Analysis Reveals Autophagy Is Involved in Early Senescence of zj-es Mutant Rice. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
27541	Impact of arsenic on microbial community structure and their metabolic potential from rice soils of West Bengal, India. <i>Science of the Total Environment</i> , 2022, 841, 156486.	3.9	9
27542	DIRECT-NET: An efficient method to discover cis-regulatory elements and construct regulatory networks from single-cell multiomics data. <i>Science Advances</i> , 2022, 8, .	4.7	21
27543	Multivariate Analysis of Metabolomic and Nutritional Profiles among Children with Autism Spectrum Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 923.	1.1	2
27544	The Dengue Virus Nonstructural Protein 1 (NS1) Interacts with the Putative Epigenetic Regulator DDO1 to Promote Flavivirus Replication in Mosquito Cells. <i>Journal of Virology</i> , 2022, 96, .	1.5	4
27545	UG/Abi: a highly diverse family of prokaryotic reverse transcriptases associated with defense functions. <i>Nucleic Acids Research</i> , 2022, 50, 6084-6101.	6.5	11
27547	Network Pharmacology Analysis and Surface Plasmon Resonance Validation of Active Compounds and Molecular Targets in Siwei Jianbu Decoction for Blood Stasis in Diabetic Patient. <i>ChemistrySelect</i> , 2022, 7, .	0.7	1
27548	Implicating effector genes at COVID-19 GWAS loci using promoter-focused Capture-C in disease-relevant immune cell types. <i>Genome Biology</i> , 2022, 23, .	3.8	12
27551	Nitrate enhances the secondary growth of storage roots in <i>Panax ginseng</i> . <i>Journal of Ginseng Research</i> , 2023, 47, 469-478.	3.0	6

#	ARTICLE	IF	CITATIONS
27552	Dysregulation of microRNAs and tRNA-derived ncRNAs in mesothelial and mesothelioma cell lines after asbestiform fiber exposure. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
27553	Network construction revealed that gestational diabetes mellitus may lead to congenital heart disease via potential lncRNAs-miRNAs regulating PPAR $\beta$ . , 2022, 33, 201062.		0
27554	Identification of the Key Genes Associated with Different Hair Types in the Inner Mongolia Cashmere Goat. <i>Animals</i> , 2022, 12, 1456.	1.0	7
27555	Heterochronic parabiosis induces stem cell revitalization and systemic rejuvenation across aged tissues. <i>Cell Stem Cell</i> , 2022, 29, 990-1005.e10.	5.2	53
27556	Expression Plasticity of Transposable Elements is Highly Associated with Organismal Re-adaptation to Ancestral Environments. <i>Genome Biology and Evolution</i> , 0, , .	1.1	0
27557	Transcriptome analysis revealed hub genes for muscle growth in Indian major carp, <i>Catla catla</i> (Hamilton, 1822). <i>Genomics</i> , 2022, 114, 110393.	1.3	3
27558	Quantitative analysis of redox proteome reveals oxidation-sensitive protein thiols acting in fundamental processes of developmental hematopoiesis. <i>Redox Biology</i> , 2022, 53, 102343.	3.9	7
27559	Arc and Homer1 are involved in comorbid epilepsy and depression: A microarray data analysis. <i>Epilepsy and Behavior</i> , 2022, 132, 108738.	0.9	4
27560	The secretome of irradiated peripheral blood mononuclear cells attenuates activation of mast cells and basophils. <i>EBioMedicine</i> , 2022, 81, 104093.	2.7	7
27561	Phosphoproteome profiling of rice tissues provides new insights into responsive mechanisms and kinase activity upon salt stress. <i>Environmental and Experimental Botany</i> , 2022, 200, 104917.	2.0	1
27562	Chemosensitizing effect of neferine on cisplatin-resistant colorectal cancer: Identification of potential candidate genes and pathways through whole transcriptome profiling. <i>Phytomedicine Plus</i> , 2022, 2, 100299.	0.9	0
27563	Carbon cycle in the microbial ecosystems of biological soil crusts. <i>Soil Biology and Biochemistry</i> , 2022, 171, 108729.	4.2	20
27564	Weighted gene co-expression network analysis reveals the mechanisms of evolutionary adaptation and selection behind blind-side hypermelanosis in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Aquaculture</i> , 2022, 558, 738394.	1.7	0
27583	Establishment and verification of a prognostic model of liver cancer by RNA-binding proteins based on the TCGA database. <i>Translational Cancer Research</i> , 2022, 11, 1925-1937.	0.4	1
27584	A potential EBV-related classifier is associated with the efficacy of immunotherapy in gastric cancer. <i>Translational Cancer Research</i> , 2022, 11, 2084-2096.	0.4	3
27585	Bioinformatics analysis identifies diagnostic biomarkers and their correlation with immune infiltration in diabetic nephropathy. <i>Annals of Translational Medicine</i> , 2022, 10, 669-669.	0.7	3
27586	Analysis of dapagliflozin-induced expression profile of long noncoding RNAs in proximal tubular epithelial cells of diabetic kidney disease. <i>Diabetic Nephropathy</i> , 2021, 1, 77-89.	0.1	0
27587	Understanding How the Relative Abundance of <i>Candida</i> Species Impacts Transcriptional Regulation in Co-culture Biofilms. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
27588	Integrative ontology and pathway-based approach identifies distinct molecular signatures in transcriptomes of esophageal squamous cell carcinoma. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 177-206.	1.0	6
27589	<i>Rbm20</i> ablation is associated with changes in the expression of titin-interacting and metabolic proteins. <i>Molecular Omics</i> , 2022, 18, 627-634.	1.4	2
27590	Implementation of an MS/MS Spectral Library for Monoterpene Indole Alkaloids. <i>Methods in Molecular Biology</i> , 2022, , 87-100.	0.4	2
27591	Allopeptimicins: unique antibacterial metabolites generated by hybrid PKS-NRPS, with original self-defense mechanism in <i>Actinoallomurus</i> . <i>RSC Advances</i> , 2022, 12, 16640-16655.	1.7	2
27592	Updates on Genomic Resources for Crop Improvement. <i>Springer Protocols</i> , 2022, , 13-29.	0.1	1
27594	FMR1 is identified as an immune-related novel prognostic biomarker for renal clear cell carcinoma: A bioinformatics analysis of TAZ/YAP. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 9295-9320.	1.0	3
27595	miR-140-3p suppresses the proliferation and migration of macrophages. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	1
27596	Finger Millet Transcriptome Analysis Using High Throughput Sequencing Technologies. <i>Compendium of Plant Genomes</i> , 2022, , 123-134.	0.3	1
27597	IR: Regulation of DNA Methylation During the Testicular Development of Shaziling Pigs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27598	Proteomic Landscape of Primary and Metastatic Brain Tumors for Heterogeneity Discovery. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27599	Investigation of differentially expressed genes and dysregulated pathways involved in multiple sclerosis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 235-259.	1.0	2
27600	Boolean modelling as a logic-based dynamic approach in systems medicine. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3161-3172.	1.9	23
27601	Transcriptome Analysis of Artificial Cultivated Mushrooms in Qinba Mountains. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27602	The Potential of Lipid Metabolism-Related&nbsp;Gene CEBPD as a Biomarker in Thoracic Aortic Dissection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27604	The Development of Mechanical Allodynia in Diabetic Rats Revealed by Single-Cell RNA-Seq. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	9
27605	Functional analysis of long non-coding RNAs involved in alkaline stress responses in wheat. <i>Journal of Experimental Botany</i> , 2022, 73, 5698-5714.	2.4	10
27606	Inflammation and remodeling pathways and risk of cardiovascular events in patients with ischemic heart failure and reduced ejection fraction. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
27608	Elastic network modeling of cellular networks unveils sensor and effector genes that control information flow. <i>PLoS Computational Biology</i> , 2022, 18, e1010181.	1.5	0

#	ARTICLE	IF	CITATIONS
27609	Presence of rare potential pathogenic variants in subjects under 65 years old with very severe or fatal COVID-19. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
27610	Identification of early neurodegenerative pathways in progressive multiple sclerosis. <i>Nature Neuroscience</i> , 2022, 25, 944-955.	7.1	55
27611	Mechanism of Action of Zhi Gan Cao Decoction for Atrial Fibrillation and Myocardial Fibrosis in a Mouse Model of Atrial Fibrillation: A Network Pharmacology-Based Study. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-22.	0.7	2
27613	Metagenomic Screening for Lipolytic Genes Reveals an Ecology-Clustered Distribution Pattern. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
27614	Identification of differentially expressed long noncoding RNAs in the ovarian tissue of Shal and Sangsari ewes using RNA-seq. <i>Veterinary Medicine and Science</i> , 2022, 8, 2138-2146.	0.6	3
27615	Deep learning driven biosynthetic pathways navigation for natural products with BioNavi-NP. <i>Nature Communications</i> , 2022, 13, .	5.8	35
27616	The dynamic cellular and molecular features during the development of radiation proctitis revealed by transcriptomic profiling in mice. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
27617	An epigenome-wide study of DNA methylation profiles and lung function among American Indians in the Strong Heart Study. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	0
27618	Network pharmacological evaluation of strigolactones efficacy as potential inhibitors against therapeutic targets of hepatocellular carcinoma. <i>Biotechnology Letters</i> , 0, , .	1.1	2
27619	Microrna-1224-5p Is a Potential Prognostic and Therapeutic Biomarker in Glioblastoma: Integrating Bioinformatics and Clinical Analyses. <i>Current Medical Science</i> , 2022, 42, 584-596.	0.7	4
27620	AddictedChem: A Data-Driven Integrated Platform for New Psychoactive Substance Identification. <i>Molecules</i> , 2022, 27, 3931.	1.7	3
27621	Analysis of the Arabidopsis <i>coilin</i> mutant reveals a positive role of AtCOILIN in plant immunity. <i>Plant Physiology</i> , 2022, 190, 745-761.	2.3	6
27623	A comprehensive bioinformatics analysis to identify potential prognostic biomarkers among CC and CXC chemokines in breast cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
27624	Identification of biomarkers for immunotherapy response in prostate cancer and potential drugs to alleviate immunosuppression. <i>Aging</i> , 2022, 14, 4839-4857.	1.4	3
27625	DNA Methylation and RNA-Sequencing Analysis to Identify Genes Related to Spontaneous Leaf Spots in a Wheat Variety "Zhongkenuomai No.1". <i>Agronomy</i> , 2022, 12, 1519.	1.3	0
27626	Gene Expression Changes of Murine Cortex Homeostasis in Response to Sleep Deprivation Hint Dysregulated Aging-like Transcriptional Responses. <i>Brain Sciences</i> , 2022, 12, 825.	1.1	2
27627	A novel 7 RNA-based signature for prediction of prognosis and therapeutic responses of wild-type BRAF cutaneous melanoma. <i>Biological Procedures Online</i> , 2022, 24, .	1.4	0
27628	SPD_0090 Negatively Contributes to Virulence of <i>Streptococcus pneumoniae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
27629	Liver cancer heterogeneity modeled by in situ genome editing of hepatocytes. <i>Science Advances</i> , 2022, 8, .	4.7	15
27630	Mitochondrial cyclophilin D promotes disease tolerance by licensing NK cell development and IL-22 production against influenza virus. <i>Cell Reports</i> , 2022, 39, 110974.	2.9	5
27632	Exonuclease 1 is a Potential Diagnostic and Prognostic Biomarker in Hepatocellular Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	5
27633	Neutrophil Infiltration Characterized by Upregulation of S100A8, S100A9, S100A12 and CXCR2 Is Associated With the Co-Occurrence of Crohn's Disease and Peripheral Artery Disease. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
27634	ERG activity is regulated by endothelial FAK coupling with TRIM25/USP9x in vascular patterning. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	4
27635	Soil Chemical Pollution and Military Actions: A Bibliometric Analysis. <i>Sustainability</i> , 2022, 14, 7138.	1.6	4
27636	Identification of peroxiredoxin II and its related molecules as potential biomarkers of dermal mesenchymal stem cell homing using network analysis. <i>Applied Biological Chemistry</i> , 2022, 65, .	0.7	1
27637	Genomic Diversity of Hospital-Acquired Infections Revealed through Prospective Whole-Genome Sequencing-Based Surveillance. <i>MSystems</i> , 2022, 7, .	1.7	10
27638	Deep Small RNA Sequencing Reveals Important miRNAs Related to Muscle Development and Intramuscular Fat Deposition in Longissimus dorsi Muscle From Different Goat Breeds. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	7
27639	Maternal age affects equine day 8 embryo gene expression both in trophoblast and inner cell mass. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
27640	Intratracheal Transplantation of Mesenchymal Stem Cells Attenuates Hyperoxia-Induced Microbial Dysbiosis in the Lungs, Brain, and Gut in Newborn Rats. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6601.	1.8	2
27641	Comprehensive analysis of KCTD family genes associated with hypoxic microenvironment and immune infiltration in lung adenocarcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
27642	Spatial centrosome proteome of human neural cells uncovers disease-relevant heterogeneity. <i>Science</i> , 2022, 376, .	6.0	25
27643	Dual-Hit Model of Parkinson's Disease: Impact of Dysbiosis on 6-Hydroxydopamine-Insulted Mice's Neuroprotective and Anti-Inflammatory Effects of Butyrate. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6367.	1.8	13
27644	An approach to cellular tropism of SARS-CoV-2 through protein-protein interaction and enrichment analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
27645	Weighted Gene Co-expression Network Analysis Identifies Specific Modules and Hub Genes Related to Subacute Ruminant Acidosis. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
27646	Identification of four serum miRNAs as potential markers to screen for thirteen cancer types. <i>PLoS ONE</i> , 2022, 17, e0269554.	1.1	6
27647	The LINC00261/MiR105-5p/SELL axis is involved in dysfunction of B cell and is associated with overall survival in hepatocellular carcinoma. <i>PeerJ</i> , 0, 10, e12588.	0.9	5



#	ARTICLE	IF	CITATIONS
27648	Synergistic anti-proliferative activity of JQ1 and GSK2801 in triple-negative breast cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	11
27649	Renal tubular gene biomarkers identification based on immune infiltrates in focal segmental glomerulosclerosis. <i>Renal Failure</i> , 2022, 44, 966-986.	0.8	2
27650	Exploring the comorbidity mechanisms between asthma and idiopathic pulmonary fibrosis and the pharmacological mechanisms of Bu-Shen-Yi-Qi decoction therapy via network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	0
27651	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. <i>Nature Cell Biology</i> , 2022, 24, 858-871.	4.6	30
27652	The Breast Cancer Protein Co-Expression Landscape. <i>Cancers</i> , 2022, 14, 2957.	1.7	3
27653	Computational epigenetic landscape analysis reveals association of CACNA1G-AS1, F11-AS1, NNT-AS1, and MSC-AS1 lncRNAs in prostate cancer progression through aberrant methylation. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
27654	Identification of prognostic candidate signatures by systematically revealing transcriptome characteristics in lung adenocarcinoma with differing tumor microenvironment immune phenotypes. <i>Aging</i> , 2022, 14, 4786-4818.	1.4	2
27655	The Transcription Factor, $\hat{\pm}1ACT$ , Acts Through a MicroRNA Network to Regulate Neurogenesis and Cell Death During Neonatal Cerebellar Development. <i>Cerebellum</i> , 0, , .	1.4	0
27656	Network Pharmacology and Data Mining Approach Reveal the Medication Rule of Traditional Chinese Medicine in the Treatment of Premenstrual Syndrome/Premenstrual Dysphoric Disorder. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
27657	Diversity of an uncommon elastic hypersaline microbial mat along a small-scale transect. <i>PeerJ</i> , 0, 10, e13579.	0.9	10
27658	Mass spectrometry methods for analysis of extracellular matrix components in neurological diseases. <i>Mass Spectrometry Reviews</i> , 2023, 42, 1848-1875.	2.8	4
27659	Metabolomics with multi-block modelling of mass spectrometry and nuclear magnetic resonance in order to discriminate Haplosclerida marine sponges. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 5929-5942.	1.9	4
27660	Epigenetic reactivation of transcriptional programs orchestrating fetal lung development in human pulmonary hypertension. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	15
27661	Microbiome function underpins the efficacy of a fiber-supplemented dietary intervention in dogs with chronic large bowel diarrhea. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	5
27662	Whole-Blood and Peripheral Mononuclear Cell Transcriptional Response to Prolonged Altitude Exposure in Well-Trained Runners. <i>Clinical Journal of Sport Medicine</i> , 2022, Publish Ahead of Print, .	0.9	2
27663	Xyloketal B Reverses Nutritional Hepatic Steatosis, Steatohepatitis, and Liver Fibrosis through Activation of the PPAR $\hat{\pm}$ /PGC1 $\hat{\pm}$ Signaling Pathway. <i>Journal of Natural Products</i> , 2022, 85, 1738-1750.	1.5	4
27664	Calculating genetic risk for dysfunction in pleiotropic biological processes using whole exome sequencing data. <i>Journal of Neurodevelopmental Disorders</i> , 2022, 14, .	1.5	0
27665	Characterization of Circular RNA Expression Profiles in Colon Specimens of Patients with Slow Transit Constipation. <i>Disease Markers</i> , 2022, 2022, 1-11.	0.6	0

#	ARTICLE	IF	CITATIONS
27667	Deepening the knowledge of rare diseases dependent on angiogenesis through semantic similarity clustering and network analysis. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	1
27668	Concurrent exercise and aerobic-resistance exercise ameliorate the serum of Retinol-Binding Protein-4 level and insulin resistance in postmenopausal women. <i>Science and Sports</i> , 2022, , .	0.2	0
27669	Comparative Analysis of Fat Composition in Marrow, Serum, and Muscle from Aging C57BL6 mice. <i>Mechanisms of Ageing and Development</i> , 2022, , 111690.	2.2	1
27670	Research on the Mechanism of Asperosaponin VI for Treating Recurrent Spontaneous Abortion by Bioinformatics Analysis and Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-17.	0.5	1
27671	Multi-Level Biological Network Analysis and Drug Repurposing Based on Leukocyte Transcriptomics in Severe COVID-19: In Silico Systems Biology to Precision Medicine. <i>Journal of Personalized Medicine</i> , 2022, 12, 1030.	1.1	7
27672	A Machine Learning Framework Predicts the Clinical Severity of Hemophilia B Caused by Point-Mutations. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	4
27673	Identification of Age-associated Proteins and Functional Alterations in Human Retinal Pigment Epithelium. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 633-647.	3.0	5
27674	Expression and prognosis analysis of mitochondrial ribosomal protein family in breast cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
27675	Integrative transcriptome-wide analysis of atopic dermatitis for drug repositioning. <i>Communications Biology</i> , 2022, 5, .	2.0	12
27676	Explainable Machine Learning for Longitudinal Multi-Omic Microbiome. <i>Mathematics</i> , 2022, 10, 1994.	1.1	3
27677	Construction and Comprehensive Analysis of the ceRNA Network to Reveal Key Genes for Benign Tracheal Stenosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
27678	Identification of Hub Genes and Immune-Related Pathways for Membranous Nephropathy by Bioinformatics Analysis. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	4
27679	Clustering analysis revealed the autophagy classification and potential autophagy regulators' sensitivity of pancreatic cancer based on multi-omics data. <i>Cancer Medicine</i> , 2023, 12, 733-746.	1.3	5
27680	Androgen receptor gene deficiency results in the reduction of steroidogenic potential in porcine luteal cells. <i>Animal Biotechnology</i> , 2023, 34, 2183-2196.	0.7	1
27682	Repositioning of Anti-Inflammatory Drugs for the Treatment of Cervical Cancer Sub-Types. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	14
27683	Disease spreading modeling and analysis: a survey. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	20
27684	Nutrient Availability Does Not Affect Community Assembly in Root-Associated Fungi but Determines Fungal Effects on Plant Growth. <i>MSystems</i> , 2022, 7, .	1.7	5
27685	Identification of Genes Related to Hair Follicle Cycle Development in Inner Mongolia Cashmere Goat by WGCNA. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	9

#	ARTICLE	IF	CITATIONS
27686	Serial-Omics and Molecular Function Study Provide Novel Insight into Cucumber Variety Improvement. <i>Plants</i> , 2022, 11, 1609.	1.6	2
27687	Extensive transgressive gene expression in testis but not ovary in the homoploid hybrid Italian sparrow. <i>Molecular Ecology</i> , 2022, 31, 4067-4077.	2.0	6
27689	Effects of water temperature on the gut microbiome and physiology of Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ) reared in a freshwater recirculating system. <i>Aquaculture</i> , 2022, 560, 738529.	1.7	14
27691	Identification of Five Hub Genes Based on Single-Cell RNA Sequencing Data and Network Pharmacology in Patients With Acute Myocardial Infarction. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	10
27692	Reproducibility of the Blood and Urine Exposome: A Systematic Literature Review and Meta-Analysis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1683-1692.	1.1	2
27693	Donor-dependent fecal microbiota transplantation efficacy against necrotizing enterocolitis in preterm pigs. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	8
27694	Substrate Utilization and Competitive Interactions Among Soil Bacteria Vary With Life-History Strategies. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
27695	Proteomic and clinical biomarkers for acute mountain sickness in a longitudinal cohort. <i>Communications Biology</i> , 2022, 5, .	2.0	6
27696	Implementation of a MS/MS database for isoquinoline alkaloids and other annonaceous metabolites. <i>Scientific Data</i> , 2022, 9, .	2.4	4
27697	Study the Mechanism of Gualou Niubang Decoction in Treating Plasma Cell Mastitis Based on Network Pharmacology and Molecular Docking. <i>BioMed Research International</i> , 2022, 2022, 1-21.	0.9	6
27698	Genome-wide association analysis and pathway enrichment provide insights into the genetic basis of photosynthetic responses to drought stress in Persian walnut. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
27699	Distinct transcriptomic profile of small arteries of hypertensive patients with chronic kidney disease identified miR-338-3p targeting GPX3 and PTPRS. <i>Journal of Hypertension</i> , 2022, 40, 1394-1405.	0.3	2
27700	A New Paradigm of Multiheme Cytochrome Evolution by Grafting and Pruning Protein Modules. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	12
27701	Structural organization, evolution, and distribution of viral pyrimidine dimer-DNA glycosylases. <i>Biophysical Reviews</i> , 0, , .	1.5	1
27702	Immune Cell Infiltration Characteristics of Pigmented Villous Nodular Synovitis and Prediction of Potential Diagnostic Markers Based on Bioinformatics. <i>BioMed Research International</i> , 2022, 2022, 1-17.	0.9	1
27703	Comprehensive Effects of Flowering Locus T-Mediated Stem Growth in Tobacco. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
27704	Variation in glucose metabolism under acidified sodium nitrite mediated nitrosative stress in <i>Saccharomyces cerevisiae</i> . <i>Journal of Applied Microbiology</i> , 0, , .	1.4	0
27705	Quantitative Succinyl-Proteome Profiling of Turnip ( <i>Brassica rapa</i> var. <i>rapa</i> ) in Response to Cadmium Stress. <i>Cells</i> , 2022, 11, 1947.	1.8	4

#	ARTICLE	IF	CITATIONS
27706	Integrated analysis reveals the pivotal interactions between immune cells in the melanoma tumor microenvironment. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
27707	Molecular Networks and Macromolecular Molar Mass Distributions for Preliminary Characterization of Danish Craft Beers. <i>Beverages</i> , 2022, 8, 35.	1.3	0
27708	Profiling and integrated analysis of differentially expressed circRNAs in cervical cancer. <i>Genomics</i> , 2022, , 110418.	1.3	0
27709	Comprehensive bioinformatic analysis reveals a cancer-associated fibroblast gene signature as a poor prognostic factor and potential therapeutic target in gastric cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	20
27710	Exploring Performance Parameters of Artificial Allosteric Protein Switches. <i>Journal of Molecular Biology</i> , 2022, 434, 167678.	2.0	4
27711	Joint profiling of gene expression and chromatin accessibility during amphioxus development at single-cell resolution. <i>Cell Reports</i> , 2022, 39, 110979.	2.9	12
27712	Identification of Dezhou donkey muscle development-related genes and long non-coding RNA based on differential expression analysis. <i>Animal Biotechnology</i> , 0, , 1-11.	0.7	1
27714	Whole-exome sequencing of Indian prostate cancer reveals a novel therapeutic target: POLQ. <i>Journal of Cancer Research and Clinical Oncology</i> , 0, , .	1.2	2
27715	Identifying Endogenous Cellular Proteins Destabilizing the Propagation of Swi1 Prion upon Overproduction. <i>Viruses</i> , 2022, 14, 1366.	1.5	0
27716	Physiological and Molecular Background of Maize Cold-Tolerance Enhancement with S-methylmethionine Salicylate. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2073-2091.	2.8	2
27717	Computational Study of Asian Propolis Compounds as Potential Anti-Type 2 Diabetes Mellitus Agents by Using Inverse Virtual Screening with the DIA-DB Web Server, Tanimoto Similarity Analysis, and Molecular Dynamic Simulation. <i>Molecules</i> , 2022, 27, 3972.	1.7	4
27718	Untargeted LC-HRMS Based-Plasma Metabolomics Reveals 3-O-Methyldopa as a New Biomarker of Poor Prognosis in High-Risk Neuroblastoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
27719	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. <i>Genome Research</i> , 2022, 32, 1112-1123.	2.4	3
27720	Quantitative proteomics and in-cell cross-linking reveal cellular reorganisation during early neuronal differentiation of SH-SY5Y cells. <i>Communications Biology</i> , 2022, 5, .	2.0	6
27721	Omics-based integrated analysis identified IKZF2 as a biomarker associated with lupus nephritis. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
27722	BCL2-associated athanogene 6 exon24 contributes to testosterone synthesis and male fertility in mammals. <i>Cell Proliferation</i> , 0, , .	2.4	3
27723	Integrated Multi-Omics Analysis Model to Identify Biomarkers Associated With Prognosis of Breast Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	12
27724	<i>Bacillus subtilis</i> biofilm matrix components target seed oil bodies to promote growth and anti-fungal resistance in melon. <i>Nature Microbiology</i> , 2022, 7, 1001-1015.	5.9	30

#	ARTICLE	IF	CITATIONS
27725	A multi-omics analysis reveals that the lysine deacetylase ABHD14B influences glucose metabolism in mammals. <i>Journal of Biological Chemistry</i> , 2022, 298, 102128.	1.6	8
27726	ggClusterNet: An R package for microbiome network analysis and modularity-based multiple network layouts. , 2022, 1, .		75
27727	The Prognostic Value of lncRNA MCM3AP-AS1 on Clinical Outcomes in Various Cancers: A Meta- and Bioinformatics Analysis. <i>Disease Markers</i> , 2022, 2022, 1-16.	0.6	0
27728	Proteomic Profiling Identifies Co-Regulated Expression of Splicing Factors as a Characteristic Feature of Intravenous Leiomyomatosis. <i>Cancers</i> , 2022, 14, 2907.	1.7	2
27730	Construction and contextualization approaches for protein-protein interaction networks. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3280-3290.	1.9	2
27731	Stress conditions induced circRNAs profile of extracellular vesicles in brain microvascular endothelial cells. <i>Metabolic Brain Disease</i> , 0, , .	1.4	0
27732	Fungal communities in European alpine soils are not affected by short-term <i>in situ</i> simulated warming than bacterial communities. <i>Environmental Microbiology</i> , 0, , .	1.8	3
27733	A Combination of Metabolomics and Machine Learning Results in the Identification of a New Cyst Nematode Hatching Factor. <i>Metabolites</i> , 2022, 12, 551.	1.3	4
27734	Icariside II Restores Vascular Smooth Muscle Cell Contractile Phenotype by Enhancing the Focal Adhesion Signaling Pathway in the Rat Vascular Remodeling Model. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
27736	Analysis of fermentation control factors on volatile compounds of primary microorganisms in Jiangsu flavor <i>Daqu</i> . <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	12
27737	Insight into the Roles of Proline-Rich Extensin-like Receptor Protein Kinases of Bread Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 TF	1.1	9
27738	Genomic Characterization of <i>Lactobacillus delbrueckii</i> Strains with Probiotics Properties. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	6
27739	Genomics analysis of <i>Drosophila sechellia</i> response to <i>Morinda citrifolia</i> fruit diet. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
27740	Identification and Characterization of Major Bile Acid 7 $\alpha$ -Dehydroxylating Bacteria in the Human Gut. <i>MSystems</i> , 2022, 7, .	1.7	12
27741	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. <i>Circulation Research</i> , 2022, 131, .	2.0	20
27742	The molecular impact of life in an indoor environment. <i>Science Advances</i> , 2022, 8, .	4.7	3
27743	Identification and functional annotation of long intergenic non-coding RNAs in Brassicaceae. <i>Plant Cell</i> , 2022, 34, 3233-3260.	3.1	22
27744	Effects of Spore-Displayed p75 Protein from <i>Lactobacillus rhamnosus</i> GG on the Transcriptional Response of HT-29 Cells. <i>Microorganisms</i> , 2022, 10, 1276.	1.6	4

#	ARTICLE	IF	CITATIONS
27745	Integrated Analysis of Immune-Related circRNA-miRNA-mRNA Regulatory Network in Ischemic Stroke. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	3
27747	Integrative analysis and prediction of human R-loop binding proteins. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
27748	The functional mechanisms of synchronizing royal jelly consumption and physical activity on rat with multiple sclerosis-like behaviors hallmarks based on bioinformatics analysis, and experimental survey. <i>BMC Neuroscience</i> , 2022, 23, .	0.8	3
27749	Expression and Regulatory Network Analysis of BICC1 for Aged Sca-1-Positive Bone Marrow Mesenchymal Stem Cells. <i>Disease Markers</i> , 2022, 2022, 1-16.	0.6	1
27750	Factors Influencing Bacterial and Fungal Skin Communities of Montane Salamanders of Central Mexico. <i>Microbial Ecology</i> , 2023, 86, 670-686.	1.4	4
27751	Disrupting the DREAM complex enables proliferation of adult human pancreatic $\hat{I}^2$ cells. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	14
27752	Bcl11a and the Correlated Key Genes Ascribable to Globin Switching: An In-silico Study. <i>Cardiovascular &amp; Hematological Disorders Drug Targets</i> , 2022, 22, 128-142.	0.2	1
27753	Network Pharmacology Approach to Investigate the Mechanism of Modified Liu Jun Zi Decoction in the Treatment of Chronic Atrophic Gastritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-12.	0.5	2
27754	A hexa-species transcriptome atlas of mammalian embryogenesis delineates metabolic regulation across three different implantation modes. <i>Nature Communications</i> , 2022, 13, .	5.8	14
27755	miRNA Regulatory Networks Associated with Peripheral Vascular Diseases. <i>Journal of Clinical Medicine</i> , 2022, 11, 3470.	1.0	1
27756	Expressed genes and their new alleles identification during fibre elongation reveal the genetic factors underlying improvements of fibre length in cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 1940-1955.	4.1	5
27757	ESRRG, ATP4A, and ATP4B as Diagnostic Biomarkers for Gastric Cancer: A Bioinformatic Analysis Based on Machine Learning. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	1
27758	Spatial Metabolomics Reveals Localized Impact of Influenza Virus Infection on the Lung Tissue Metabolome. <i>MSystems</i> , 2022, 7, .	1.7	6
27759	Identification of HOX signatures contributing to oral cancer phenotype. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
27760	Qinzhi Zhudan formula improves memory and alleviates neuroinflammation in vascular dementia rats partly by inhibiting the TNFR1-mediated TNF pathway. <i>Journal of Traditional Chinese Medical Sciences</i> , 2022, 9, 298-310.	0.1	3
27761	Data-dependent visualization of biological networks in the web-browser with NDEdit. <i>PLoS Computational Biology</i> , 2022, 18, e1010205.	1.5	1
27762	Decoding RNA Editing Sites Through Transcriptome Analysis in Rice Under Alkaline Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
27763	Brevilin A Isolated from <i>Centipeda minima</i> Induces Apoptosis in Human Gastric Cancer Cells via an Extrinsic Apoptotic Signaling Pathway. <i>Plants</i> , 2022, 11, 1658.	1.6	11



#	ARTICLE	IF	CITATIONS
27764	Network pharmacology integrated molecular dynamics reveals the bioactive compounds and potential targets of <i>Tinospora crispa</i> Linn. as insulin sensitizer. <i>PLoS ONE</i> , 2022, 17, e0251837.	1.1	6
27765	Genome-wide CRISPR screens of T <sub>H</sub> 1 cell exhaustion identify chromatin remodeling factors that limit T <sub>H</sub> 1 cell persistence. <i>Cancer Cell</i> , 2022, 40, 768-786.e7.	7.7	104
27766	Dynamic succession of microbial community in Nongxiangxing daqu and microbial roles involved in flavor formation. <i>Food Research International</i> , 2022, 159, 111559.	2.9	23
27767	Identification of molecular mechanism of the anti-lung cancer effect of Jin Ning Fang using network pharmacology and its experimental verification. <i>International Journal of Transgender Health</i> , 2022, 15, 745-759.	1.1	2
27768	A Novel Overall Survival Prediction Signature Based on Comprehensive Research in Prostate Cancer Bone Metastases. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	2
27769	Tubulin TUBB4B Is Involved in Spermatogonia Proliferation and Cell Cycle Processes. <i>Genes</i> , 2022, 13, 1082.	1.0	3
27770	Metabolite Effect on Angiogenesis: Insights from Transcriptome Analysis. <i>Cell Biochemistry and Biophysics</i> , 2022, 80, 519-536.	0.9	2
27771	A Necroptosis-Related lncRNA Signature Predicts Prognosis and Indicates the Immune Microenvironment in Soft Tissue Sarcomas. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
27772	Using network analysis to model the effects of the SARS Cov2 pandemic on acute patient care within a healthcare system. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
27773	Drug repositioning in non-small cell lung cancer (NSCLC) using gene co-expression and drug-gene interaction networks analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	10
27774	A Novel Drug Combination of Mangiferin and Cinnamic Acid Alleviates Rheumatoid Arthritis by Inhibiting TLR4/NF- $\kappa$ B/NLRP3 Activation-Induced Pyroptosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	24
27777	Distinct mechanisms of innate and adaptive immune regulation underlie poor oncologic outcomes associated with KRAS-TP53 co-alteration in pancreatic cancer. <i>Oncogene</i> , 2022, 41, 3640-3654.	2.6	17
27778	Gut virome dysbiosis following focal cerebral ischemia in mice. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2022, 42, 1597-1602.	2.4	4
27779	Yi-Shen-Hua-Shi Granule Alleviates Adriamycin-Induced Glomerular Fibrosis by Suppressing the BMP2/Smad Signaling Pathway. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
27781	Exploring Ganweikang Tablet as a Candidate Drug for NAFLD Through Network Pharmacology Analysis and Experimental Validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
27782	Cardiac fibroblasts regulate the development of heart failure via Htra3-TGF- $\beta$ 2-IGFBP7 axis. <i>Nature Communications</i> , 2022, 13, .	5.8	35
27783	Multi-omics profiling reveals comprehensive microbe-plant-metabolite regulation patterns for medicinal plant <i>Glycyrrhiza uralensis</i> Fisch. <i>Plant Biotechnology Journal</i> , 2022, 20, 1874-1887.	4.1	27
27784	A genome-wide atlas of antibiotic susceptibility targets and pathways to tolerance. <i>Nature Communications</i> , 2022, 13, .	5.8	12

#	ARTICLE	IF	CITATIONS
27786	Small-extracellular vesicles and their microRNA cargo from porcine follicular fluids: the potential association with oocyte quality. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	6
27787	In vitro ve in silico analizi ile metforminin meme t $\frac{1}{4}$ m $\frac{1}{4}$ r $\frac{1}{4}$ h $\frac{1}{4}$ crelerinde protein profili $\frac{1}{4}$ zerindeki etkinli $\frac{1}{4}$ yi. <i>Ege T<math>\frac{1}{4}</math>p Dergisi</i> , 0, , 215-224.	0.1	0
27788	Identification of Prognosis-Related Molecular Subgroups and Construction of a Prognostic Prediction Model Using Immune-Related Genes in Pancreatic Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-21.	0.6	1
27789	Exosomes derived from magnetically actuated bone mesenchymal stem cells promote tendon-bone healing through the miR-21-5p/SMAD7 pathway. <i>Materials Today Bio</i> , 2022, 15, 100319.	2.6	15
27790	Exposure of Keratinocytes to <i>Candida Albicans</i> in the Context of Atopic Milieu Induces Changes in the Surface Glycosylation Pattern of Small Extracellular Vesicles to Enhance Their Propensity to Interact With Inhibitory Siglec Receptors. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
27791	Genome-wide transcriptome profiling of human trabecular meshwork cells treated with TGF- $\beta$ 2. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
27792	A Pan-Cancer Analysis Revealing the Dual Roles of Lysine (K)-Specific Demethylase 6B in Tumorigenesis and Immunity. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
27793	Genome-Wide Identification and Analysis of the NF- $\kappa$ B Transcription Factor Family Reveal Its Potential Roles in Salt Stress in Alfalfa ( <i>Medicago sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 6426.	1.8	6
27794	Comparative Transcriptome Analysis of Organ-Specific Adaptive Responses to Hypoxia Provides Insights to Human Diseases. <i>Genes</i> , 2022, 13, 1096.	1.0	2
27795	Construction of a Novel circRNA/miRNA/mRNA Regulatory Network to Explore the Potential Pathogenesis of Wilson's Disease. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
27797	Pharmacological mechanisms of sodium-glucose co-transporter 2 inhibitors in heart failure with preserved ejection fraction. <i>BMC Cardiovascular Disorders</i> , 2022, 22, .	0.7	4
27798	ARL4C Regulates the Progression of Clear Cell Renal Cell Carcinoma by Affecting the Wnt/ $\beta$ -Catenin Signaling Pathway. <i>Journal of Oncology</i> , 2022, 2022, 1-24.	0.6	4
27799	SNHG5/miR-299-5p/ATF2 Axis as a Biomarker in Immune Microenvironment of Intervertebral Disc Degeneration. <i>Mediators of Inflammation</i> , 2022, 2022, 1-14.	1.4	1
27800	Screening potential immune signatures for early-stage basal-like/triple-negative breast cancer. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	0
27801	REPS1 as a Potential Biomarker in Alzheimer's Disease and Vascular Dementia. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	8
27802	A genome-wide association study of the occurrence of genetic variations in <i>Edwardsiella piscicida</i> , <i>Vibrio harveyi</i> , and <i>Streptococcus parauberis</i> under stressed environments. <i>Journal of Fish Diseases</i> , 2022, 45, 1373-1388.	0.9	2
27804	Inhibition of cell survival and invasion by Tanshinone AIIA via FTH1: A key therapeutic target and biomarker in head and neck squamous cell carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2022, 24, .	0.8	11
27805	Identification and Validation of Immune-Related Biomarker Gene and Construction of ceRNA Networks in Septic Cardiomyopathy. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3

#	ARTICLE	IF	CITATIONS
27806	Construction of a four-mRNA prognostic signature with its ceRNA network in CESC. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
27808	Transcriptome analysis reveals regulation mechanism of methyl jasmonate-induced terpenes biosynthesis in <i>Curcuma wenyujin</i> . <i>PLoS ONE</i> , 2022, 17, e0270309.	1.1	9
27809	Recognition of Key Genes in Human Anaplastic Thyroid Cancer via the Weighing Gene Coexpression Network. <i>BioMed Research International</i> , 2022, 2022, 1-17.	0.9	4
27810	Variation of Grain Yield, Grain Protein Content and Nitrogen Use Efficiency Components under Different Nitrogen Rates in Mediterranean Durum Wheat Genotypes. <i>Agriculture (Switzerland)</i> , 2022, 12, 916.	1.4	9
27811	Deciphering the Crosstalk Mechanisms of Wheat-Stem Rust Pathosystem: Genome-Scale Prediction Unravels Novel Host Targets. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
27812	Construction of an Expression Classifier Based on an Immune-related Ten-gene Panel for Rapid Diagnosis of Papillary Thyroid Carcinoma Risks. <i>Current Bioinformatics</i> , 2022, 17, 924-936.	0.7	0
27813	SARS-CoV-2 ORF10 impairs cilia by enhancing CUL2ZYG11B activity. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	22
27814	RNF144B stimulates the proliferation and inhibits the apoptosis of human spermatogonial stem cells via the FCER2/NOTCH2/HES1 pathway and its abnormality is associated with azoospermia. <i>Journal of Cellular Physiology</i> , 2022, 237, 3565-3577.	2.0	7
27815	Holliday Cross-Recognition Protein HJURP: Association With the Tumor Microenvironment in Hepatocellular Carcinoma and With Patient Prognosis. <i>Pathology and Oncology Research</i> , 0, 28, .	0.9	6
27816	Alterations of Cardiac Protein Kinases in Cyclic Nucleotide-Dependent Signaling Pathways in Human Ischemic Heart Failure. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
27817	Integrated Transcriptomics and Widely Targeted Metabolomics Analyses Provide Insights Into Flavonoid Biosynthesis in the Rhizomes of Golden Buckwheat ( <i>Fagopyrum cymosum</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
27818	Comparative Transcriptomic Analyses of Nitrate-Response in Rice Genotypes With Contrasting Nitrogen Use Efficiency Reveals Common and Genotype-Specific Processes, Molecular Targets and Nitrogen Use Efficiency-Candidates. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
27819	Genetic association and single-cell transcriptome analyses reveal distinct features connecting autoimmunity with cancers. <i>IScience</i> , 2022, 25, 104631.	1.9	3
27820	Large-scale comparative transcriptome analysis of <i>Nicotiana tabacum</i> response to <i>Ralstonia solanacearum</i> infection. <i>Plant Biotechnology Reports</i> , 2022, 16, 757-775.	0.9	2
27821	An Integrated Mass Spectrometry-Based Glycomics-Driven Glycoproteomics Analytical Platform to Functionally Characterize Glycosylation Inhibitors. <i>Molecules</i> , 2022, 27, 3834.	1.7	6
27822	The <i>rolB</i> transgenic <i>Nicotiana tabacum</i> plants exhibit upregulated <i>ARF7</i> and <i>ARF19</i> gene expression. <i>Plant Direct</i> , 2022, 6, .	0.8	1
27823	Comparative Analysis of Transcriptomes of <i>Ophiostoma novo-ulmi</i> ssp. <i>americana</i> Colonizing Resistant or Sensitive Genotypes of American Elm. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 637.	1.5	5
27824	Circulating microRNAs Suggest Networks Associated with Biological Functions in Aggressive Refractory Type 2 Celiac Disease. <i>Biomedicines</i> , 2022, 10, 1408.	1.4	2

#	ARTICLE	IF	CITATIONS
27825	Proteomic Signatures of Monocytes in Hereditary Recurrent Fevers. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
27826	Humanized yeast to model human biology, disease and evolution. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	22
27827	Generating FAIR research data in experimental tribology. <i>Scientific Data</i> , 2022, 9, .	2.4	7
27828	Damage-responsive neuro-glial clusters coordinate the recruitment of dormant neural stem cells in <i>Drosophila</i> . <i>Developmental Cell</i> , 2022, 57, 1661-1675.e7.	3.1	9
27831	Identification and Validation of Candidate Gene Module Along With Immune Cells Infiltration Patterns in Atherosclerosis Progression to Plaque Rupture via Transcriptome Analysis. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	8
27832	The Bioinformatic Study Uncovers Probable Critical Genes Involved in the Pathophysiology of Biliary Atresia. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	1
27833	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of <i>Bicyclus anynana</i> Butterflies. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
27834	Genome-Wide Analysis of the Peptidase M24 Superfamily in <i>Triticum aestivum</i> Demonstrates That TaM24-9 Is Involved in Abiotic Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6904.	1.8	0
27835	CircRNAs in Xiang pig ovaries among diestrus and estrus stages. <i>Porcine Health Management</i> , 2022, 8, .	0.9	4
27836	Identification of Differentially Expressed Long Noncoding RNAs as Functional Biomarkers and Construction of Function Enrichment Network in Oral Squamous Cell Carcinoma. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-9.	0.5	2
27837	Comparative Transcriptome Analysis Reveals Common and Developmental Stage-Specific Genes That Respond to Low Nitrogen in Maize Leaves. <i>Plants</i> , 2022, 11, 1550.	1.6	1
27838	Microvascular and proteomic signatures overlap in COVID-19 and bacterial sepsis: the MICROCODE study. <i>Angiogenesis</i> , 0, , .	3.7	8
27839	Immune Cell Networks Uncover Candidate Biomarkers of Melanoma Immunotherapy Response. <i>Journal of Personalized Medicine</i> , 2022, 12, 958.	1.1	0
27841	The Potential Mechanisms of Cinobufotalin Treating Colon Adenocarcinoma by Network Pharmacology. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
27842	Rings in Clinical Trials and Drugs: Present and Future. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 8699-8712.	2.9	105
27843	Comprehensive Bioinformatics Analysis to Reveal Key RNA Targets and Hub Competitive Endogenous RNA Network of <i>Keratoconus</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
27844	Study on the Mechanism of Treating Femoral Head Necrosis with <i>Drynariae Rhizoma</i> Based on Network Pharmacology. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-8.	0.7	3
27845	Gene Co-expression Network Analysis of the Comparative Transcriptome Identifies Hub Genes Associated With Resistance to <i>Aspergillus flavus</i> L. in Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	11

#	ARTICLE	IF	CITATIONS
27846	Prioritizing Candidate Genes for Type 2 Diabetes Mellitus using Integrated Network and Pathway Analysis. <i>Avicenna Journal of Medical Biotechnology</i> , 0, , .	0.2	0
27847	Gene Differential Expression and Interaction Networks Illustrate the Biomarkers and Molecular Biological Mechanisms of Unsaponifiable Matter in Kanglaite Injection for Pancreatic Ductal Adenocarcinoma. <i>BioMed Research International</i> , 2022, 2022, 1-19.	0.9	5
27848	Characterization of Expression and Epigenetic Features of Core Genes in Common Wheat. <i>Genes</i> , 2022, 13, 1112.	1.0	1
27850	Integrated Analysis of a Ferroptosis-Related LncRNA Signature for Evaluating the Prognosis of Patients with Colorectal Cancer. <i>Genes</i> , 2022, 13, 1094.	1.0	8
27851	The Underlying Molecular Basis and Mechanisms of Venous Thrombosis in Patients with Osteomyelitis: A Data-Driven Analysis. <i>Genetical Research</i> , 2022, 2022, 1-11.	0.3	2
27852	<i>Coralococcus soli</i> sp. Nov., a Soil Myxobacterium Isolated from Subtropical Climate, Chalus County, Iran, and Its Potential to Produce Secondary Metabolites. <i>Microorganisms</i> , 2022, 10, 1262.	1.6	7
27853	Whole Transcriptome Sequencing of Peripheral Blood Shows That Immunity/GnRH/PI3K-Akt Pathways Are Associated With Opioid Use Disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	5
27854	Identification of Hub Genes for Early Diagnosis and Predicting Prognosis in Colon Adenocarcinoma. <i>BioMed Research International</i> , 2022, 2022, 1-21.	0.9	3
27855	Identification of key apoptosis-related genes and immune infiltration in the pathogenesis of psoriasis. <i>Hereditas</i> , 2022, 159, .	0.5	3
27856	Effects of <i>Pasteurella multocida</i> on Histopathology, miRNA and mRNA Expression Dynamics in Lung of Goats. <i>Animals</i> , 2022, 12, 1529.	1.0	2
27857	Neuroendocrine-Immune Regulatory Network of <i>Eucommia ulmoides</i> Oliver. <i>Molecules</i> , 2022, 27, 3697.	1.7	6
27858	Genome-Wide Identification and Characterization of CPR5 Genes in <i>Gossypium</i> Reveals Their Potential Role in Trichome Development. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
27859	Network pharmacology-based strategy to investigate pharmacological mechanisms of Qingbutongluo Pill for treatment of brucellosis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	0
27860	STAT6 inhibits ferroptosis and alleviates acute lung injury via regulating P53/SLC7A11 pathway. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	44
27862	Comprehensive molecular evaluation of the histone methyltransferase gene family and their important roles in two-line hybrid wheat. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
27863	Phoenicin Switch: Discovering the Trigger for Radical Phoenicin Production in Multiple Wild-Type <i>Penicillium</i> Species. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	3
27864	Combining QTL mapping and gene co-expression network analysis for prediction of candidate genes and molecular network related to yield in wheat. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	8
27865	Mechanistic insight of the potential of geraniol against Alzheimer's disease. <i>European Journal of Medical Research</i> , 2022, 27, .	0.9	3

#	ARTICLE	IF	CITATIONS
27866	Genome-wide identification of R2R3-MYB gene family and association with anthocyanin biosynthesis in Brassica species. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
27867	Development and Validation of a Novel Ferroptosis-Related LncRNA Signature for Predicting Prognosis and the Immune Landscape Features in Uveal Melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	10
27868	Posttranscriptional Regulation in Response to Different Environmental Stresses in <i>Campylobacter jejuni</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
27869	Investigating the AC079305/DUSP1 Axis as Oxidative Stress-Related Signatures and Immune Infiltration Characteristics in Ischemic Stroke. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-19.	1.9	8
27870	CompositeView: A Network-Based Visualization Tool. <i>Big Data and Cognitive Computing</i> , 2022, 6, 66.	2.9	4
27871	Integrating genomics and transcriptomics to identify candidate genes for subcutaneous fat deposition in beef cattle. <i>Genomics</i> , 2022, 114, 110406.	1.3	11
27872	Feasibility and Acceptability of HIV Self-Test Kit Distribution Through PrEP Clients' Social and Sexual Networks to Increase HIV Testing and PrEP Information. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 90, S105-S113.	0.9	7
27873	Porcine Circovirus type 2 infected myocardial tissue transcriptome signature. <i>Gene</i> , 2022, 836, 146670.	1.0	7
27874	Pharmacokinetic and gut microbiota analyses revealed the effect of <i>Lactobacillus acidophilus</i> on the metabolism of Olsalazine in ulcerative colitis rats. <i>European Journal of Pharmaceutical Sciences</i> , 2022, 175, 106235.	1.9	3
27875	Immunoregulation of Ghrelin in neurocognitive sequelae associated with COVID-19: an in silico investigation. <i>Gene</i> , 2022, 834, 146647.	1.0	5
27876	Computational approach to decode the mechanism of curcuminoids against neuropathic pain. <i>Computers in Biology and Medicine</i> , 2022, 147, 105739.	3.9	5
27877	Tri-n-butyl phosphate delays tissue repair by dysregulating neutrophil function in zebrafish. <i>Toxicology and Applied Pharmacology</i> , 2022, 449, 116114.	1.3	3
27878	Identification of ceRNA network to explain the mechanism of cognitive dysfunctions induced by PS NPs in mice. <i>Ecotoxicology and Environmental Safety</i> , 2022, 241, 113785.	2.9	10
27879	Traditional herbal formula Jiao-tai-wan improves chronic restrain stress-induced depression-like behaviors in mice. <i>Biomedicine and Pharmacotherapy</i> , 2022, 153, 113284.	2.5	7
27880	Dysfunction of calcium-regulated exocytosis at a single-cell level causes catecholamine hypersecretion in patients with pheochromocytoma. <i>Cancer Letters</i> , 2022, 543, 215765.	3.2	4
27881	Multiomics analyses uncover nanoceria triggered oxidative injury and nutrient imbalance in earthworm <i>Eisenia fetida</i> . <i>Journal of Hazardous Materials</i> , 2022, 437, 129354.	6.5	11
27882	An acceleration of carotenoid production and growth of <i>Haematococcus lacustris</i> induced by host-microbiota network interaction. <i>Microbiological Research</i> , 2022, 262, 127097.	2.5	4
27883	In silico drug repurposing against SARS-CoV-2 using an integrative transcriptomic profiling approach: Hydrocortisone and Benzhydrocodone as potential drug candidates against COVID-19. <i>Infection, Genetics and Evolution</i> , 2022, 103, 105318.	1.0	3



#	ARTICLE	IF	CITATIONS
27884	Temporal heterogeneity of bacterial communities and their responses to <i>Raphidiopsis raciborskii</i> blooms. <i>Microbiological Research</i> , 2022, 262, 127098.	2.5	1
27885	Insights into microbial contamination in multi-type manure-amended soils: The profile of human bacterial pathogens, virulence factor genes and antibiotic resistance genes. <i>Journal of Hazardous Materials</i> , 2022, 437, 129356.	6.5	34
27886	2D-DIGE based urinary proteomics and functional enrichment studies to reveal novel <i>Mycobacterium tuberculosis</i> and human protein biomarker candidates for pulmonary tuberculosis. <i>Biochemical and Biophysical Research Communications</i> , 2022, 619, 15-21.	1.0	3
27887	Comparative coexpression networks pinpoint acyltransferases decorating structures of major iridoid glycosides in a medicinal herb, <i>Picrorhiza kurroa</i> . <i>Plant Gene</i> , 2022, 31, 100366.	1.4	1
27888	Investigation on the potential targets of Astragaloside IV against intracerebral hemorrhage based on network pharmacology and experimental validation. <i>Bioorganic Chemistry</i> , 2022, 127, 105975.	2.0	6
27889	Network analysis reveals the root endophytic fungi associated with <i>Fusarium</i> root rot invasion. <i>Applied Soil Ecology</i> , 2022, 178, 104567.	2.1	10
27890	Scopolin obtained from <i>Smilax china</i> L. against hepatocellular carcinoma by inhibiting glycolysis: A network pharmacology and experimental study. <i>Journal of Ethnopharmacology</i> , 2022, 296, 115469.	2.0	6
27891	Neuronal differentiation pathways and compound-induced developmental neurotoxicity in the human neural progenitor cell test (hNPT) revealed by RNA-seq. <i>Chemosphere</i> , 2022, 304, 135298.	4.2	6
27892	Comprehensive understanding the impacts of dietary exposure to polyethylene microplastics on genetically improved farmed tilapia ( <i>Oreochromis niloticus</i> ): tracking from growth, microbiota, metabolism to gene expressions. <i>Science of the Total Environment</i> , 2022, 841, 156571.	3.9	15
27893	Influences of the alcoholic extract of <i>Artemisia annua</i> on gastrointestinal microbiota and performance of Nile tilapia. <i>Aquaculture</i> , 2022, 560, 738521.	1.7	5
27894	An Update on the Multifaceted Role of NF- $\kappa$ B in Endometriosis. <i>International Journal of Biological Sciences</i> , 2022, 18, 4400-4413.	2.6	22
27895	Transcriptome profiling during double-flower development provides insight into stamen petaloid in cultivated <i>Lilium</i> . <i>Ornamental Plant Research</i> , 2022, 2, 1-11.	0.2	4
27896	Taohong Siwu Decoction exerts anticancer effects on breast cancer via regulating MYC, BIRC5, EGF and PIK3R1 revealed by HTS2 technology. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3461-3472.	1.9	4
27897	Vibsanoids A–D, four new subtypes of vibsane diterpenoids with a distinctive tricyclo[8.2.1.0 <sup>2,9</sup> ]tridecane core from <i>Viburnum odoratissimum</i> . <i>Organic Chemistry Frontiers</i> , 2022, 9, 4561-4568.	2.3	5
27898	Stem-Cell-Based Modeling and Single-Cell Multiomics Reveal Gene Regulatory Mechanisms Underlying Human Skeletal Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27899	Identification of osteoporosis based on gene biomarkers using support vector machine. <i>Open Medicine (Poland)</i> , 2022, 17, 1216-1227.	0.6	2
27900	MiR-4763-3p targeting <i>RASD2</i> as a Potential Biomarker and Therapeutic Target for Schizophrenia. , 2022, 13, 1278.		1
27901	Integrating network pharmacology and molecular docking to explore the potential mechanism of Xinguan No. 3 in the treatment of COVID-19. <i>Open Chemistry</i> , 2022, 20, 570-582.	1.0	3

#	ARTICLE	IF	CITATIONS
27903	The role of miR-4469 as a tumor suppressor regulating inflammatory cell infiltration in colorectal cancer. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3755-3763.	1.9	2
27904	Prior exposure to ciprofloxacin disrupts intestinal homeostasis and predisposes ayu (<i>Plecoglossus altivelis</i>) to subsequent <i>Pseudomonas plecoglossicida</i>-induced infection. <i>Zoological Research</i> , 2022, 43, 648-665.	0.9	3
27905	Analysis of the potential role of photocurable hydrogel in patient-derived glioblastoma organoid culture through RNA sequencing. <i>Biomaterials Science</i> , 2022, 10, 4902-4914.	2.6	3
27906	Transcriptome-Based Network Analysis Cell Cycle-Related Genes in Response to Blue and Red Light of Maize. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27907	Transcriptomic landscape of sodium butyrate-induced growth inhibition of human colorectal cancer organoids. <i>Molecular Omics</i> , 0, , .	1.4	2
27908	Tracing the cell-type-specific modules of immune responses during COVID-19 progression using scDisProcema. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3545-3555.	1.9	1
27909	Network Analysis of Differentially Expressed Genes (DEGs) Identified in Zebrafish after Infection with Spring Viremia of Carp Virus (SVCV) – an in Silico Approach. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27910	Elite networks in public private partnerships: mapping the enabling field in Ontario. <i>Studies in Political Economy</i> , 2022, 103, 36-54.	0.5	1
27911	Study on Medication Rules of Traditional Chinese Medicine Against Inflammatory Breast Cancer Based on Bioinformatics and Network Pharmacology. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27912	Comparative genomic analysis reveals new evidence of genus boundary for family Iridoviridae and explores qualified hallmark genes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3493-3502.	1.9	5
27913	Applying Synteny Networks (SynNet) to Study Genomic Arrangements of Protein-Coding Genes in Plants. <i>Methods in Molecular Biology</i> , 2022, , 199-215.	0.4	2
27914	Protective Effects of Polydatin on Reproductive Injury Induced by Ionizing Radiation. <i>Dose-Response</i> , 2022, 20, 155932582211075.	0.7	2
27915	Modularity of the hydrophobic core and evolution of functional diversity in fold A glycosyltransferases. <i>Journal of Biological Chemistry</i> , 2022, 298, 102212.	1.6	3
27916	Convergent and Divergent Age Patterning of Gut Microbiota Diversity in Humans and Nonhuman Primates. <i>MSystems</i> , 2022, 7, .	1.7	5
27917	MAPPINGS, a tool for network analysis of large phospho-signalling datasets: application to host erythrocyte response to Plasmodium infection. <i>Current Research in Microbial Sciences</i> , 2022, , 100149.	1.4	1
27918	Network-based machine learning approach to predict immunotherapy response in cancer patients. <i>Nature Communications</i> , 2022, 13, .	5.8	56
27919	Transcriptome profiling of the ventral pallidum reveals a role for pallido-thalamic neurons in cocaine reward. <i>Molecular Psychiatry</i> , 2022, 27, 3980-3991.	4.1	12
27921	Spanish Melon Landraces: Revealing Useful Diversity by Genomic, Morphological, and Metabolomic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7162.	1.8	2

#	ARTICLE	IF	CITATIONS
27922	Gpx3 and Egr1 Are Involved in Regulating the Differentiation Fate of Cardiac Fibroblasts under Pressure Overload. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-21.	1.9	3
27923	N(6)-methyladenosine methylation-regulated polo-like kinase 1 cell cycle homeostasis as a potential target of radiotherapy in pancreatic adenocarcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	13
27924	Comparative Use of Contralateral and Sham-Operated Controls Reveals Traces of a Bilateral Genetic Response in the Rat Brain after Focal Stroke. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7308.	1.8	5
27926	STAT3 and NTRK2 Genes Predicted by the Bioinformatics Approach May Play Important Roles in the Pathogenesis of Multiple Sclerosis and Obsessive-Compulsive Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 1043.	1.1	3
27927	Next-Generation Grade and Survival Expression Biomarkers of Human Gliomas Based on Algorithmically Reconstructed Molecular Pathways. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7330.	1.8	6
27928	Time Course Analysis of Transcriptome in Human Myometrium Depending on Labor Duration and Correlating With Postpartum Blood Loss. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
27929	Identification and expression analysis of GARP superfamily genes in response to nitrogen and phosphorus stress in <i>Spirodela polyrhiza</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
27930	Analysis of Competitive Endogenous Mechanism and Survival Prognosis of Serum Exosomes in Ovarian Cancer Patients Based on Sequencing Technology and Bioinformatics. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
27931	Effects and associated transcriptomic landscape changes of methamphetamine on immune cells. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	2
27932	Identification of Estrus in Sows Based on Salivary Proteomics. <i>Animals</i> , 2022, 12, 1656.	1.0	3
27935	Integrative Analysis of Genes Involved in the Global Response to Potato Wart Formation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
27936	Rapid growth of Moso bamboo ( <i>Phyllostachys edulis</i> ): Cellular roadmaps, transcriptome dynamics, and environmental factors. <i>Plant Cell</i> , 2022, 34, 3577-3610.	3.1	50
27937	Aberrant Gene Expression Profiling in Men With Sertoli Cell-Only Syndrome. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
27938	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	8
27939	Bmp5 Mutation Alters circRNA Expression During Embryonic External Ear Development. <i>Journal of Craniofacial Surgery</i> , 2022, 33, 1934-1938.	0.3	1
27940	Analyzing the Systems Biology Effects of COVID-19 mRNA Vaccines to Assess Their Safety and Putative Side Effects. <i>Pathogens</i> , 2022, 11, 743.	1.2	11
27941	Exploring Quercetin Anti-Osteoporosis Pharmacological Mechanisms with In Silico and In Vivo Models. <i>Life</i> , 2022, 12, 980.	1.1	10
27942	Immuno-Modulatory Effects of Intervertebral Disc Cells. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	20

#	ARTICLE	IF	CITATIONS
27943	Identification of JUN as determinant of osteoarthritis and its inhibition by the Chinese herbal formulae Zhuanggu Huoxue Tang. <i>Computers in Biology and Medicine</i> , 2022, 148, 105786.	3.9	2
27944	CD137 Regulates Bone Loss via the p53 Wnt/ $\beta$ 2-Catenin Signaling Pathways in Aged Mice. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	6
27945	Comparative genomics of <i>Acinetobacter baumannii</i> and therapeutic bacteriophages from a patient undergoing phage therapy. <i>Nature Communications</i> , 2022, 13, .	5.8	20
27946	Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. <i>Nature Microbiology</i> , 2022, 7, 962-973.	5.9	21
27949	Integrative Proteomic and Phosphoproteomic Analyses of Hypoxia-Treated Pulmonary Artery Smooth Muscle Cells. <i>Proteomes</i> , 2022, 10, 23.	1.7	3
27950	Perinatal Hypoxia Aggravates Occlusive Pulmonary Vasculopathy In SU5416/Hypoxia-Treated Rats Later In Life. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 0, , .	1.3	0
27951	Differential Transcriptional Responses in Two Old World <i>Bemisia tabaci</i> Cryptic Species Post Acquisition of Old and New World Begomoviruses. <i>Cells</i> , 2022, 11, 2060.	1.8	11
27952	Deeper insights into long-term survival heterogeneity of pancreatic ductal adenocarcinoma (PDAC) patients using integrative individual- and group-level transcriptome network analyses. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
27953	Immunolipidomics Reveals a Globoside Network During the Resolution of Pro-Inflammatory Response in Human Macrophages. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
27954	Establishment and verification of potential biomarkers for cholangiocarcinoma. <i>Experimental and Therapeutic Medicine</i> , 2022, 24, .	0.8	2
27955	Single-cell transcriptomic analysis identifies an immune-prone population in erythroid precursors during human ontogenesis. <i>Nature Immunology</i> , 2022, 23, 1109-1120.	7.0	30
27956	Transfer learning in proteins: evaluating novel protein learned representations for bioinformatics tasks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	8
27957	Comprehensive bioinformatics analyses reveal immune genes responsible for altered immune microenvironment in intervertebral disc degeneration. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1229-1242.	1.0	6
27958	Guts of the Urban Ecosystem: Microbial Ecology of Sewer Infrastructure. <i>MSystems</i> , 0, , .	1.7	5
27959	Machine Learning Predictor of Immune Checkpoint Blockade Response in Gastric Cancer. <i>Cancers</i> , 2022, 14, 3191.	1.7	8
27960	Identification of Therapeutic Targets for Amyotrophic Lateral Sclerosis Using PandaOmics – An AI-Enabled Biological Target Discovery Platform. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	32
27961	Mixotrophy in a Local Strain of <i>Nannochloropsis</i> <i>granulata</i> for Renewable High-Value Biomass Production on the West Coast of Sweden. <i>Marine Drugs</i> , 2022, 20, 424.	2.2	4
27962	Transcriptomic analysis reveals pathophysiological relationship between chronic obstructive pulmonary disease (COPD) and periodontitis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	8

#	ARTICLE	IF	CITATIONS
27963	Comparative transcriptome analysis of Indian domestic duck reveals candidate genes associated with egg production. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
27964	The regulatory role of <i>HOX</i> interacting lncRNA in oral cancer—An <i>in silico</i> analysis. <i>Journal of Oral Pathology and Medicine</i> , 2022, 51, 684-693.	1.4	2
27965	Virioplankton assemblages from challenger deep, the deepest place in the oceans. <i>IScience</i> , 2022, 25, 104680.	1.9	7
27966	Lack of TRPV1 Channel Modulates Mouse Gene Expression and Liver Proteome with Glucose Metabolism Changes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7014.	1.8	8
27967	Genome of the bee <i>Holcopasites calliopsidis</i> —a species showing the common apid trait of brood parasitism. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
27968	Construction and validation of gastric cancer diagnosis model based on machine learning. <i>Exploration of Medicine</i> , 0, , 300-313.	1.5	1
27969	Connectome Mapper 3: A Flexible and Open-Source Pipeline Software for Multiscale Multimodal Human Connectome Mapping. <i>Journal of Open Source Software</i> , 2022, 7, 4248.	2.0	11
27970	Cyclic immonium ion of lactyllysine reveals widespread lactylation in the human proteome. <i>Nature Methods</i> , 2022, 19, 854-864.	9.0	60
27971	Integrated Bioinformatics Analysis for Identifying the Significant Genes as Poor Prognostic Markers in Gastric Adenocarcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	0
27972	Comprehensive Characterization of a Novel E3-Related Gene Signature With Implications in Prognosis and Immunotherapy of Low-Grade Gliomas. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
27973	Protective Effect of <i>Hedyotis diffusa</i> Willd. Ethanol Extract on Isoniazid-Induced Liver Injury in the Zebrafish Model. <i>Drug Design, Development and Therapy</i> , 0, Volume 16, 1995-2015.	2.0	4
27974	<i>miR-548d-3p</i> inhibits the invasion and migration of gastric cancer cells by targeting <i>GKN1</i> . <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, .	0.9	3
27975	Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic component. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1301-1312.	0.5	21
27976	ABC transporters mined through comparative transcriptomics associate with organ-specific accumulation of picosides in a medicinal herb, <i>Picrorhiza kurroa</i> . <i>Protoplasma</i> , 0, , .	1.0	1
27977	The close interaction between hypoxia-related proteins and metastasis in pancarcinomas. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
27979	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. <i>Nature Microbiology</i> , 2022, 7, 953-961.	5.9	17
27980	The case for the Humanities Citation Index (HuCI): a citation index by the humanities, for the humanities. <i>International Journal on Digital Libraries</i> , 2023, 24, 191-204.	1.1	4
27981	One-Week Dynamic Changes in Cardiac Proteomes After Cardiac Radioablation in Experimental Rat Model. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	3

#	ARTICLE	IF	CITATIONS
27982	Identification of hub genes predicting the development of prostate cancer from benign prostate hyperplasia and analyzing their clinical value in prostate cancer by bioinformatic analysis. <i>Discover Oncology</i> , 2022, 13, .	0.8	5
27983	Ferroptosis and Autophagy-Related Genes in the Pathogenesis of Ischemic Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	9
27985	Meta-Analysis of Altered Gut Microbiota Reveals Microbial and Metabolic Biomarkers for Colorectal Cancer. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	30
27986	Global cellular response to chemical perturbation of PLK4 activity and abnormal centrosome number. <i>ELife</i> , 0, 11, .	2.8	2
27987	Anti-colon Cancer Effects of <i>Dendrobium officinale</i> Kimura & Migo Revealed by Network Pharmacology Integrated With Molecular Docking and Metabolomics Studies. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	4
27988	Investigation on Metabolites in Structural Diversity from the Deep-Sea Sediment-Derived Bacterium <i>Agrococcus</i> sp. SCSIO 52902 and Their Biosynthesis. <i>Marine Drugs</i> , 2022, 20, 431.	2.2	4
27989	Reduction of Cardiac Fibrosis by Interference With YAP-Dependent Transactivation. <i>Circulation Research</i> , 2022, 131, 239-257.	2.0	26
27990	Mass Spectral Molecular Networking to Profile the Metabolome of Biostimulant <i>Bacillus</i> Strains. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
27991	Potential metabolic and genetic interaction among viruses, methanogen and methanotrophic archaea, and their syntrophic partners. <i>ISME Communications</i> , 2022, 2, .	1.7	5
27992	The SKBR3 cell-membrane proteome reveals telltales of aberrant cancer cell proliferation and targets for precision medicine applications. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
27993	Insights into the Antimicrobial Activities and Metabolomes of <i>Aquimarina</i> (Flavobacteriaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	2.2	11
27995	TMED2/9/10 Serve as Biomarkers for Poor Prognosis in Head and Neck Squamous Carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
27996	Dissecting the Genetic Structure of Maize Leaf Sheaths at Seedling Stage by Image-Based High-Throughput Phenotypic Acquisition and Characterization. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
27997	Long Non-coding RNA and mRNA Co-expression Network Reveals Novel Players in Pleomorphic Xanthoastrocytoma. <i>Molecular Neurobiology</i> , 0, , .	1.9	0
27998	Dynamics of Small Non-coding RNA Profiles and the Intestinal Microbiome of High and Low Weight Chickens. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
27999	Benzyladenine affects polyamine contents and proteomic profiles during in vitro shoot development and ex vitro rooting in <i>Dalbergia nigra</i> (Vell.) Allemão ex Benth. (Fabaceae). <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 151, 75-92.	1.2	5
28000	Identification of hub genes and regulatory networks in histologically unstable carotid atherosclerotic plaque by bioinformatics analysis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	6
28002	Total Flavonoids of <i>Drynariae Rhizoma</i> Improve Glucocorticoid-Induced Osteoporosis of Rats: UHPLC-MS-Based Qualitative Analysis, Network Pharmacology Strategy and Pharmacodynamic Validation. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3



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28004	Vinegar Volatile Organic Compounds: Analytical Methods, Constituents, and Formation Processes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
28005	The RNA virome of echinoderms. <i>Journal of General Virology</i> , 2022, 103, .	1.3	1
28006	GenX induces fibroinflammatory gene expression in primary human hepatocytes. <i>Toxicology</i> , 2022, 477, 153259.	2.0	13
28007	An Immune Signature for Risk Stratification and Therapeutic Prediction in <i>Helicobacter pylori</i> -Infected Gastric Cancer. <i>Cancers</i> , 2022, 14, 3276.	1.7	6
28008	Differences of core genes in liver fibrosis and hepatocellular carcinoma: Evidence from integrated bioinformatics and immunohistochemical analysis. <i>World Journal of Gastrointestinal Oncology</i> , 2022, 14, 1265-1280.	0.8	4
28009	Exploring the Anti-inflammatory Effects of Protopine Total Alkaloids of <i>Macleaya Cordata</i> (Willd.) R. Br.. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
28010	Gene Co-Expression Network Analysis Identifies Hubs in Hepatitis B Virus-Associated Hepatocellular Carcinoma. <i>Journal of the Chinese Medical Association</i> , 0, Publish Ahead of Print, .	0.6	3
28011	The Impact of Varying Food Availability on Gene Expression in the Liver: Testing the Match-Mismatch Hypothesis. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
28012	A Systematic Review and Integrated Bioinformatic Analysis of Candidate Genes and Pathways in the Endometrium of Patients With Polycystic Ovary Syndrome During the Implantation Window. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
28013	Identification and integrated analysis of lncRNAs and miRNAs in IPEC-J2 cells provide novel insight into the regulation of the innate immune response by PDCoV infection. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
28014	A novel signature derived from metabolism-related genes GPT and SMS to predict prognosis of laryngeal squamous cell carcinoma. <i>Cancer Cell International</i> , 2022, 22, .	1.8	3
28015	Identifying Urban Agriculture Needs and Challenges for the Implementation of Green Labeling in Xochimilco, Mexico. <i>Frontiers in Sustainable Cities</i> , 0, 4, .	1.2	2
28016	Comparison of the co-occurrence patterns of the gut microbial community between Bt-susceptible and Bt-resistant strains of the rice stem borer, <i>Chilo suppressalis</i> . <i>Journal of Pest Science</i> , 2023, 96, 299-315.	1.9	6
28017	Integrative Bioinformatics Analysis Reveals CHEK1 and UBE2C as Luminal A Breast Cancer Subtype Biomarkers. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
28018	An Integrated Bioinformatics Analysis towards the Identification of Diagnostic, Prognostic, and Predictive Key Biomarkers for Urinary Bladder Cancer. <i>Cancers</i> , 2022, 14, 3358.	1.7	9
28019	Distinct nuclear and cytoplasmic assemblies and interactomes of the mammalian CTLH E3 ligase complex. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	4
28020	Construction of <sc>miRNA&#x2013;lncRNA&#x2013;mRNA</sc> co&#x2013;expression network affecting <sc>EMT&#x2013;/sc>-mediated cisplatin resistance in ovarian cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 4530-4547.	1.6	6
28021	Scalable multiplex co-fractionation/mass spectrometry platform for accelerated protein interactome discovery. <i>Nature Communications</i> , 2022, 13, .	5.8	20

#	ARTICLE	IF	CITATIONS
28023	Reduction of LPAR1 Expression in Neuroblastoma Promotes Tumor Cell Migration. <i>Cancers</i> , 2022, 14, 3346.	1.7	2
28024	Bioinformatics roadmap for therapy selection in cancer genomics. <i>Molecular Oncology</i> , 2022, 16, 3881-3908.	2.1	6
28025	The Construction and Analysis of Infiltrating Immune Cell and ceRNA Networks in Diabetic Foot Ulcer. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
28026	Integrated transcriptomic and regulatory network analyses uncovers the role of let-7b-5p, SPIB, and HLA-DPB1 in sepsis. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
28027	In-Silico Analysis of Deleterious SNPs of FGF4 Gene and Their Impacts on Protein Structure, Function and Bladder Cancer Prognosis. <i>Life</i> , 2022, 12, 1018.	1.1	5
28028	<i>Pseudomonas</i> spp. Enriched in Endophytic Community of Healthy Cotton Plants Inhibit Cotton Verticillium Wilt. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
28029	STAY-GREEN (SGR) genes in tomato ( <i>Solanum lycopersicum</i> ): genome-wide identification, and expression analyses reveal their involvements in ripening and salinity stress responses. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 557-569.	0.7	3
28031	Exploring the potential targets of Sanshimaof formula for hepatocellular carcinoma treatment by a method of network pharmacology combined with molecular biology. <i>Journal of Ethnopharmacology</i> , 2022, , 115531.	2.0	3
28033	Metagenomic Characterization of Resistance Genes in Deception Island and Their Association with Mobile Genetic Elements. <i>Microorganisms</i> , 2022, 10, 1432.	1.6	5
28034	Multiomics reveal the central role of pentose phosphate pathway in resident thymic macrophages to cope with efferocytosis-associated stress. <i>Cell Reports</i> , 2022, 40, 111065.	2.9	8
28035	A Regulatory Axis between Epithelial Splicing Regulatory Proteins and Estrogen Receptor $\hat{\pm}$ Modulates the Alternative Transcriptome of Luminal Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7835.	1.8	3
28036	A de novo YY1 missense variant expanding the Gabriele-de Vries syndrome phenotype and affecting X-chromosome inactivation. <i>Metabolic Brain Disease</i> , 2022, 37, 2431-2440.	1.4	3
28037	Integrated analysis of Wnt signalling system component gene expression. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	3
28038	Potential ferroptosis-related diagnostic and prognostic biomarkers in laryngeal cancer. <i>European Archives of Oto-Rhino-Laryngology</i> , 2022, 279, 5277-5288.	0.8	2
28039	Alternative splicing patterns reveal prognostic indicator in muscle-invasive bladder cancer. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	2
28040	Sequential rescue and repair of stalled and damaged ribosome by bacterial PrfH and RtcB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
28041	Lilac ( <i>Syringa oblata</i> ) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	2.0	13
28042	Comorbidities and ethnic health disparities in the UK biobank. <i>JAMIA Open</i> , 2022, 5, .	1.0	1

#	ARTICLE	IF	CITATIONS
28043	Rare Carbon-Bridged Citrinin Dimers from the Starfish-Derived Symbiotic Fungus <i>Penicillium</i> sp. GGF16-1-2. <i>Marine Drugs</i> , 2022, 20, 443.	2.2	9
28044	Uncoupling of Mitosis and Cytokinesis Upon a Prolonged Arrest in Metaphase Is Influenced by Protein Phosphatases and Mitotic Transcription in Fission Yeast. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
28045	Comprehensive mutations analyses of FTO (fat mass and obesity-associated gene) and their effects on FTO's substrate binding implicated in obesity. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
28047	Characterisation of sequence-structure-function space in sensor-effector integrators of phytochrome-regulated diguanylate cyclases. <i>Photochemical and Photobiological Sciences</i> , 2022, 21, 1761-1779.	1.6	3
28048	Screening of Human Circular RNAs as Biomarkers for Early Onset Detection of Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	2
28049	Highly perturbed genes and hub genes associated with type 2 diabetes in different tissues of adult humans: a bioinformatics analytic workflow. <i>Functional and Integrative Genomics</i> , 2022, 22, 1003-1029.	1.4	3
28051	T Cells With Activated STAT4 Drive the High-Risk Rejection State to Renal Allograft Failure After Kidney Transplantation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
28052	The Circadian Molecular Machinery in CNS Cells: A Fine Tuner of Neuronal and Glial Activity With Space/Time Resolution. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
28053	Multi-omics personalized network analyses highlight progressive disruption of central metabolism associated with COVID-19 severity. <i>Cell Systems</i> , 2022, 13, 665-681.e4.	2.9	17
28054	Differential expression profile of plasma exosomal microRNAs in acute type A aortic dissection with acute lung injury. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
28055	Inflammation in Preeclampsia: Genetic Biomarkers, Mechanisms, and Therapeutic Strategies. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	27
28056	Novel Drug Candidate Prediction for Intrahepatic Cholangiocarcinoma via Hub Gene Network Analysis and Connectivity Mapping. <i>Cancers</i> , 2022, 14, 3284.	1.7	11
28057	Effects of long-term exposure to MST312 on lung cancer cells tumorigenesis: Role of SHH/GLI1 axis. <i>Cell Biology International</i> , 2022, 46, 1468-1479.	1.4	1
28058	Organic Connection of Holobiont Components and the Essential Roles of Core Microbes in the Holobiont Formation of Feral <i>Brassica napus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
28059	A Novel Multitasking Ant Colony Optimization Method for Detecting Multiorder SNP Interactions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 814-832.	2.2	8
28060	Regular combined training and vitamins modulated the apoptosis process in diabetic rats: Bioinformatics analysis of heart failure's differential genes expression network correlated with anti-apoptotic process. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	2
28061	Multiplexed Visualization Method to Explore Complete Targeting Regulatory Relationships Among Circadian Genes for Insomnia Treatment. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	1
28062	Differential expression profile and in-silico functional analysis of long noncoding RNA and mRNA in duck embryo fibroblasts infected with duck plague virus. <i>BMC Genomics</i> , 2022, 23, .	1.2	1

#	ARTICLE	IF	CITATIONS
28064	Auxiliary Metabolic Gene Functions in Pelagic and Benthic Viruses of the Baltic Sea. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	21
28065	Prune homolog 2 with BCH domain (PRUNE2) gene expression is associated with feed efficiency-related traits in Nelore steers. <i>Mammalian Genome</i> , 2022, 33, 629-641.	1.0	1
28066	The role of NAD metabolism in neuronal differentiation. <i>Neurochemistry International</i> , 2022, 159, 105402.	1.9	3
28067	Identification of key genes and biological regulatory mechanisms in diabetic nephropathy: Meta-analysis of gene expression datasets. <i>Nefrologia</i> , 2023, 43, 575-586.	0.2	1
28068	Integrated Analysis of LncRNA-Mediated ceRNA Network in Calcific Aortic Valve Disease. <i>Cells</i> , 2022, 11, 2204.	1.8	5
28069	Identifying potential prognosis markers in hepatocellular carcinoma via integrated bioinformatics analysis and biological experiments. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28070	Immune infiltration and clinical significance analyses of the coagulation-related genes in hepatocellular carcinoma. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	34
28071	A novel therapeutic approach for IPF: Based on the "Autophagy - Apoptosis" balance regulation of Zukamu Granules in alveolar macrophages. <i>Journal of Ethnopharmacology</i> , 2022, 297, 115568.	2.0	3
28072	Comprehensive Analysis of TRIM Family Genes in Hepatitis Virus B-Related Hepatoma Carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
28073	Investigation into potential mechanisms of metabolic syndrome by integrative analysis of metabolomics and proteomics. <i>PLoS ONE</i> , 2022, 17, e0270593.	1.1	5
28074	LTBP2 inhibits prostate cancer progression and metastasis via the PI3K/AKT signaling pathway. <i>Experimental and Therapeutic Medicine</i> , 2022, 24, .	0.8	3
28075	Approaches in Gene Coexpression Analysis in Eukaryotes. <i>Biology</i> , 2022, 11, 1019.	1.3	4
28076	Conformational selection guides $\beta$ 2-arrestin recruitment at a biased G protein-coupled receptor. <i>Science</i> , 2022, 377, 222-228.	6.0	16
28077	TritiKBdb: A Functional Annotation Resource for Deciphering the Complete Interaction Networks in Wheat-Karnal Bunt Pathosystem. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7455.	1.8	1
28078	Identification and Characterization of Long Non-coding RNA in Tomato Roots Under Salt Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
28079	High PANX1 Expression Leads to Neutrophil Recruitment and the Formation of a High Adenosine Immunosuppressive Tumor Microenvironment in Basal-like Breast Cancer. <i>Cancers</i> , 2022, 14, 3369.	1.7	5
28080	Investigating evolutionary relationships through cluster analysis: A teaching science with big data workshop session. <i>Biochemistry and Molecular Biology Education</i> , 0, , .	0.5	1
28081	Orthology-based analysis helps map evolutionary diversification and predict substrate class use of <sc>BAHD</sc> acyltransferases. <i>Plant Journal</i> , 2022, 111, 1453-1468.	2.8	10

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28082	Application of <i>Sophora alopecuroides</i> organic fertilizer changes the rhizosphere microbial community structure of melon plants and increases the fruit sugar content. <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 164-175.	1.7	3
28083	Evolutionary analysis of globin domains from kinetoplastids. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	0
28084	Tumor treating fields affect mesothelioma cell proliferation by exerting histotype-dependent cell cycle checkpoint activations and transcriptional modulations. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	2
28085	Construction of circRNA-Mediated Immune-Related ceRNA Network and Identification of Circulating circRNAs as Diagnostic Biomarkers in Acute Ischemic Stroke. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4087-4104.	1.6	5
28086	Exploring the dynamic variations of viral genomes via a novel genetic network. <i>Molecular Phylogenetics and Evolution</i> , 2022, , 107583.	1.2	0
28089	A multiomics and network pharmacological study reveals the neuroprotective efficacy of Fu-Fang-Dan-Zhi tablets against glutamate-induced oxidative cell death. <i>Computers in Biology and Medicine</i> , 2022, 148, 105873.	3.9	8
28090	SYNGR2 serves as a prognostic biomarker and correlates with immune infiltrates in esophageal squamous cell carcinoma. <i>Journal of Gene Medicine</i> , 0, , .	1.4	1
28091	Prokineticins as a Prognostic Biomarker for Low-Grade Gliomas: A Study Based on The Cancer Genome Atlas Data. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	5
28092	Interconnectedness between periodontitis stage, oral hygiene habits, adherence to the Mediterranean diet and nutritional status in Dalmatian kidney transplant recipients: a cross-sectional study. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
28093	Large-Scale Multi-Omics Studies Provide New Insights into Blood Pressure Regulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7557.	1.8	10
28094	Industrializing AI-powered drug discovery: lessons learned from the <i>Patrimony</i> computing platform. <i>Expert Opinion on Drug Discovery</i> , 2022, 17, 815-824.	2.5	5
28095	Landscape of Global Gene Expression Reveals Distinctive Tissue Characteristics in Bactrian Camels ( <i>Camelus bactrianus</i> ). <i>Agriculture (Switzerland)</i> , 2022, 12, 958.	1.4	0
28096	Network Pharmacology-Based Strategy to Reveal the Mechanism of Cassiae Semen against Cataracts. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-18.	0.7	0
28097	Identification of Endoplasmic Reticulum Stress-Related Subtypes, Infiltration Analysis of Tumor Microenvironment, and Construction of a Prognostic Model in Colorectal Cancer. <i>Cancers</i> , 2022, 14, 3326.	1.7	2
28098	Genome-Wide Identification and Characterization of Receptor-Like Protein Kinase 1 (RPK1) Gene Family in <i>Triticum aestivum</i> Under Drought Stress. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
28099	Identification of Ferroptosis-Associated Genes in Prostate Cancer by Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28100	Identification of functional pathways and molecular signatures in neuroendocrine neoplasms by multi-omics analysis. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	14
28101	Diet-Induced Hypercholesterolemia Leads to Cardiac Dysfunction and Alterations in the Myocardial Proteome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7387.	1.8	1

#	ARTICLE	IF	CITATIONS
28102	Integrated transcriptome and hormonal analysis of naphthalene acetic acid-induced adventitious root formation of tea cuttings ( <i>Camellia sinensis</i> ). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	11
28103	Qing'e Pill Inhibits Osteoblast Ferroptosis via ATM Serine/Threonine Kinase (ATM) and the PI3K/AKT Pathway in Primary Osteoporosis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	12
28104	Exploring the fuzzy border between senolytics and senomorphics with chemoinformatics and systems pharmacology. <i>Biogerontology</i> , 2022, 23, 453-471.	2.0	4
28105	Circulating circular RNAs as biomarkers for the diagnosis of essential hypertension with carotid plaque. <i>Clinical and Experimental Hypertension</i> , 0, , 1-9.	0.5	0
28106	Identification of hub salt-responsive genes in <i>Cucumis sativus</i> using a long non-coding RNA and mRNA interaction network. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 539-556.	0.7	1
28107	Systematic Investigation of Immune-Related lncRNA Landscape Reveals a Potential Long Non-Coding RNA Signature for Predicting Prognosis in Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28108	Metabolome and transcriptome profiling reveal regulatory network and mechanism of flavonoid biosynthesis during color formation of <i>Dioscorea cirrhosa</i> L. <i>PeerJ</i> , 0, 10, e13659.	0.9	2
28109	Microarray-Based Prediction of Polycythemia after Exposure to High Altitudes. <i>Genes</i> , 2022, 13, 1193.	1.0	1
28110	Chromatin Separation Regulators Predict the Prognosis and Immune Microenvironment Estimation in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28113	Genome-wide identification of resistance genes and transcriptome regulation in yeast to accommodate ammonium toxicity. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
28114	Effects of Soybean Lecithin on Growth Performance, Intestine Morphology, and Liver Tissue Metabolism in Rock Bream ( <i>Oplegnathus fasciatus</i> ) Larvae. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	8
28115	Gene expression data analysis using Hellinger correlation in weighted gene co-expression networks (WGCNA). <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3851-3863.	1.9	21
28116	Transcriptomic Analysis Reveals the Role of tmRNA on Biofilm Formation in <i>Bacillus subtilis</i> . <i>Microorganisms</i> , 2022, 10, 1338.	1.6	4
28117	A comprehensive analysis of ncRNA-mediated interactions reveals potential prognostic biomarkers in prostate adenocarcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3839-3850.	1.9	1
28118	Identification of genes and key pathways underlying the pathophysiological association between nonalcoholic fatty liver disease and atrial fibrillation. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	4
28119	SimPLIT: Simplified Sample Preparation for Large-Scale Isobaric Tagging Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1842-1856.	1.8	9
28120	Homology-based reconstruction of regulatory networks for bacterial and archaeal genomes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
28121	Early steps of embryo implantation are regulated by exchange of extracellular vesicles between the embryo and the endometrium. <i>FASEB Journal</i> , 2022, 36, .	0.2	12



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28122	The structural and functional divergence of a neglected three-finger toxin subfamily in lethal elapids. <i>Cell Reports</i> , 2022, 40, 111079.	2.9	11
28123	Network-based quantitative proteomics identified significant proteins associated with growth heterosis in triploid fish. <i>Aquaculture Research</i> , 0, , .	0.9	0
28124	Identification and Validation of a Potential Stemness-Associated Biomarker in Hepatocellular Carcinoma. <i>Stem Cells International</i> , 2022, 2022, 1-18.	1.2	1
28125	Rhizosphere soil bacterial communities and nitrogen cycling affected by deciduous and evergreen tree species. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	8
28126	Qin Huang formula enhances the effect of Adriamycin in B-cell lymphoma via increasing tumor infiltrating lymphocytes by targeting toll-like receptor signaling pathway. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	2
28127	RNA-sequencing of human aortic valves identifies that miR-629-3p and TAGLN miRNA-mRNA pair involving in calcified aortic valve disease. <i>Journal of Physiology and Biochemistry</i> , 2022, 78, 819-831.	1.3	7
28128	Bioinformatics Analysis Reveals FOXM1/BUB1B Signaling Pathway as a Key Target of Neosetophomone B in Human Leukemic Cells: A Gene Network-Based Microarray Analysis. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
28129	Wheat Rhizosphere Microbiota Respond to Changes in Plant Genotype, Chemical Inputs, and Plant Phenotypic Plasticity. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	7
28130	An Outdoor Access Period Improves Chicken Cecal Microbiota and Potentially Increases Micronutrient Biosynthesis. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
28131	Tumor antigens and immune subtypes of glioblastoma: the fundamentals of mRNA vaccine and individualized immunotherapy development. <i>Journal of Big Data</i> , 2022, 9, .	6.9	21
28132	Comparisons of Metastatic Patterns, Survival Outcomes and Tumor Immune Microenvironment Between Young and Non-Young Breast Cancer Patients. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	10
28133	Glia Maturation Factor 1 as a Novel Independent Prognostic Biomarker and Potential Therapeutic Target of Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
28134	Single-cell RNA Sequencing Analysis Reveals New Immune Disorder Complexities in Hypersplenism. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
28135	Multi-Omics Integration-Based Prioritisation of Competing Endogenous RNA Regulation Networks in Small Cell Lung Cancer: Molecular Characteristics and Drug Candidates. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
28136	Identification and Validation of Immune-Related Long Non-Coding RNA Signature for Predicting Immunotherapeutic Response and Prognosis in NSCLC Patients Treated With Immunotherapy. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
28137	Isolation and Molecular Characterization of a Novel Lytic Bacteriophage That Inactivates MDR <i>Klebsiella pneumoniae</i> Strains. <i>Pharmaceutics</i> , 2022, 14, 1421.	2.0	13
28138	Identification of Immune-Associated Genes in Diagnosing Aortic Valve Calcification With Metabolic Syndrome by Integrated Bioinformatics Analysis and Machine Learning. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	28
28139	ATRPred: A machine learning based tool for clinical decision making of anti-TNF treatment in rheumatoid arthritis patients. <i>PLoS Computational Biology</i> , 2022, 18, e1010204.	1.5	4

#	ARTICLE	IF	CITATIONS
28140	Anti-liver fibrosis effects of the total flavonoids of litchi semen on CCl <sub>4</sub> -induced liver fibrosis in rats associated with the upregulation of retinol metabolism. <i>Pharmaceutical Biology</i> , 2022, 60, 1264-1277.	1.3	3
28141	Deciphering the pharmacological mechanisms of <i>Chaenomeles Fructus</i> against rheumatoid arthritis by integrating network pharmacology and experimental validation. <i>Food Science and Nutrition</i> , 2022, 10, 3380-3394.	1.5	2
28142	In Silico Comparative Structural and Residue Interaction Network Analysis of MATE Efflux Proteins in <i>P. aeruginosa</i> and <i>S. aureus</i> . <i>Chemistry Africa</i> , 0, , .	1.2	0
28143	Comprehensive Analysis of Immune-Related Metabolic Genes in Lung Adenocarcinoma. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
28144	Chlorogenic acid exerts antibacterial effects by affecting lipid metabolism and scavenging ROS in <i>Streptococcus pyogenes</i> . <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	12
28145	Transcriptomic Profiling Revealed Signaling Pathways Associated with the Spawning of Female Zebrafish under Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7494.	1.8	5
28146	Shared Genetic Risk Factors Between Cancer and Cardiovascular Diseases. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	6
28147	Identification of circRNA-miRNA-mRNA Regulatory Network and Crucial Signaling Pathway Axis Involved in Tetralogy of Fallot. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28148	Comparative bioinformatics analysis and abiotic stress responses of expansin proteins in Cucurbitaceae members: watermelon and melon. <i>Protoplasma</i> , 2023, 260, 509-527.	1.0	7
28149	HIF-1 $\alpha$ induces glycolytic reprogramming in tissue-resident alveolar macrophages to promote cell survival during acute lung injury. <i>ELife</i> , 0, 11, .	2.8	8
28150	Statistical Bioinformatics to Uncover the Underlying Biological Mechanisms That Linked Smoking with Type 2 Diabetes Patients Using Transcriptomic and GWAS Analysis. <i>Molecules</i> , 2022, 27, 4390.	1.7	2
28151	Comprehensive Computational Analysis of Honokiol Targets for Cell Cycle Inhibition and Immunotherapy in Metastatic Breast Cancer Stem Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	1
28152	Context-dependent regulation of ferroptosis sensitivity. <i>Cell Chemical Biology</i> , 2022, 29, 1409-1418.e6.	2.5	42
28153	In Silico Identification of lncRNAs Regulating Sperm Motility in the Turkey ( <i>Meleagris gallopavo</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7642.	1.8	2
28154	Characterization of LipS1 and LipS2 from <i>Thermococcus kodakarensis</i> : Proteins Annotated as Biotin Synthases, which Together Catalyze Formation of the Lipoyl Cofactor. <i>ACS Bio &amp; Med Chem Au</i> , 2022, 2, 509-520.	1.7	3
28155	Vitamin D boosts immune response of macrophages through a regulatory network of microRNAs and mRNAs. <i>Journal of Nutritional Biochemistry</i> , 2022, 109, 109105.	1.9	11
28156	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	9.4	25
28157	Foxh1 engages in chromatin regulation revealed by protein interactome analyses. <i>Development Growth and Differentiation</i> , 0, , .	0.6	1

#	ARTICLE	IF	CITATIONS
28158	Looking for the Genes Related to Lung Cancer From Nasal Epithelial Cells by Network and Pathway Analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28159	Light-induced asymmetries in embryonic retinal gene expression are mediated by the vascular system and extracellular matrix. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
28160	Partial root-zone simulated drought induces greater flavonoid accumulation than full root-zone simulated water deficiency in the leaves of <i>Ginkgo biloba</i> . <i>Environmental and Experimental Botany</i> , 2022, 201, 104998.	2.0	9
28161	17q21.31 sub-haplotypes underlying H1-associated risk for Parkinson's disease are associated with LRR37A/2 expression in astrocytes. <i>Molecular Neurodegeneration</i> , 2022, 17, .	4.4	15
28162	Identification and Verification of Potential Biomarkers in Gastric Cancer By Integrated Bioinformatic Analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
28163	Prospective role and immunotherapeutic targets of sideroflexin protein family in lung adenocarcinoma: evidence from bioinformatics validation. <i>Functional and Integrative Genomics</i> , 2022, 22, 1057-1072.	1.4	30
28164	The Pharmacological Mechanism of Xiyanning Injection for the Treatment of Novel Coronavirus Pneumonia (COVID-19): Based on Network Pharmacology Strategy. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	0
28165	Bioinformatics strategies for studying the molecular mechanisms of fungal extracellular vesicles with a focus on infection and immune responses. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
28166	Systemic approaches using single cell transcriptome reveal that C/EBP $\beta$ regulates autophagy under amino acid starved condition. <i>Nucleic Acids Research</i> , 2022, 50, 7298-7309.	6.5	3
28167	The therapeutic effect of Fufang Zhenshu Tiaozhi (FTZ) on osteoclastogenesis and ovariectomized-induced bone loss: evidence from network pharmacology, molecular docking and experimental validation. <i>Aging</i> , 2022, 14, 5727-5748.	1.4	3
28168	High expression of eIF4A1 predicts unfavorable prognosis in clear cell renal cell carcinoma. <i>Molecular and Cellular Probes</i> , 2022, , 101845.	0.9	4
28169	SARS-CoV-2 potential drugs, drug targets, and biomarkers: a viral-host interaction network-based analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
28170	Transcriptional networks regulating suberin and lignin in endodermis link development and ABA response. <i>Plant Physiology</i> , 2022, 190, 1165-1181.	2.3	16
28171	Molecular networking-based discovery of anti-inflammatory chromene dimers from <i>Melicope pteleifolia</i> . <i>Phytochemistry</i> , 2022, 202, 113322.	1.4	4
28172	EEF1A1 transcription cofactor gene polymorphism is associated with muscle gene expression and residual feed intake in Nelore cattle. <i>Mammalian Genome</i> , 2022, 33, 619-628.	1.0	1
28173	Quantitative proteomic analysis of Bi Zhong Xiao decoction against collagen-induced arthritis rats in the early and late stages. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	2
28174	Identification of Key Genes Related to the Obesity Patients with Osteoarthritis Based on Weighted Gene Coexpression Network Analysis (WGCNA). <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-17.	0.7	1
28175	Knockdown of Lamin B1 and the Corresponding Lamin B Receptor Leads to Changes in Heterochromatin State and Senescence Induction in Malignant Melanoma. <i>Cells</i> , 2022, 11, 2154.	1.8	10

#	ARTICLE	IF	CITATIONS
28176	INK4 cyclin-dependent kinase inhibitors as potential prognostic biomarkers and therapeutic targets in hepatocellular carcinoma. <i>Bioscience Reports</i> , 2022, 42, .	1.1	2
28177	Identification of Ferroptotic Genes in Spinal Cord Injury at Different Time Points: Bioinformatics and Experimental Validation. <i>Molecular Neurobiology</i> , 2022, 59, 5766-5784.	1.9	11
28179	Platelet proteome reveals features of cell death, antiviral response and viral replication in covid-19. <i>Cell Death Discovery</i> , 2022, 8, .	2.0	15
28180	Construction of a circular RNA-based competing endogenous RNA network to screen biomarkers related to intervertebral disc degeneration. <i>BMC Musculoskeletal Disorders</i> , 2022, 23, .	0.8	1
28181	Network Pharmacology Integrated Molecular Docking to Explore the Mechanism of Blister Beetle Therapy for Lung Adenocarcinoma. <i>Contrast Media and Molecular Imaging</i> , 2022, 2022, 1-21.	0.4	0
28182	A systematic exploration of ginsenoside Rg5 reveals anti-inflammatory functions in airway mucosa cells. <i>Journal of Ginseng Research</i> , 2023, 47, 97-105.	3.0	6
28183	The State of the Catatonia Literature: Employing Bibliometric Analysis of Articles From 1965â€“2020 to Identify Current Research Gaps. <i>Journal of the Academy of Consultation-Liaison Psychiatry</i> , 2023, 64, 13-27.	0.2	5
28184	Differential gene screening and bioinformatics analysis of epidermal stem cells and dermal fibroblasts during skin aging. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
28185	Study on the Potential Mechanism of Tonifying Kidney and Removing Dampness Formula in the Treatment of Postmenopausal Dyslipidemia Based on Network Pharmacology, Molecular Docking and Experimental Evidence. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
28187	MiR-487b suppressed inflammation and neuronal apoptosis in spinal cord injury by targeted Ifitm3. <i>Metabolic Brain Disease</i> , 2022, 37, 2405-2415.	1.4	7
28188	Molecular Pathways and Key Genes Associated With Breast Width and Protein Content in White Striping and Wooden Breast Chicken Pectoral Muscle. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	4
28189	Genome-Wide Analysis of microRNAs Identifies the Lipid Metabolism Pathway to Be a Defining Factor in Adipose Tissue From Different Sheep. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
28191	Molecular landscapes of human hippocampal immature neurons across lifespan. <i>Nature</i> , 2022, 607, 527-533.	13.7	116
28192	Hypoxia reveals a new function of Foxn1 in the keratinocyte antioxidant defense system. <i>FASEB Journal</i> , 2022, 36, .	0.2	5
28193	Effect of Selenium Treatment on Central Insulin Sensitivity: A Proteomic Analysis in Î²-Amyloid Precursor Protein/Presenilin-1 Transgenic Mice. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	2
28194	Target Metabolome and Transcriptome Analysis Reveal Molecular Mechanism Associated with Changes of Tea Quality at Different Development Stages. <i>Molecular Biotechnology</i> , 0, , .	1.3	0
28195	Dysbiosis and Predicted Functions of the Dental Biofilm of Dairy Goats with Periodontitis. <i>Microbial Ecology</i> , 2023, 86, 687-698.	1.4	5
28196	Study on the Anti-demyelination Mechanism of Bu-Shen-Yi-Sui Capsule in the Central Nervous System Based on Network Pharmacology and Experimental Verification. <i>Mediators of Inflammation</i> , 2022, 2022, 1-23.	1.4	1

#	ARTICLE	IF	CITATIONS
28197	Altered mitochondrial microenvironment at the spotlight of musculoskeletal aging and Alzheimer's disease. <i>Scientific Reports</i> , 2022, 12, .	1.6	10
28198	Identification of molecular mechanisms underlying the therapeutic effects of Xintong granule in coronary artery disease by a network pharmacology and molecular docking approach. <i>Medicine (United States)</i> , 2022, 101, e29829.	0.4	2
28199	Mechanism and Molecular Targets of Ejiao Siwu Decoction for Treating Primary Immune Thrombocytopenia Based on High-Performance Liquid Chromatograph, Network Pharmacology, Molecular Docking and Cytokines Validation. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	1
28200	Orientation algorithm for PPI networks based on network propagation approach. <i>Journal of Biosciences</i> , 2022, 47, .	0.5	2
28201	Keeping time in the dark: Potato diel and circadian rhythmic gene expression reveals tissue-specific circadian clocks. <i>Plant Direct</i> , 2022, 6, .	0.8	6
28202	Proteomic characterisation of triple negative breast cancer cells following CDK4/6 inhibition. <i>Scientific Data</i> , 2022, 9, .	2.4	4
28203	A protein-protein interaction map reveals that the <i>Coxiella burnetii</i> effector CirB inhibits host proteasome activity. <i>PLoS Pathogens</i> , 2022, 18, e1010660.	2.1	12
28204	Online Mathematics Education during the COVID-19 Pandemic: Didactic Strategies, Educational Resources, and Educational Contexts. <i>Education Sciences</i> , 2022, 12, 492.	1.4	12
28205	Epigenomics of conventional type-I dendritic cells depicted preferential control of TLR9 versus TLR3 response by NCoR1 through differential IRF3 activation. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	2
28206	Host Species Influence the Gut Microbiota of Endemic Cold-Water Fish in Upper Yangtze River. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
28207	Altered Transcriptional Regulation of Glycolysis in Circulating CD8+ T Cells of Rheumatoid Arthritis Patients. <i>Genes</i> , 2022, 13, 1216.	1.0	3
28208	Spatially resolved proteomic map shows that extracellular matrix regulates epidermal growth. <i>Nature Communications</i> , 2022, 13, .	5.8	26
28210	Pyroptosis may play a crucial role in modifications of the immune microenvironment in periodontitis. <i>Journal of Periodontal Research</i> , 2022, 57, 977-990.	1.4	11
28211	Multi-omics study identifies novel signatures of DNA/RNA, amino acid, peptide, and lipid metabolism by simulated diabetes on coronary endothelial cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
28212	The Effect of Residual Pesticide Application on Microbiomes of the Storage Mite <i>Tyrophagus putrescentiae</i> . <i>Microbial Ecology</i> , 2023, 85, 1527-1540.	1.4	3
28213	A Chromosome Level Genome Assembly of a Winter Turnip Rape ( <i>Brassica rapa</i> L.) to Explore the Genetic Basis of Cold Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
28214	Investigation of Biomarkers Associated with Low Platelet Counts in Normal Karyotype Acute Myeloid Leukemia. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7772.	1.8	3
28215	Englerin A Rewires Phosphosignaling via Hsp27 Hyperphosphorylation to Induce Cytotoxicity in Renal Cancer Cells. <i>Journal of Proteome Research</i> , 2022, 21, 1948-1960.	1.8	3

#	ARTICLE	IF	CITATIONS
28216	Untargeted LC-MS/MS-Based Multi-Informative Molecular Networking for Targeting the Antiproliferative Ingredients in <i>Tetradium ruticarpum</i> Fruit. <i>Molecules</i> , 2022, 27, 4462.	1.7	4
28218	Inner membrane complex proteomics reveals a palmitoylation regulation critical for intraerythrocytic development of malaria parasite. <i>ELife</i> , 0, 11, .	2.8	9
28219	Transcriptome and Network Analyses Reveal the Gene Set Involved in PST Accumulation and Responses to Toxic <i>Alexandrium minutum</i> Exposure in the Gills of <i>Chlamys farreri</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7912.	1.8	0
28220	EPH receptor tyrosine kinases phosphorylate the PAR-3 scaffold protein to modulate downstream signaling networks. <i>Cell Reports</i> , 2022, 40, 111031.	2.9	8
28221	Identification of the KCNQ1OT1/ miR-378a-3p/ RBMS1 Axis as a Novel Prognostic Biomarker Associated With Immune Cell Infiltration in Gastric Cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28222	A Method for Bridging Population-Specific Genotypes to Detect Gene Modules Associated with Alzheimer's Disease. <i>Cells</i> , 2022, 11, 2219.	1.8	0
28223	Dynamics of the Gut Bacteriome During a Laboratory Adaptation Process of the Mediterranean Fruit Fly, <i>Ceratitis capitata</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
28224	Molecular network-guided chemical profile and mass spectrometry, volatile compounds, and antimicrobial activity of <i>Scaptotrigona depilis</i> propolis. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, .	0.7	2
28225	Pan-Cancer Analysis Reveals the Prognostic Potential of the THAP9/THAP9-AS1 Sense-Antisense Gene Pair in Human Cancers. <i>Non-coding RNA</i> , 2022, 8, 51.	1.3	0
28228	Hsa-let-7c-5p, hsa-miR-130b-3p, and hsa-miR-142-3p as Novel miRNA Biomarkers for Melanoma Progression. <i>Genetical Research</i> , 2022, 2022, 1-12.	0.3	4
28229	Early Systemic Glycolytic Shift After Aneurysmal Subarachnoid Hemorrhage is Associated with Functional Outcomes. <i>Neurocritical Care</i> , 0, , .	1.2	1
28230	COL5A1 Promotes the Progression of Gastric Cancer by Acting as a ceRNA of miR-137-3p to Upregulate FSTL1 Expression. <i>Cancers</i> , 2022, 14, 3244.	1.7	5
28231	Functional analysis of <i>Escherichia coli</i> K12 toxin-antitoxin systems as novel drug targets using a network biology approach. <i>Microbial Pathogenesis</i> , 2022, 169, 105683.	1.3	5
28232	Microbial pathways to subvert host immunity generate citrullinated neoantigens targeted in rheumatoid arthritis. <i>Current Opinion in Structural Biology</i> , 2022, 75, 102423.	2.6	3
28233	Proteomics of the phase angle: Results from the population-based KORA S4 study. <i>Clinical Nutrition</i> , 2022, 41, 1818-1826.	2.3	3
28234	Pathophysiology and system biology of rat c-BSA induced immune complex glomerulonephritis and pathway comparison with human gene sequencing data. <i>International Immunopharmacology</i> , 2022, 109, 108891.	1.7	6
28235	Long non-coding RNAs are involved in immune resistance to <i>Aeromonas hydrophila</i> in black carp ( <i>Mylopharyngodon piceus</i> ). <i>Fish and Shellfish Immunology</i> , 2022, 127, 366-374.	1.6	2
28236	Genome-wide association meta-analysis of 88,250 individuals highlights pleiotropic mechanisms of five ocular diseases in UK Biobank. <i>EBioMedicine</i> , 2022, 82, 104161.	2.7	21



#	ARTICLE	IF	CITATIONS
28237	Organ-specific host differential gene expression analysis in systemic candidiasis: A systems biology approach. <i>Microbial Pathogenesis</i> , 2022, 169, 105677.	1.3	2
28238	Weighted gene co-expression network analysis identifies potential regulators in response to <i>Salmonella</i> Enteritidis challenge in the reproductive tract of laying ducks. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2384-2398.	1.7	2
28239	Examining the relations between semantic memory structure and creativity in second language. <i>Thinking Skills and Creativity</i> , 2022, 45, 101067.	1.9	5
28240	Network analysis for elucidating the mechanisms of Shenfu injection in preventing and treating COVID-19 combined with heart failure. <i>Computers in Biology and Medicine</i> , 2022, 148, 105845.	3.9	3
28241	Exploration and validation of <i>Taraxacum mongolicum</i> anti-cancer effect. <i>Computers in Biology and Medicine</i> , 2022, 148, 105819.	3.9	2
28242	Inhibitory role of LINC00332 in gastric cancer progression through regulating cell EMT and stemness. <i>Life Sciences</i> , 2022, 305, 120759.	2.0	5
28243	Application of a pharmacological transcriptome filter identifies a shortlist of mouse glucocorticoid receptor target genes associated with memory consolidation. <i>Neuropharmacology</i> , 2022, 216, 109186.	2.0	4
28244	<i>Porphyromonas gingivalis</i> resistance and virulence: An integrated functional network analysis. <i>Gene</i> , 2022, 839, 146734.	1.0	4
28245	A review on computational approaches that support the researches on traditional Chinese medicines (TCM) against COVID-19. <i>Phytomedicine</i> , 2022, 104, 154324.	2.3	2
28246	Integrating network pharmacology and experimental models to investigate the efficacy of QYHJ on pancreatic cancer. <i>Journal of Ethnopharmacology</i> , 2022, 297, 115516.	2.0	5
28247	Contribution of prognostic ferroptosis-related subtypes classification and hub genes of sepsis. <i>Transplant Immunology</i> , 2022, 74, 101660.	0.6	1
28248	Localized intensification of arsenic methylation within landfill leachate-saturated zone. <i>Science of the Total Environment</i> , 2022, 842, 156979.	3.9	0
28249	Dynamic metabolic and transcriptomic profiling reveal synthetic characters and regulators of flavonoid biosynthesis in <i>Camellia oleifera</i> seeds. <i>Industrial Crops and Products</i> , 2022, 186, 115295.	2.5	15
28250	Tandem Mass Tag-based proteomics analysis reveals the vital role of inflammation in traumatic brain injury in a mouse model. <i>Neural Regeneration Research</i> , 2023, 18, 155.	1.6	4
28252	Sex chromosome aneuploidies give rise to changes in the circular RNA profile: A circular transcriptome-wide study of Turner and Klinefelter syndrome across different tissues. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
28253	APE1 controls DICER1 expression in NSCLC through miR-33a and miR-130b. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	12
28254	Transcriptome Analysis and HPLC Profiling of Flavonoid Biosynthesis in <i>Citrus aurantium</i> L. during Its Key Developmental Stages. <i>Biology</i> , 2022, 11, 1078.	1.3	1
28255	Host genetic determinants drive compartment-specific assembly of tea plant microbiomes. <i>Plant Biotechnology Journal</i> , 2022, 20, 2174-2186.	4.1	10

#	ARTICLE	IF	CITATIONS
28256	Lipid-related FABP5 activation of tumor-associated monocytes fosters immune privilege via PD-L1 expression on Treg cells in hepatocellular carcinoma. <i>Cancer Gene Therapy</i> , 2022, 29, 1951-1960.	2.2	17
28257	Temporal Cortex Microarray Analysis Revealed Impaired Ribosomal Biogenesis and Hyperactivity of the Glutamatergic System: An Early Signature of Asymptomatic Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	3
28258	Establishment of a circular RNA regulatory stemness-related gene pair signature for predicting prognosis and therapeutic response in colorectal cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
28259	<i>Margaritaria nobilis</i> L.F. (Phyllanthaceae): Ethnopharmacology and Application of Computational Tools in the Annotation of Bioactive Molecules. <i>Metabolites</i> , 2022, 12, 681.	1.3	6
28260	Rethinking the Intrinsic Sensitivity of Fungi to Glyphosate. <i>BioTech</i> , 2022, 11, 28.	1.3	2
28261	Identifying potential signatures for atherosclerosis in the context of predictive, preventive, and personalized medicine using integrative bioinformatics approaches and machine-learning strategies. <i>EPMA Journal</i> , 2022, 13, 433-449.	3.3	5
28262	Global transcriptomic response of <i>Escherichia coli</i> to p-coumaric acid. <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	1
28263	A Network-Guided Approach to Discover Phytochemical-Based Anticancer Therapy: Targeting MARK4 for Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	9
28264	The Identification by Exome Sequencing of Candidate Genes in BRCA-Negative Tunisian Patients at a High Risk of Hereditary Breast/Ovarian Cancer. <i>Genes</i> , 2022, 13, 1296.	1.0	2
28265	Sex-biased admixture and assortative mating shape genetic variation and influence demographic inference in admixed Cabo Verdeans. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
28266	Novel Interactions Between Phytoplankton and Bacteria Shape Microbial Seasonal Dynamics in Coastal Ocean Waters. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
28268	Integrated transcriptome and small RNA sequencing in revealing miRNA-mediated regulatory network of floral bud break in <i>Prunus mume</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
28271	Network Pharmacology and Molecular Docking on the Molecular Mechanism of Jiawei-Huang Lian-Gan Jiang Decoction in the Treatment of Colorectal Adenomas. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-15.	0.5	0
28272	Bioinformatics analysis of potential common pathogenic mechanisms for COVID-19 infection and primary Sjogren's syndrome. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
28273	Proteome-Wide Differential Effects of Peritoneal Dialysis Fluid Properties in an In Vitro Human Endothelial Cell Model. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8010.	1.8	4
28274	Identification of key genes and their association with immune infiltration in adipose tissue of obese patients: a bioinformatic analysis. <i>Adipocyte</i> , 2022, 11, 401-412.	1.3	6
28275	Molecular Networking-Guided Isolation of Cycloartane-type Triterpenoids from <i>Curculigo orchioides</i> and Their Inhibitory Effect on Nitric Oxide Production. <i>ACS Omega</i> , 2022, 7, 26853-26862.	1.6	3
28276	Key features of the genetic architecture and evolution of host-microbe interactions revealed by high-resolution genetic mapping of the mucosa-associated gut microbiome in hybrid mice. <i>ELife</i> , 0, 11, .	2.8	9

#	ARTICLE	IF	CITATIONS
28277	Treatable traits in the NOVELTY study. <i>Respirology</i> , 2022, 27, 929-940.	1.3	29
28278	Untargeted Metabolomics Sheds Light on the Secondary Metabolism of Fungi Triggered by Choline-Based Ionic Liquids. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
28279	A framework for non-preserved consensus gene module detection in Johne's disease. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
28280	Urine Proteomics Reveals Sex-Specific Response to Total Pancreatectomy With Islet Autotransplantation. <i>Pancreas</i> , 2022, 51, 435-444.	0.5	2
28281	Genome-wide identification and expression pattern analysis of lipoxygenase gene family in turnip ( <i>Brassica rapa</i> L. subsp. <i>rapa</i> ). <i>PeerJ</i> , 0, 10, e13746.	0.9	5
28282	Drug discovery and potential gene and pathway associated with polycystic ovary syndrome through text mining and biomedical databases. <i>Reproductive and Developmental Medicine</i> , 2023, 7, 44-49.	0.2	0
28283	Common Core Genes Play Vital Roles in Gastric Cancer With Different Stages. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28284	Microbial succession and its effect on key aroma components during light-aroma-type Xiaoqu Baijiu brewing process. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	9
28285	Comprehensive Analysis of Quantitative Proteomics With DIA Mass Spectrometry and ceRNA Network in Intrahepatic Cholestasis of Pregnancy. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	6
28286	Exploration of molecular targets and mechanisms of Chinese medicinal formula <i>Acacia Catechu</i> <i>Scutellariae Radix</i> in the treatment of COVID-19 by a systems pharmacology strategy. <i>Phytotherapy Research</i> , 2022, 36, 4210-4229.	2.8	7
28287	Identification of potential predictive biomarkers and biological pathways and the correction with immune infiltration in the activation of Crohn's disease. <i>Immunogenetics</i> , 2022, 74, 527-537.	1.2	1
28288	Rice co-expression network analysis identifies gene modules associated with agronomic traits. <i>Plant Physiology</i> , 2022, 190, 1526-1542.	2.3	6
28289	Prediction of the Active Components and Mechanism of <i>Forsythia suspensa</i> Leaf against Respiratory Syncytial Virus Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	0
28290	A supervised protein complex prediction method with network representation learning and gene ontology knowledge. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
28291	lncRNA-miRNA-mRNA ceRNA Network Involved in Sheep Prolificacy: An Integrated Approach. <i>Genes</i> , 2022, 13, 1295.	1.0	12
28292	Effect of Pyroptosis-Related Genes on the Prognosis of Breast Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
28293	Integrated analysis using ToppMiR uncovers altered miRNA-mRNA regulatory networks in pediatric hepatocellular carcinoma: A pilot study. <i>Cancer Reports</i> , 0, , .	0.6	1
28294	Identifying General Tumor and Specific Lung Cancer Biomarkers by Transcriptomic Analysis. <i>Biology</i> , 2022, 11, 1082.	1.3	6

#	ARTICLE	IF	CITATIONS
28296	Bioinformatics-Based Approach for Exploring the Immune Cell Infiltration Patterns in Alzheimer's Disease and Determining the Intervention Mechanism of Liuwei Dihuang Pill. <i>Dose-Response</i> , 2022, 20, 155932582211155.	0.7	1
28297	Mechanistic Studies on the Stereoselectivity of FFAR1 Modulators. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 3664-3675.	2.5	4
28298	Whole transcriptome analysis reveals non-coding RNA's competing endogenous gene pairs as novel form of motifs in serous ovarian cancer. <i>Computers in Biology and Medicine</i> , 2022, 148, 105881.	3.9	10
28299	A joint learning approach for genomic prediction in polyploid grasses. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
28300	Liver transcriptome analysis reveals changes in energy metabolism, oxidative stress, and apoptosis in pearl gentian grouper exposed to acute hypoxia. <i>Aquaculture</i> , 2022, 561, 738635.	1.7	16
28301	Comparative analysis of differentially abundant proteins between high and low intramuscular fat content groups in donkeys. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
28302	Identification and characterization of four immune-related signatures in keloid. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
28303	MTHSA-DHEI: multitasking harmony search algorithm for detecting high-order SNP epistatic interactions. <i>Complex &amp; Intelligent Systems</i> , 2023, 9, 637-658.	4.0	11
28304	Differential MicroRNA Expression in Porcine Endometrium Related to Spontaneous Embryo Loss during Early Pregnancy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8157.	1.8	4
28305	A Novel Prognostic Risk Model for Cervical Cancer Based on Immune Checkpoint HLA-G-Driven Differentially Expressed Genes. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
28306	Mechanism of the Combination of KuShen and XiYangShen on Myocarditis Based on Network Pharmacology and Animal Experiments. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, , 100141.	0.5	0
28309	Bioinformatic Analysis of a Set of 14 Temperate Bacteriophages Isolated from Staphylococcus aureus Strains Highlights Their Massive Genetic Diversity. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
28310	A comprehensive multi-omics analysis reveals molecular features associated with cancer via RNA cross-talks in the Notch signaling pathway. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3972-3985.	1.9	2
28311	The SARS-CoV-2 targeted human RNA binding proteins network biology to investigate COVID-19 associated manifestations. <i>International Journal of Biological Macromolecules</i> , 2022, 217, 853-863.	3.6	5
28312	Gene Ontology Analysis Highlights Biological Processes Influencing Non-Response to Anti-TNF Therapy in Rheumatoid Arthritis. <i>Biomedicines</i> , 2022, 10, 1808.	1.4	2
28313	miRNA-mRNA associations with inosine monophosphate specific deposition in the muscle of Jingyuan chicken. <i>British Poultry Science</i> , 2022, 63, 821-832.	0.8	5
28314	Comprehensive analysis of the large and small ribosomal proteins in breast cancer: Insights on proteomic and transcriptomic expression patterns, regulation, mutational landscape, and prognostic significance. <i>Computational Biology and Chemistry</i> , 2022, 100, 107746.	1.1	2
28315	Remarkable immune and clinical value of novel ferroptosis-related genes in glioma. <i>Scientific Reports</i> , 2022, 12, .	1.6	2

#	ARTICLE	IF	CITATIONS
28316	Quantitative Proteomics and Network Analysis of Differentially Expressed Proteins in Proteomes of Icefish Muscle Mitochondria Compared with Closely Related Red-Blooded Species. <i>Biology</i> , 2022, 11, 1118.	1.3	0
28317	Transcriptome Analysis Identifies Key Metabolic Changes in the Brain of Takifugu rubripes in Response to Chronic Hypoxia. <i>Genes</i> , 2022, 13, 1347.	1.0	11
28318	Global and precise identification of functional <i>miRNA</i> targets in <i>mESCs</i> by integrative analysis. <i>EMBO Reports</i> , 2022, 23, .	2.0	5
28319	Integrated Analysis of Gene Expression and Methylation Data to Identify Potential Biomarkers Related to Atherosclerosis Onset. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-13.	1.9	0
28320	The genome of <i>Dioscorea zingiberensis</i> sheds light on the biosynthesis, origin and evolution of the medicinally important diosgenin saponins. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
28321	Ultra-high performance liquid chromatography combined with electrospray ionization quadrupole time-of-flight mass spectrometry and molecular networking analysis to investigate the chemodiversity of bioactive extracts of <i>Annona jahnii</i> Saff. fungi from the Brazilian Amazon. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, .	0.7	0
28322	Amnion Cells in Tailored Hydrogels Deposit Human Amnion Native Extracellular Matrix. <i>Advanced Functional Materials</i> , 2022, 32, .	7.8	3
28323	Fructus Zanthoxyli extract improves glycolipid metabolism disorder of type 2 diabetes mellitus via activation of AMPK/PI3K/Akt pathway: Network pharmacology and experimental validation. <i>Journal of Integrative Medicine</i> , 2022, 20, 543-560.	1.4	6
28324	Identification of gut metabolites associated with Parkinson's disease using bioinformatic analyses. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	5
28325	Mapping the network biology of metabolic response to stress in posttraumatic stress disorder and obesity. <i>Frontiers in Psychology</i> , 0, 13, .	1.1	1
28326	Analysis of mechanisms of Shenhuang Granule in treating severe COVID-19 based on network pharmacology and molecular docking. <i>Journal of Integrative Medicine</i> , 2022, 20, 561-574.	1.4	2
28327	Integration of multi-omics data reveals interplay between brassinosteroid and Target of Rapamycin Complex signaling in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2022, 236, 893-910.	3.5	15
28329	Proteomic Assessment of C57BL/6 Hippocampi after Non-Selective Pharmacological Inhibition of Nitric Oxide Synthase Activity: Implications of Seizure-like Neuronal Hyperexcitability Followed by Tauopathy. <i>Biomedicines</i> , 2022, 10, 1772.	1.4	3
28330	Identification of Molecular Targets and Potential Mechanisms of Yinchen Wuling San Against Head and Neck Squamous Cell Carcinoma by Network Pharmacology and Molecular Docking. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
28331	Molecular Network-Based Identification of Tramadol Metabolites in a Fatal Tramadol Poisoning. <i>Metabolites</i> , 2022, 12, 665.	1.3	12
28332	Introduction of exotic species <i>Sonneratia apetala</i> alters diazotrophic community and stimulates nitrogen fixation in mangrove sediments. <i>Ecological Indicators</i> , 2022, 142, 109179.	2.6	4
28333	Mechanism of action of Bu Zhong Yi Qi Decoction in the treatment of chronic fatigue syndrome based on network pharmacology and molecular docking. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 4, 100139.	0.5	0
28334	The microbiome and its association with antibiotic resistance genes in the hadal biosphere at the Yap Trench. <i>Journal of Hazardous Materials</i> , 2022, 439, 129543.	6.5	3

#	ARTICLE	IF	CITATIONS
28335	Integrative analysis of the metabolome and transcriptome provides novel insights into the mechanisms of flavonoid biosynthesis in <i>Camellia lanceoleosa</i> . <i>Scientia Horticulturae</i> , 2022, 304, 111357.	1.7	5
28336	Integrated transcriptomics and metabolomics analysis to characterize the optimal picking time in yellowhorn ( <i>Xanthoceras sorbifolium</i> ) flowers. <i>Industrial Crops and Products</i> , 2022, 187, 115389.	2.5	4
28337	Analysis of the multi-physiological and functional mechanism of wheat alkylresorcinols based on reverse molecular docking and network pharmacology. <i>Food and Function</i> , 2022, 13, 9091-9107.	2.1	3
28338	Research on the Evaluation and Utilization of Constitutional Diagnosis by Korean Doctors using AI-based Evaluation Tool. <i>Journal of Physiology &amp; Pathology in Korean Medicine</i> , 2022, 36, 73-78.	0.2	0
28339	Trends & Opportunities in Visualization for Physiology: A Multiscale Overview. <i>Computer Graphics Forum</i> , 2022, 41, 609-643.	1.8	1
28340	Network Pharmacology and Molecular Docking Analysis on Mechanisms of Isobavachalcone in Parkinson's Disease. , 2022, 2, 1-9.		0
28341	Application of process mining approach to the developmental process of the roundworm <i>C. elegans</i> . , 2022, , .		0
28342	Therapeutic targets and functions of curcumol against COVID-19 and colon adenocarcinoma. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
28343	The spatiotemporal regulations of epicatechin biosynthesis under normal flowering and the continuous inflorescence removal treatment in <i>Fagopyrum dibotrys</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
28344	Household-level sanitation in Ethiopia and its influencing factors: a systematic review. <i>BMC Public Health</i> , 2022, 22, .	1.2	8
28345	Abnormal bile acid metabolism is an important feature of gut microbiota and fecal metabolites in patients with slow transit constipation. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
28349	Biochemical and Proteome Analysis Reveal Different Nutritional Compound Compositions and Chloroplast Development Situations between Purple-Red and White-Yellow Tea Plant Cultivars. <i>Horticulturae</i> , 2022, 8, 685.	1.2	2
28350	Identification of the Key Pathways and Genes Involved in the Wax Biosynthesis of the Chinese White Wax Scale Insect ( <i>Ericerus pela</i> Chavannes) by Integrated Weighted Gene Coexpression Network Analysis. <i>Genes</i> , 2022, 13, 1364.	1.0	5
28351	Genome-wide identification and expression pattern of short-wavelength light responsive members of the NAC family in turnip. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 581-594.	0.7	0
28352	System analysis of <i>Lipomyces starkeyi</i> during growth on various plant-based sugars. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 5629-5642.	1.7	1
28353	Elucidation of the Underlying Mechanism of Gujian Oral Liquid Acting on Osteoarthritis through Network Pharmacology, Molecular Docking, and Experiment. <i>BioMed Research International</i> , 2022, 1-19.	0.9	1
28354	Innate Immune Training of Human Macrophages by Cathelicidin Analogs. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
28355	PROTEOMIC STUDY OF CARBAPENEM-RESISTANT <i>K. PNEUMONIAE</i> CLINICAL ISOLATES. <i>International Journal of Applied Pharmaceutics</i> , 0, , 89-94.	0.3	0



#	ARTICLE	IF	CITATIONS
28357	Interaction between endometrial microbiota and host gene regulation in recurrent implantation failure. <i>Journal of Assisted Reproduction and Genetics</i> , 0, .	1.2	2
28358	Shared mechanisms across the major psychiatric and neurodegenerative diseases. <i>Nature Communications</i> , 2022, 13, .	5.8	48
28359	An Updated Genome Assembly Improves Understanding of the Transcriptional Regulation of Coloration in Midas Cichlid. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
28360	Paladin, overexpressed in colon cancer, is required for actin polymerisation and liver metastasis dissemination. <i>Oncogenesis</i> , 2022, 11, .	2.1	1
28361	Molecular Circuit Discovery for Mechanobiology of Cardiovascular Disease. <i>Regenerative Engineering and Translational Medicine</i> , 0, , .	1.6	0
28362	Secondary Metabolites Produced during <i>Aspergillus fumigatus</i> and <i>Pseudomonas aeruginosa</i> Biofilm Formation. <i>MBio</i> , 2022, 13, .	1.8	6
28363	Urinary microRNAome in healthy cats and cats with pyelonephritis or other urological conditions. <i>PLoS ONE</i> , 2022, 17, e0270067.	1.1	0
28364	Integrated bioinformatic analysis of dysregulated <sc>microRNA</sc> expression network in ovarian endometriosis. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2022, 101, 1074-1084.	1.3	4
28365	Changes in the liver proteome in apoE knockout mice exposed to inhalation of silica nanoparticles indicate mitochondrial damage and impairment of ER stress responses associated with microvesicular steatosis. <i>Environmental Science and Pollution Research</i> , 2023, 30, 699-709.	2.7	3
28366	Genome-wide identification and functional exploration of the legume lectin genes in <i>Brassica napus</i> and their roles in Sclerotinia disease resistance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
28367	Mouse fetal growth restriction through parental and fetal immune gene variation and intercellular communications cascade. <i>Nature Communications</i> , 2022, 13, .	5.8	4
28368	Discovery, structure and mechanism of a tetraether lipid synthase. <i>Nature</i> , 2022, 609, 197-203.	13.7	25
28369	Ferroptosis-related lncRNA signature predicts prognosis and immunotherapy efficacy in cutaneous melanoma. <i>Frontiers in Surgery</i> , 0, 9, .	0.6	4
28371	Candidate genes for tick resistance in cattle: a systematic review combining post-GWAS analyses with sequencing data. <i>Journal of Applied Animal Research</i> , 2022, 50, 460-470.	0.4	2
28372	Identification of photoperiod-induced specific miRNAs in the adrenal glands of Sunite sheep ( <i>Ovis</i> )	0.9	1
28373	Immunomodulatory mechanisms of abatacept: A therapeutic strategy for COVID-19. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	1
28374	Temporal Dynamics of the Intestinal Microbiome Following Short-Term Dietary Restriction. <i>Nutrients</i> , 2022, 14, 2785.	1.7	5
28375	Mechanism of Danhong Injection in the Treatment of Arrhythmia Based on Network Pharmacology, Molecular Docking, and In Vitro Experiments. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	3

#	ARTICLE	IF	CITATIONS
28376	Multi-Omics Study on the Molecular Mechanisms of Tetraodon Nigroviridis Resistance to Exogenous <i>Vibrio Parahaemolyticus</i> Infection. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
28377	Bioinformatics Strategies to Identify Shared Molecular Biomarkers That Link Ischemic Stroke and Moyamoya Disease with Glioblastoma. <i>Pharmaceutics</i> , 2022, 14, 1573.	2.0	1
28378	RNA Sequencing Reveals the Expression Profiles of circRNAs and Indicates Hsa_circ_0070562 as a Pro-osteogenic Factor in Bone Marrow-Derived Mesenchymal Stem Cells of Patients With Ankylosing Spondylitis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28379	Identification of Metabolic Syndrome-Related miRNA-mRNA Regulatory Networks and Key Genes Based on Bioinformatics Analysis. <i>Biochemical Genetics</i> , 2023, 61, 428-447.	0.8	1
28380	Sustainable environmental remediation via biomimetic multifunctional lignocellulosic nano-framework. <i>Nature Communications</i> , 2022, 13, .	5.8	26
28381	Toxoplasma infection in male mice alters dopamine-sensitive behaviors and host gene expression patterns associated with neuropsychiatric disease. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010600.	1.3	0
28382	Carbonic: A Framework for Creating and Visualizing Complex Compound Graphs. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 7541.	1.3	1
28383	Identification of risk genes for Alzheimer's disease by gene embedding. <i>Cell Genomics</i> , 2022, 2, 100162.	3.0	12
28384	Insights into male androgenetic alopecia using comparative transcriptome profiling: hypoxia-inducible factor-1 and Wnt/ $\beta$ -catenin signalling pathways. <i>British Journal of Dermatology</i> , 2022, 187, 936-947.	1.4	11
28385	The Effect of Traditional Korean Medicine Treatment and Herbal Network Analysis in Postoperative Hip Fracture Inpatients. <i>Journal of Korean Medicine Rehabilitation</i> , 2022, 32, 119-129.	0.2	0
28386	Proteomics Evidence of a Systemic Response to Desiccation in the Resurrection Plant <i>Haberlea rhodopensis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8520.	1.8	7
28387	Low abundance members of the gut microbiome exhibit high immunogenicity. <i>Gut Microbes</i> , 2022, 14, .	4.3	8
28388	The Effect of <i>Septoria glycines</i> and Fungicide Application on the Soybean Phyllosphere Mycobiome. <i>Phytobiomes Journal</i> , 2023, 7, 220-232.	1.4	4
28391	Proteomic and phosphoproteomic measurements enhance ability to predict ex vivo drug response in AML. <i>Clinical Proteomics</i> , 2022, 19, .	1.1	9
28392	Hub genes associated with immune cell infiltration in breast cancer, identified through bioinformatic analyses of multiple datasets. <i>Cancer Biology and Medicine</i> , 0, , 1-28.	1.4	3
28393	Dietary fat composition shapes bile acid metabolism and severity of liver injury in a pig model of pediatric NAFLD. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 0, , .	1.8	4
28394	Differential expression of miRNAs in the body wall of the sea cucumber <i>Apostichopus japonicus</i> under heat stress. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
28395	Effect of the FA2H Gene on cashmere fineness of Jiangnan cashmere goats based on transcriptome sequencing. <i>BMC Genomics</i> , 2022, 23, .	1.2	5

#	ARTICLE	IF	CITATIONS
28396	Graph Properties of Mass-Difference Networks for Profiling and Discrimination in Untargeted Metabolomics. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
28397	Integrated Analysis of Microarray, Small RNA, and Degradome Datasets Uncovers the Role of MicroRNAs in Temperature-Sensitive Genic Male Sterility in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8057.	1.8	2
28398	Oncogenic Role of miR-217 During Clear Cell Renal Carcinoma Progression. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	8
28400	Exploration and validation of metastasis-associated genes for skin cutaneous melanoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
28401	Myasthenia gravis-specific aberrant neuromuscular gene expression by medullary thymic epithelial cells in thymoma. <i>Nature Communications</i> , 2022, 13, .	5.8	27
28402	Nitidine Chloride Alleviates Inflammation and Cellular Senescence in Murine Osteoarthritis Through Scavenging ROS. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
28403	Analysis of characteristic genes and ceRNA regulation mechanism of endometriosis based on full transcriptional sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28404	orsum: a Python package for filtering and comparing enrichment analyses using a simple principle. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	8
28405	Potential of ATP5MG to Treat Metabolic Syndrome-Associated Cardiovascular Diseases. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
28406	Cyst stem cell lineage eIF5 non-autonomously prevents testicular germ cell tumor formation via eIF1A/eIF2 <sup>3</sup> -mediated pre-initiation complex. <i>Stem Cell Research and Therapy</i> , 2022, 13, .	2.4	4
28407	Network Tau spreading is vulnerable to the expression gradients of <i>APOE</i> and glutamatergic-related genes. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	19
28409	Integration of probabilistic functional networks without an external Gold Standard. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	0
28410	Comparative transcriptomics of tropical woody plants supports fast and furious strategy along the leaf economics spectrum in lianas. <i>Biology Open</i> , 2022, 11, .	0.6	3
28411	Analysis of <i>Streptomyces</i> Volatilomes Using Global Molecular Networking Reveals the Presence of Metabolites with Diverse Biological Activities. <i>Microbiology Spectrum</i> , 0, , .	1.2	2
28412	Genome-wide identification of long non-coding (lncRNA) in <i>Nilaparvata lugens</i> ™s adaptability to resistant rice. <i>PeerJ</i> , 0, 10, e13587.	0.9	2
28413	Effects of short-term feeding with high fiber diets on growth, utilization of dietary fiber, and microbiota in pigs. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
28414	Comparative analysis of the gut microbiota of sand fly vectors of zoonotic visceral leishmaniasis (ZVL) in Iran; host-environment interplay shapes diversity. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010609.	1.3	6
28416	Graphia: A platform for the graph-based visualisation and analysis of high dimensional data. <i>PLoS Computational Biology</i> , 2022, 18, e1010310.	1.5	30

#	ARTICLE	IF	CITATIONS
28417	Ganga River sediments of India predominate with aerobic and chemo-heterotrophic bacteria majorly engaged in the degradation of xenobiotic compounds. <i>Environmental Science and Pollution Research</i> , 2023, 30, 752-772.	2.7	6
28418	Phosphoproteomics of three exercise modalities identifies canonical signaling and C18ORF25 as an AMPK substrate regulating skeletal muscle function. <i>Cell Metabolism</i> , 2022, 34, 1561-1577.e9.	7.2	26
28419	Identification of proteome markers for drug-induced liver injury in zebrafish embryos. <i>Toxicology</i> , 2022, 477, 153262.	2.0	1
28420	HelR is a helicase-like protein that protects RNA polymerase from rifamycin antibiotics. <i>Molecular Cell</i> , 2022, 82, 3151-3165.e9.	4.5	4
28421	Comprehensive Phylogenomics of <i>Methylobacterium</i> Reveals Four Evolutionary Distinct Groups and Underappreciated Phyllosphere Diversity. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
28423	Characterization of the rare microbiome of rice paddy soil from arsenic contaminated hotspot of West Bengal and their interrelation with arsenic and other geochemical parameters. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	1
28425	Study on the Action Mechanism of the Yifei Jianpi Tongfu Formula in Treatment of Colorectal Cancer Lung Metastasis Based on Network Analysis, Molecular Docking, and Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	2
28427	Production of Fungal Quinones: Problems and Prospects. <i>Biomolecules</i> , 2022, 12, 1041.	1.8	1
28428	Co-Expression Network and Integrative Analysis of Metabolome and Transcriptome Uncovers Biological Pathways for Fertility in Beef Heifers. <i>Metabolites</i> , 2022, 12, 708.	1.3	4
28429	Mechanism of Zhinao Capsule in Treating Alzheimer's Disease Based on Network Pharmacology Analysis and Molecular Docking Validation. <i>Journal of Healthcare Engineering</i> , 2022, 2022, 1-12.	1.1	0
28430	Mistimed sleep and waking activity in humans disrupts glucocorticoid signalling transcripts and SP1, but not plasma cortisol rhythms. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	2
28431	Spatial Gene Expression Changes in the Mouse Heart After Base-Targeted Irradiation. <i>International Journal of Radiation Oncology Biology Physics</i> , 2023, 115, 453-463.	0.4	8
28432	Computational prediction and experimental validation of Salmonella Typhimurium SopE-mediated fine-tuning of autophagy in intestinal epithelial cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
28433	Pathogenesis and Therapeutic Targets of Focal Cortical Dysplasia Based on Bioinformatics Analysis. <i>Neurochemical Research</i> , 2022, 47, 3506-3521.	1.6	3
28434	Revvng an Engine of Human Metabolism: Activity Enhancement of Triosephosphate Isomerase via Hemi-Phosphorylation. <i>ACS Chemical Biology</i> , 2022, 17, 2769-2780.	1.6	5
28435	Functional Diversity and Evolution of the Drosophila Sperm Proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100281.	2.5	6
28436	Network pharmacology and molecular docking analysis reveal insights into the molecular mechanism of shiliao decoction in the treatment of cancer-associated malnutrition. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	3
28437	Identification of programmed cell death-related gene signature and associated regulatory axis in cerebral ischemia/reperfusion injury. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	12

#	ARTICLE	IF	CITATIONS
28438	The Extract of Ilex cornuta Bark Promotes Bone Healing by Activating Adenosine A2A Receptor. <i>Drug Design, Development and Therapy</i> , 0, Volume 16, 2569-2587.	2.0	1
28439	Lysosomal GPCR-like protein LYCHOS signals cholesterol sufficiency to mTORC1. <i>Science</i> , 2022, 377, 1290-1298.	6.0	33
28440	m6A regulator-mediated RNA methylation modification patterns are involved in immune microenvironment regulation of coronary heart disease. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	3
28441	Network analysis of hepatocellular carcinoma liquid biopsies augmented by single-cell sequencing data. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
28442	Methodological Verification-based Screening of the Representative Ingredients for Traditional Chinese Medicine: Taking Astragalus as an Example for Interfering with Cervical Cancer. <i>Current Computer-Aided Drug Design</i> , 2022, 18, 347-362.	0.8	0
28443	Exploring the Target and Mechanism of Radix Paeoniae Alba on Sjogren's Syndrome. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	0
28444	Genome wide identification of lncRNAs and circRNAs having regulatory role in fruit shelf life in health crop cucumber ( <i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
28445	Identification of blood-based inflammatory biomarkers for the early-stage detection of acute myocardial infarction. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2022, 11, .	1.2	7
28446	Cancer-Associated Stromal Fibroblast-Derived Transcriptomes Predict Poor Clinical Outcomes and Immunosuppression in Colon Cancer. <i>Pathology and Oncology Research</i> , 0, 28, .	0.9	9
28447	Integrative Analysis Between Genome-Wide Association Study and Expression Quantitative Trait Loci Reveals Bovine Muscle Gene Expression Regulatory Polymorphisms Associated With Intramuscular Fat and Backfat Thickness. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
28448	Molecular Mechanism of Xingnao Kaiqiao Pill for Perioperative Neurocognitive Disorder and Its Correlation With Immune and Inflammatory Signaling Pathways Based on Network Pharmacology and Molecular Docking. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	0
28452	eQTL analysis of laying hens divergently selected for feather pecking identifies KLF14 as a potential key regulator for this behavioral disorder. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28453	Targeted inhibition of ubiquitin signaling reverses metabolic reprogramming and suppresses glioblastoma growth. <i>Communications Biology</i> , 2022, 5, .	2.0	6
28454	Comprehensive deciphering prophages in genus <i>Acetobacter</i> on the ecology, genomic features, toxin-antitoxin system, and linkage with CRISPR-Cas system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
28455	Genetic networks underlying salinity tolerance in wheat uncovered with genome-wide analyses and selective sweeps. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2925-2941.	1.8	7
28456	Transcriptomic and histochemical analysis reveal the complex regulatory networks in equine Chorioallantois during spontaneous term labor. <i>Biology of Reproduction</i> , 0, , .	1.2	0
28457	Using Machine Learning to Identify Biomarkers Affecting Fat Deposition in Pigs by Integrating Multisource Transcriptome Information. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 10359-10370.	2.4	6
28458	Artificial Intelligence-Assisted Bioinformatics, Microneedle, and Diabetic Wound Healing: A New Deal of an Old Drug. <i>ACS Applied Materials &amp; Interfaces</i> , 2022, 14, 37396-37409.	4.0	16

#	ARTICLE	IF	CITATIONS
28459	Construction of an immune-related gene signature for the prognosis and diagnosis of glioblastoma multiforme. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
28460	microRNA Expression Levels Change in Neonatal Patients During and After Exposure to Cardiopulmonary Bypass. <i>Journal of the American Heart Association</i> , 2022, 11, .	1.6	0
28461	Co-expression network analysis of genes and networks associated with wheat pistillody. <i>PeerJ</i> , 0, 10, e13902.	0.9	1
28462	Characteristics and particularities of bacterial community variation in the offshore shellfish farming waters of the North Yellow Sea. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
28463	Regulators of early maize leaf development inferred from transcriptomes of laser capture microdissection (LCM)-isolated embryonic leaf cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
28464	Upregulation of XIAP promotes lung adenocarcinoma brain metastasis by modulating ceRNA network. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
28465	Global patterns and rates of habitat transitions across the eukaryotic tree of life. <i>Nature Ecology and Evolution</i> , 2022, 6, 1458-1470.	3.4	19
28466	Review and assessment of Boolean approaches for inference of gene regulatory networks. <i>Heliyon</i> , 2022, 8, e10222.	1.4	9
28467	Whole-transcriptome RNA sequencing reveals the global molecular responses and circRNA/lncRNA-miRNA-mRNA ceRNA regulatory network in chicken fat deposition. <i>Poultry Science</i> , 2022, 101, 102121.	1.5	10
28468	Novel Online Three-Dimensional Separation Expands the Detectable Functional Landscape of Cellular Phosphoproteome. <i>Analytical Chemistry</i> , 0, , .	3.2	0
28469	Manpixiao Decoction Halted the Malignant Transformation of Precancerous Lesions of Gastric Cancer: From Network Prediction to In-Vivo Verification. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
28470	Identification of CXCL10 and CXCL11 as the candidate genes involving the development of colitis-associated colorectal cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28471	Gemin5-dependent RNA association with polysomes enables selective translation of ribosomal and histone mRNAs. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	4
28472	Comprehensive Multiomics Analysis Reveals Potential Diagnostic and Prognostic Biomarkers in Adrenal Cortical Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-33.	0.7	0
28473	Soil and Soilless Tomato Cultivation Promote Different Microbial Communities That Provide New Models for Future Crop Interventions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8820.	1.8	10
28475	Bioinformatics and System Biological Approaches for the Identification of Genetic Risk Factors in the Progression of Cardiovascular Disease. <i>Cardiovascular Therapeutics</i> , 2022, 2022, 1-14.	1.1	7
28476	SETD2 regulates gene transcription patterns and is associated with radiosensitivity in lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28477	Transcriptome Analysis of Developing Xylem Provides New Insights into Shade Response in Three Poplar Hybrids. <i>Forests</i> , 2022, 13, 1261.	0.9	1



#	ARTICLE	IF	CITATIONS
28478	Expression dynamics of metabolites in diploid and triploid watermelon in response to flooding. PeerJ, 0, 10, e13814.	0.9	3
28479	Prediction of potential molecular markers of bovine mastitis by meta-analysis of differentially expressed genes using combined p value and robust rank aggregation. Tropical Animal Health and Production, 2022, 54, .	0.5	3
28480	A novel algorithm for lung adenocarcinoma based on <sc>N6</sc> methyladenosine-related immune long noncoding <sc>RNAs</sc> as a reliable biomarker for predicting survival outcomes and selecting sensitive anti-tumor therapies. Journal of Clinical Laboratory Analysis, 0, , .	0.9	3
28481	Subgroup-Enriched Pathways and Kinase Signatures in Medulloblastoma Patient-Derived Xenografts. Journal of Proteome Research, 2022, 21, 2124-2136.	1.8	3
28482	Hallmark-guided subtypes of hepatocellular carcinoma for the identification of immune-related gene classifiers in the prediction of prognosis, treatment efficacy, and drug candidates. Frontiers in Immunology, 0, 13, .	2.2	11
28483	HDACi promotes inflammatory remodeling of the tumor microenvironment to enhance epitope spreading and antitumor immunity. Journal of Clinical Investigation, 2022, 132, .	3.9	3
28484	Pinelliae rhizoma alleviated acute lung injury induced by lipopolysaccharide via suppressing endoplasmic reticulum stress-mediated NLRP3 inflammasome. Frontiers in Pharmacology, 0, 13, .	1.6	6
28485	Response and Regulatory Network Analysis of Roots and Stems to Abiotic Stress in Populus trichocarpa. Forests, 2022, 13, 1300.	0.9	2
28486	Association between BMP15 Gene Polymorphisms of Growth Traits and Litter Size in Qinghai Bamei Pigs. Russian Journal of Genetics, 2022, 58, 997-1006.	0.2	0
28487	Interactome of PTH-Regulated miRNAs and Their Predicted Target Genes for Investigating the Epigenetic Effects of PTH (1-34) in Bone Metabolism. Genes, 2022, 13, 1443.	1.0	2
28488	Characterization of the SGLT2 Interaction Network and Its Regulation by SGLT2 Inhibitors: A Bioinformatic Analysis. Frontiers in Pharmacology, 0, 13, .	1.6	12
28489	Local burn wound environment versus systemic response: Comparison of proteins and metabolites. Wound Repair and Regeneration, 2022, 30, 560-572.	1.5	3
28491	Development of actionable targets of multi-kinase inhibitors (AToMI) screening platform to dissect kinase targets of staurosporines in glioblastoma cells. Scientific Reports, 2022, 12, .	1.6	1
28492	Preclinical insights into fucoidan as a nutraceutical compound against perfluorooctanoic acid-associated obesity via targeting endoplasmic reticulum stress. Frontiers in Nutrition, 0, 9, .	1.6	4
28493	Genome-wide analysis of HSP20 gene family and expression patterns under heat stress in cucumber (Cucumis sativus L.). Frontiers in Plant Science, 0, 13, .	1.7	7
28494	Integrated analysis to reveal potential therapeutic targets and prognostic biomarkers of skin cutaneous melanoma. Frontiers in Immunology, 0, 13, .	2.2	3
28496	Identification of Four Biomarkers of Human Skin Aging by Comprehensive Single Cell Transcriptome, Transcriptome, and Proteomics. Frontiers in Genetics, 0, 13, .	1.1	4
28498	The regulatory landscape of neurite development in Caenorhabditis elegans. Frontiers in Molecular Neuroscience, 0, 15, .	1.4	3

#	ARTICLE	IF	CITATIONS
28499	Altered expression of ACOX2 in non-small cell lung cancer. BMC Pulmonary Medicine, 2022, 22, .	0.8	5
28500	Identification of Candidate Therapeutic Target Genes and Profiling of Tumor-Infiltrating Immune Cells in Pancreatic Cancer via Integrated Transcriptomic Analysis. Disease Markers, 2022, 2022, 1-14.	0.6	1
28501	Homeodomain-interacting protein kinase HIPK4 regulates phosphorylation of manchette protein RIMBP3 during spermiogenesis. Journal of Biological Chemistry, 2022, 298, 102327.	1.6	7
28502	Convergent evolution of AP2/ERF III and IX subfamilies through recurrent polyploidization and tandem duplication during eudicot adaptation to paleoenvironmental changes. Plant Communications, 2022, 3, 100420.	3.6	14
28503	Interactome overlap between risk genes of epilepsy and targets of anti-epileptic drugs. PLoS ONE, 2022, 17, e0272428.	1.1	0
28504	Analysis of the Mechanism of GuizhiFuling Wan in Treating Adenomyosis Based on Network Pharmacology Combined with Molecular Docking and Experimental Verification. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	0
28505	The expression of Hexokinase 2 and its hub genes are correlated with the prognosis in glioma. BMC Cancer, 2022, 22, .	1.1	8
28506	De novo variants in genes regulating stress granule assembly associate with neurodevelopmental disorders. Science Advances, 2022, 8, .	4.7	16
28507	Identification and Validation of Three Hub Genes Involved in Cell Proliferation and Prognosis of Castration-Resistant Prostate Cancer. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-27.	1.9	2
28508	Vascular Proteome Responses Precede Organ Dysfunction in a Murine Model of Staphylococcus aureus Bacteremia. MSystems, 2022, 7, .	1.7	3
28509	Therapeutic effects of shaogan fuzi decoction in rheumatoid arthritis: Network pharmacology and experimental validation. Frontiers in Pharmacology, 0, 13, .	1.6	7
28510	Physiology and Proteomic Basis of Lung Adaptation to High-Altitude Hypoxia in Tibetan Sheep. Animals, 2022, 12, 2134.	1.0	4
28511	Systematic review of gastric cancer-associated genetic variants, gene-based meta-analysis, and gene-level functional analysis to identify candidate genes for drug development. Frontiers in Genetics, 0, 13, .	1.1	4
28512	The calcium sensor CBL7 is required for <i>Serendipita indica</i> -induced growth stimulation in <i>Arabidopsis thaliana</i> , controlling defense against the endophyte and K <sup>+</sup> homeostasis in the symbiosis. Plant, Cell and Environment, 2022, 45, 3367-3382.	2.8	5
28513	ER $\alpha$ -LBD, an isoform of estrogen receptor alpha, promotes breast cancer proliferation and endocrine resistance. Npj Breast Cancer, 2022, 8, .	2.3	5
28514	Combined QTL Mapping across Multiple Environments and Co-Expression Network Analysis Identified Key Genes for Embryogenic Callus Induction from Immature Maize Embryos. International Journal of Molecular Sciences, 2022, 23, 8786.	1.8	2
28516	Genome-wide characterization of the Rho family in cotton provides insights into fiber development. Journal of Cotton Research, 2022, 5, .	1.0	1
28518	High-affinity SOAT1 ligands remodeled cholesterol metabolism program to inhibit tumor growth. BMC Medicine, 2022, 20, .	2.3	8

#	ARTICLE	IF	CITATIONS
28519	Construction of a solid Cox model for AML patients based on multiomics bioinformatic analysis. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
28520	Identifying the tumor location-associated candidate genes in development of new drugs for colorectal cancer using machine-learning-based approach. <i>Medical and Biological Engineering and Computing</i> , 0, , .	1.6	0
28522	K-Clique Multiomics Framework: A Novel Protocol to Decipher the Role of Gut Microbiota Communities in Nutritional Intervention Trials. <i>Metabolites</i> , 2022, 12, 736.	1.3	4
28523	Circulating microRNA signatures associated with disease severity and outcome in COVID-19 patients. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	23
28524	Novel Driver Strength Index highlights important cancer genes in TCGA PanCanAtlas patients. <i>PeerJ</i> , 0, 10, e13860.	0.9	1
28525	Proteogenomics reveals sex-biased aging genes and coordinated splicing in cardiac aging. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2022, 323, H538-H558.	1.5	11
28526	Screening of crosstalk and pyroptosis-related genes linking periodontitis and osteoporosis based on bioinformatics and machine learning. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
28527	Evaluation of the early defoliation trait and identification of resistance genes through a comprehensive transcriptome analysis in pears. <i>Journal of Integrative Agriculture</i> , 2023, 22, 120-138.	1.7	1
28528	Proteomics analysis of chronic skin injuries caused by mustard gas. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	1
28529	TcMYC2 regulates Pyrethrin biosynthesis in <i>Tanacetum cinerariifolium</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	9
28530	RNA-Seq analysis reveals the important co-expressed genes associated with polyphyllin biosynthesis during the developmental stages of <i>Paris polyphylla</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	4
28531	ReDisX, a machine learning approach, rationalizes rheumatoid arthritis and coronary artery disease patients uniquely upon identifying subpopulation differentiation markers from their genomic data. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	0
28532	Metadata analysis to explore hub of the hub-genes highlighting their functions, pathways and regulators for cervical cancer diagnosis and therapies. <i>Discover Oncology</i> , 2022, 13, .	0.8	4
28533	Oral squamous cell carcinoma gene patterns connected with <i>RNA</i> methylation for prognostic prediction. <i>Oral Diseases</i> , 0, , .	1.5	8
28534	Shared and contrasting associations in the dynamic nano- and picoplankton communities of two close but contrasting sites from the Bay of Biscay. <i>Environmental Microbiology</i> , 2022, 24, 6052-6070.	1.8	1
28535	Qingfei Jiedu decoction inhibits PD-L1 expression in lung adenocarcinoma based on network pharmacology analysis, molecular docking and experimental verification. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	9
28536	Adverse outcome pathways and linkages to transcriptomic effects relevant to ionizing radiation injury. <i>International Journal of Radiation Biology</i> , 0, , 1-13.	1.0	3
28537	Conformation-Dependent Influences of Hydrophobic Amino Acids in Two In-Register Parallel $\beta$ -Sheet Amyloids, an $\alpha$ -Synuclein Amyloid and a Local Structural Model of PrP <sup>Sc</sup> . <i>ACS Omega</i> , 2022, 7, 31271-31288.	1.6	1

#	ARTICLE	IF	CITATIONS
28538	Characteristics of members of IGT family genes in controlling rice root system architecture and tiller development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
28539	Integrative Analysis of Metabolome and Transcriptome Reveals the Role of Strigolactones in Wounding-Induced Rice Metabolic Re-Programming. <i>Metabolites</i> , 2022, 12, 789.	1.3	10
28540	Diversity and dynamics of the CRISPR-Cas systems associated with <i>Bacteroides fragilis</i> in human population. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
28541	Solonamides, a Group of Cyclodepsipeptides, Influence Motility in the Native Producer <i>Photobacterium galathea</i> S2753. <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	0
28542	Failure of diet-induced transcriptional adaptations in alpha-synuclein transgenic mice. <i>Human Molecular Genetics</i> , 0, , .	1.4	0
28543	Network pharmacology and molecular docking approaches to elucidate the potential compounds and targets of Saeng-Ji-Hwang-Ko for treatment of type 2 diabetes mellitus. <i>Computers in Biology and Medicine</i> , 2022, , 106041.	3.9	4
28545	M6A-related lncRNAs predict clinical outcome and regulate the tumor immune microenvironment in hepatocellular carcinoma. <i>BMC Cancer</i> , 2022, 22, .	1.1	6
28546	Identification of Potential Prognostic Biomarkers Associated with Monocyte Infiltration in Lung Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2022, 2022, 1-19.	0.9	1
28547	Whole Transcriptome-Based Study to Speculate upon the Silkworm Yellow Blood Inhibitor (I) Gene and Analyze the miRNA-Mediated Gene Regulatory Network. <i>Processes</i> , 2022, 10, 1556.	1.3	0
28548	Integrative small and long RNA omics analysis of human healing and nonhealing wounds discovers cooperating microRNAs as therapeutic targets. <i>ELife</i> , 0, 11, .	2.8	12
28549	Genome-Wide Characterization of Ascorbate Peroxidase Gene Family in Peanut ( <i>Arachis hypogea</i> L.) Revealed Their Crucial Role in Growth and Multiple Stress Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	17
28550	<i>FAT2</i> mutation is associated with better prognosis and responsiveness to immunotherapy in uterine corpus endometrial carcinoma. <i>Cancer Medicine</i> , 0, , .	1.3	0
28551	Proinflammatory changes in the maternal circulation, maternal-fetal interface, and placental transcriptome in preterm birth. <i>American Journal of Obstetrics and Gynecology</i> , 2023, 228, 332.e1-332.e17.	0.7	10
28552	CDNF Interacts with ER Chaperones and Requires UPR Sensors to Promote Neuronal Survival. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9489.	1.8	14
28553	Diurnal Alterations in Gene Expression Across Striatal Subregions in Psychosis. <i>Biological Psychiatry</i> , 2023, 93, 137-148.	0.7	5
28554	Identification of G6PC as a potential prognostic biomarker in hepatocellular carcinoma based on bioinformatics analysis. <i>Medicine (United States)</i> , 2022, 101, e29548.	0.4	3
28555	Glioblastoma hijacks neuronal mechanisms for brain invasion. <i>Cell</i> , 2022, 185, 2899-2917.e31.	13.5	168
28556	Multi-omics analysis reveals RNA splicing alterations and their biological and clinical implications in lung adenocarcinoma. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	7.1	7

#	ARTICLE	IF	CITATIONS
28557	Exploration of molecular features of PCOS with different androgen levels and immune-related prognostic biomarkers associated with implantation failure. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
28558	Integrating knowledge of protein sequence with protein function for the prediction and validation of new MALT1 substrates. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4717-4732.	1.9	8
28559	Identification of potential targets of the curcumin analog CCA-1.1 for glioblastoma treatment : integrated computational analysis and in vitro study. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
28560	Characterizations of MYB Transcription Factors in <i>Camellia oleifera</i> Reveal the Key Regulators Involved in Oil Biosynthesis. <i>Horticulturae</i> , 2022, 8, 742.	1.2	3
28561	Combining Deep Phenotyping of Serum Proteomics and Clinical Data via Machine Learning for COVID-19 Biomarker Discovery. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9161.	1.8	7
28562	Transcriptome and Metabolome Analyses Revealed the Response Mechanism of Sugar Beet to Salt Stress of Different Durations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9599.	1.8	8
28563	Tandem mass tag-based quantitative proteomic analysis of cervical cancer. <i>Proteomics - Clinical Applications</i> , 2023, 17, .	0.8	3
28564	Neuroprotection of Bone Marrow-Derived Mesenchymal Stem Cell-Derived Extracellular Vesicle-Enclosed miR-410 Correlates with HDAC4 Knockdown in Hypoxic-Ischemic Brain Damage. <i>Neurochemical Research</i> , 2022, 47, 3150-3166.	1.6	3
28565	The quality of organic amendments affects soil microbiome and nitrogen-cycling bacteria in an organic farming system. <i>Frontiers in Soil Science</i> , 0, 2, .	0.8	4
28566	The dynamic proteome in <i>Arabidopsis thaliana</i> early embryogenesis. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
28567	NCOA4-Mediated Ferritinophagy Is a Pancreatic Cancer Dependency via Maintenance of Iron Bioavailability for Iron-Sulfur Cluster Proteins. <i>Cancer Discovery</i> , 2022, 12, 2180-2197.	7.7	40
28569	Association Between Circulating CD4+ T Cell Methylation Signatures of Network-Oriented SOCS3 Gene and Hemodynamics in Patients Suffering Pulmonary Arterial Hypertension. <i>Journal of Cardiovascular Translational Research</i> , 2023, 16, 17-30.	1.1	24
28570	Dysbiosis and predicted function of dental and ruminal microbiome associated with bovine periodontitis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
28571	Mapping the cell-membrane proteome of the SKBR3/HER2+ cell line to the cancer hallmarks. <i>PLoS ONE</i> , 2022, 17, e0272384.	1.1	0
28572	Exploring direct and indirect targets of current antileishmanial drugs using a novel thermal proteomics profiling approach. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
28573	Integrative, In Silico and Comparative Analysis of Breast Cancer Secretome Highlights Invasive-Ductal-Carcinoma-Grade Progression Biomarkers. <i>Cancers</i> , 2022, 14, 3854.	1.7	0
28574	Global signalling network analysis of luminal T47D breast cancer cells in response to progesterone. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
28576	Identification of key genes and pathways in chronic rhinosinusitis with nasal polyps and asthma comorbidity using bioinformatics approaches. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5

#	ARTICLE	IF	CITATIONS
28577	A complete twelve-gene deletion null mutant reveals that cyclic di-GMP is a global regulator of phase-transition and host colonization in <i>Erwinia amylovora</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010737.	2.1	6
28579	Transcriptome analysis of peripheral blood mononuclear cells in patients with type 1 diabetes mellitus. <i>Endocrine</i> , 2022, 78, 270-279.	1.1	1
28580	The fate of antibiotic resistance genes in the coastal lagoon with multiple functional zones. <i>Journal of Environmental Sciences</i> , 2023, 128, 93-106.	3.2	5
28581	Single-cell RNA profiling of <i>Plasmodium vivax</i> -infected hepatocytes reveals parasite- and host- specific transcriptomic signatures and therapeutic targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	14
28582	Integrative analysis of circulating microRNAs and the placental transcriptome in recurrent pregnancy loss. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
28583	Long noncoding RNA <i>CHROMR</i> regulates antiviral immunity in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
28584	Mitochondrial dynamics maintain muscle stem cell regenerative competence throughout adult life by regulating metabolism and mitophagy. <i>Cell Stem Cell</i> , 2022, 29, 1298-1314.e10.	5.2	48
28585	Bacterial species metabolic interaction network for deciphering the lignocellulolytic system in fungal cultivating termite gut microbiota. <i>BioSystems</i> , 2022, 221, 104763.	0.9	2
28586	SCNIC: Sparse correlation network investigation for compositional data. <i>Molecular Ecology Resources</i> , 2023, 23, 312-325.	2.2	13
28587	Screening for severe drug-drug interactions in patients with multiple sclerosis: A comparison of three drug interaction databases. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
28589	Identification of miRNA-mRNA Pairs in Relation to TNF- $\alpha$ /IL-1 $\beta$ Induced Inflammatory Response in Intervertebral Disc Degeneration. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-10.	0.5	1
28590	Integration of transcriptomics, proteomics, and metabolomics data to reveal HER2-associated metabolic heterogeneity in gastric cancer with response to immunotherapy and neoadjuvant chemotherapy. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	46
28592	Identification of molecular signatures associated with sleep disorder and Alzheimer's disease. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	8
28593	Candidate genes for infertility: an in-silico study based on cytogenetic analysis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	3
28594	Network pharmacology reveals multitarget mechanism of action of drugs to be repurposed for COVID-19. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	8
28595	DNA- and RNA-Binding Proteins Linked Transcriptional Control and Alternative Splicing Together in a Two-Layer Regulatory Network System of Chronic Myeloid Leukemia. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
28596	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. <i>Microbiome</i> , 2022, 10, .	4.9	12
28597	Identification of key genes and immune cell infiltration in recurrent implantation failure: A study based on integrated analysis of multiple microarray studies. <i>American Journal of Reproductive Immunology</i> , 0, , .	1.2	8



#	ARTICLE	IF	CITATIONS
28598	Evaluating the therapeutic role of selected active compounds in Plumula Nelumbinis on pulmonary hypertension via network pharmacology and experimental analysis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	6
28599	Lipid/water interface of galactolipid bilayers in different lyotropic liquid-crystalline phases. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
28600	Anti-protozoal activity and metabolomic analyses of <i>Cichorium intybus</i> L. against <i>Trypanosoma cruzi</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2022, 20, 43-53.	1.4	0
28602	Assembly and dynamics of the apple carposphere microbiome during fruit development and storage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
28603	Novel Diagnostic Biomarkers for High-Grade Serous Ovarian Cancer Uncovered by Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2022, 21, 2146-2159.	1.8	6
28604	Identification of Chemokines-related miRNAs as Potential Biomarkers in Psoriasis based on Integrated Bioinformatics Analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	0
28605	Humanized substitutions of <i>Vmat1</i> in mice alter amygdala-dependent behaviors associated with the evolution of anxiety. <i>IScience</i> , 2022, 25, 104800.	1.9	1
28606	Metabolomic and transcriptomic signatures of influenza vaccine response in healthy young and older adults. <i>Aging Cell</i> , 2022, 21, .	3.0	9
28607	Nanoscale Mapping of EGFR and c-MET Protein Environments on Lung Cancer Cell Surfaces via Therapeutic Antibody Photocatalyst Conjugates. <i>ACS Chemical Biology</i> , 2022, 17, 2304-2314.	1.6	3
28609	Enhanced proteostasis, lipid remodeling, and nitrogen remobilization define barley flag leaf senescence. <i>Journal of Experimental Botany</i> , 2022, 73, 6816-6837.	2.4	6
28610	Unraveling the multi-targeted curative potential of bioactive molecules against cervical cancer through integrated omics and systems pharmacology approach. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
28611	Network Pharmacology and Molecular Docking Validation to Reveal the Pharmacological Mechanisms of Kangai Injection against Colorectal Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	2
28612	Honghua extract mediated potent inhibition of COVID-19 host cell pathways. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
28613	Collaboration between Antagonistic Cell Type Regulators Governs Natural Variation in the <i>Candida albicans</i> Biofilm and Hyphal Gene Expression Network. <i>MBio</i> , 2022, 13, .	1.8	14
28615	Exploring the Underlying Mechanism of Ren-Shen-Bai-Du Powder for Treating Inflammatory Bowel Disease Based on Network Pharmacology and Molecular Docking. <i>Pharmaceuticals</i> , 2022, 15, 1038.	1.7	2
28616	hCoCena: horizontal integration and analysis of transcriptomics datasets. <i>Bioinformatics</i> , 2022, 38, 4727-4734.	1.8	4
28617	Bizarre parosteal osteochondromatous proliferation in pediatric: A case report and literature review. <i>Pediatric Hematology Oncology Journal</i> , 2022, , .	0.1	0
28619	Automatic Diverse Subset Selection From Enzyme Families by Solving the Maximum Diversity Problem. , 2022, , .		0

#	ARTICLE	IF	CITATIONS
28620	Possible Contribution of Alternative Transcript Isoforms in Mature Biofilm Growth Phase of <i>Candida glabrata</i> . <i>Indian Journal of Microbiology</i> , 2022, 62, 583-601.	1.5	1
28621	Retinal degeneration induced in a mouse model of ischemiaâ€“reperfusion injury and its management by pemaflibrate treatment. <i>FASEB Journal</i> , 2022, 36, .	0.2	10
28622	Dichotomous <i>cis</i>-regulatory motifs mediate the maturation of the neuromuscular junction by retrograde BMP signaling. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
28623	Role of Long Non-Coding RNA in Regulating ER Stress Response to the Progression of Diabetic Complications. <i>Current Gene Therapy</i> , 2023, 23, 96-110.	0.9	3
28624	Chemical and genomic analyses of a marine-derived <i>Streptomyces</i> sp. V17-9 producing amino acid derivatives and siderophores. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
28625	Upregulation of key genes <i>Eln</i> and <i>Tgfb3</i> were associated with the severity of cardiac hypertrophy. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
28626	PrMYB5 activates anthocyanin biosynthetic PrDFR to promote the distinct pigmentation pattern in the petal of <i>Paeonia rockii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
28627	By characterizing metabolic and immune microenvironment reveal potential prognostic markers in the development of colorectal cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	4
28628	Identifying Drug-Induced Liver Injury Associated With Inflammation-Drug and Drug-Drug Interactions in Pharmacologic Treatments for COVID-19 by Bioinformatics and System Biology Analyses: The Role of Pregnane X Receptor. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
28629	Doxorubicin-Induced Cardiotoxicity May Be Alleviated by Bone Marrow Mesenchymal Stem Cell-Derived Exosomal lncRNA via Inhibiting Inflammation. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4467-4486.	1.6	4
28630	The Role of CD28 and CD8+ T Cells in Keloid Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8862.	1.8	6
28631	Pyroptosis in sepsis: Comprehensive analysis of research hotspots and core genes in 2022. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	6
28632	Antiphospholipid antibodies in patients with calcific aortic valve stenosis. <i>Rheumatology</i> , 2023, 62, 1187-1196.	0.9	3
28634	Bioinformatic analysis of circular RNA expression profiles in a rat lumbosacral spinal root avulsion model. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
28635	Gene expression analysis reveals a 5-gene signature for progression-free survival in prostate cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
28636	Functional networks of the human bromodomain-containing proteins. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
28637	Association of N-Acetyl Asparagine with QTc in Diabetes: A Metabolomics Study. <i>Biomedicines</i> , 2022, 10, 1955.	1.4	0
28639	HTT-OMNI: A Web-based Platform for Huntingtin Interaction Exploration and Multi-omics Data Integration. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100275.	2.5	3

#	ARTICLE	IF	CITATIONS
28640	A Novel hepatocellular carcinoma specific hypoxic related signature for predicting prognosis and therapeutic responses. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
28641	Pulmonate slug evolution is reflected in the de novo genome of <i>Arion vulgaris</i> Moquin-Tandon, 1855. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
28642	The comprehensive expression and functional analysis of m6A modification "readers" in hepatocellular carcinoma. <i>Aging</i> , 2022, 14, 6269-6298.	1.4	5
28643	A new gene set identifies senescent cells and predicts senescence-associated pathways across tissues. <i>Nature Communications</i> , 2022, 13, .	5.8	167
28644	Bioactive Natural Products Identification Using Automation of Molecular Networking Software. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 6378-6385.	2.5	5
28645	Classifying Integrated Signature Molecules in Macrophages of Rheumatoid Arthritis, Osteoarthritis, and Periodontal Disease: An Omics-Based Study. <i>Current Issues in Molecular Biology</i> , 2022, 44, 3496-3517.	1.0	2
28646	Regulation of Protein Transport Pathways by the Cytosolic Hsp90s. <i>Biomolecules</i> , 2022, 12, 1077.	1.8	6
28647	An integrative approach to uncover the components, mechanisms, and functions of traditional Chinese medicine prescriptions on male infertility. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
28648	Transcriptomic Immune Profiles Can Represent the Tumor Immune Microenvironment Related to the Tumor Budding Histology in Uterine Cervical Cancer. <i>Genes</i> , 2022, 13, 1405.	1.0	4
28649	A comprehensive comparison of fecal microbiota in three ecological bird groups of raptors, waders, and waterfowl. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
28650	Game-theoretic link relevance indexing on genome-wide expression dataset identifies putative salient genes with potential etiological and diapeutics role in colorectal cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
28654	The impact of PrsA over-expression on the <i>Bacillus subtilis</i> transcriptome during fed-batch fermentation of alpha-amylase production. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
28657	Exploring the mechanism of action of Xuanfei Baidu granule (XFBD) in the treatment of COVID-19 based on molecular docking and molecular dynamics. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
28658	Comparative Transcriptome Analysis Reveals Genes Associated with the Gossypol Synthesis and Gland Morphogenesis in <i>Gossypium hirsutum</i> . <i>Genes</i> , 2022, 13, 1452.	1.0	0
28659	Identification of <i>PIK3CG</i> as a hub in septic myocardial injury using network pharmacology and weighted gene co-expression network analysis. <i>Bioengineering and Translational Medicine</i> , 2023, 8, .	3.9	5
28660	Network Pharmacology and Molecular Docking-Based Mechanism Study to Reveal Antihypertensive Effect of Gedan Jiangya Decoction. <i>BioMed Research International</i> , 2022, 2022, 1-17.	0.9	4
28661	<i>UaEIE</i> [juE-siE]: Color encoding of high-dimensional data. <i>Protein Science</i> , 2022, 31, .	3.1	2
28663	Transcriptome profiling of somatic embryogenesis in wheat ( <i>Triticum aestivum</i> L.) influenced by auxin, calcium and brassinosteroid. <i>Plant Growth Regulation</i> , 2022, 98, 599-612.	1.8	3

#	ARTICLE	IF	CITATIONS
28665	In silico analysis and preclinical findings uncover potential targets of anti-cervical carcinoma and COVID-19 in laminarin, a promising nutraceutical. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
28666	A Ferroptosis-Related LncRNA Signature Associated with Prognosis, Tumor Immune Environment, and Genome Instability in Hepatocellular Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-19.	0.7	4
28667	The cyanobactericidal bacterium <i>Paucibacter aquatile</i> DH15 caused the decline of <i>Microcystis</i> and aquatic microbial community succession: A mesocosm study. <i>Environmental Pollution</i> , 2022, 311, 119849.	3.7	8
28668	Genome-wide identification and expression analysis of the Hsp20, Hsp70 and Hsp90 gene family in <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
28669	Coexpression Network Analysis Based Characterisation of the R2R3-MYB Family Genes in Tolerant Poplar Infected with <i>Melampsora larici-populina</i> . <i>Forests</i> , 2022, 13, 1255.	0.9	1
28670	Comprehensive metabolomics study on the pathogenesis of anaplastic astrocytoma via UPLC-Q/TOF-MS. <i>Medicine (United States)</i> , 2022, 101, e29594.	0.4	1
28671	Investigation of proteinsâ€™ interaction network and the expression pattern of genes involved in the ABA biogenesis and antioxidant system under methanol spray in drought-stressed rapeseed. <i>3 Biotech</i> , 2022, 12, .	1.1	5
28672	Transcriptome Analysis Reveals Gene Expression Changes during Repair from Mechanical Wounding in <i>Aquilaria sinensis</i> . <i>Forests</i> , 2022, 13, 1258.	0.9	1
28673	Prognostic value of SOX9 in cervical cancer: Bioinformatics and experimental approaches. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
28674	Integrated Analysis of Crucial Genes and miRNAs Associated with Osteoporotic Fracture of Type 2 Diabetes. <i>BioMed Research International</i> , 2022, 2022, 1-18.	0.9	7
28675	Expression profiles analysis identifies specific interferon-stimulated signatures as potential diagnostic and predictive indicators of JAK2V617F+ myelofibrosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
28676	Thrombosis-related circulating miR-16-5p is associated with disease severity in patients hospitalised for COVID-19. <i>RNA Biology</i> , 2022, 19, 963-979.	1.5	11
28677	Identification and validation of ferroptosis key genes in bone mesenchymal stromal cells of primary osteoporosis based on bioinformatics analysis. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
28678	Metataxonomic Mapping of the Microbial Diversity of Irish and Eastern Mediterranean Cheeses. <i>Foods</i> , 2022, 11, 2483.	1.9	11
28679	Disease similarity network analysis of Autism Spectrum Disorder and comorbid brain disorders. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	5
28680	Temporal and Sex-Linked Protein Expression Dynamics in a Familial Model of Alzheimerâ€™s Disease. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100280.	2.5	8
28682	The Risk Correlation between N7-Methylguanosine Modification-Related lncRNAs and Survival Prognosis of Oral Squamous Cell Carcinoma Based on Comprehensive Bioinformatics Analysis. <i>Applied Bionics and Biomechanics</i> , 2022, 2022, 1-11.	0.5	3
28683	mRNAsi-related metabolic risk score model identifies poor prognosis, immunoevasive contexture, and low chemotherapy response in colorectal cancer patients through machine learning. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4

#	ARTICLE	IF	CITATIONS
28684	Convergent cerebrospinal fluid proteomes and metabolic ontologies in humans and animal models of Rett syndrome. <i>IScience</i> , 2022, 25, 104966.	1.9	4
28686	Comparative transcriptome and metabolome analysis reveal key regulatory defense networks and genes involved in enhanced salt tolerance of <i>Actinidia</i> (kiwifruit). <i>Horticulture Research</i> , 2022, 9, .	2.9	14
28687	WNT Activation and TGF $\beta$ 2-Smad Inhibition Potentiate Stemness of Mammalian Auditory Neuroprogenitors for High-Throughput Generation of Functional Auditory Neurons In Vitro. <i>Cells</i> , 2022, 11, 2431.	1.8	0
28688	A microRNA microRNA crosstalk network inferred from genome-wide single nucleotide polymorphism variants in natural populations of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
28689	Rational Design of the Soluble Variant of <i>l</i> -Pipicolic Acid Hydroxylase using the $\pm$ -Helix Rule and the Hydrophathy Contradiction Rule. <i>ACS Omega</i> , 2022, 7, 29508-29516.	1.6	0
28690	Epigenetic and integrative cross-omics analyses of cerebral white matter hyperintensities on MRI. <i>Brain</i> , 2023, 146, 492-506.	3.7	12
28691	Exploring Lead loci shared between schizophrenia and Cardiometabolic traits. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
28693	Altered macronutrient composition and genetics influence the complex transcriptional network associated with adiposity in the Collaborative Cross. <i>Genes and Nutrition</i> , 2022, 17, .	1.2	2
28694	<i>Entamoeba histolytica</i> HM-1: IMSS gene expression profiling identifies key hub genes, potential biomarkers, and pathways in Amoebiasis infection: a systematic network meta-analysis. <i>Bioscience Reports</i> , 2022, 42, .	1.1	7
28695	Identification and Validation in a Novel Classification of Helicase Patterns for the Prediction of Tumor Proliferation and Prognosis. <i>Journal of Hepatocellular Carcinoma</i> , 0, Volume 9, 885-900.	1.8	1
28696	Identification of crucial hub genes and potential molecular mechanisms in breast cancer by integrated bioinformatics analysis and experimental validation. <i>Computers in Biology and Medicine</i> , 2022, 149, 106036.	3.9	5
28698	Identification of key genes of the ccRCC subtype with poor prognosis. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
28700	Regulation of DNA methylation during the testicular development of Shaziling pigs. <i>Genomics</i> , 2022, 114, 110450.	1.3	4
28701	Comprehensive analysis of differentially expressed profiles of mRNA, lncRNA, and miRNA of Yili geese ovary at different egg-laying stages. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
28703	Similar protein segments shared between domains of different evolutionary lineages. <i>Protein Science</i> , 2022, 31, .	3.1	8
28704	Using Advanced Bioinformatics Tools to Identify Novel Therapeutic Candidates for Age-Related Macular Degeneration. <i>Translational Vision Science and Technology</i> , 2022, 11, 10.	1.1	9
28705	Identifying potential pharmacological targets and mechanisms of vitamin D for hepatocellular carcinoma and COVID-19. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
28706	Ecosystem size-induced environmental fluctuations affect the temporal dynamics of community assembly mechanisms. <i>ISME Journal</i> , 2022, 16, 2635-2643.	4.4	8

#	ARTICLE	IF	CITATIONS
28707	Immuno-genomic profiling of biopsy specimens predicts neoadjuvant chemotherapy response in esophageal squamous cell carcinoma. <i>Cell Reports Medicine</i> , 2022, 3, 100705.	3.3	5
28708	Targets for Renal Carcinoma Growth Control Identified by Screening FOXD1 Cell Proliferation Pathways. <i>Cancers</i> , 2022, 14, 3958.	1.7	4
28709	Hepatoprotective Effect Associated with Alkaloids from <i>Corydalis tomentella</i> Franch. based on Network Pharmacology, Molecular Docking and <i>In Vitro</i> Experiment. <i>Chemistry and Biodiversity</i> , 2022, 19, .	1.0	2
28711	Copper starvation induces antimicrobial isocyanide integrated into two distinct biosynthetic pathways in fungi. <i>Nature Communications</i> , 2022, 13, .	5.8	9
28712	Comprehensive proteomic analysis reveals dynamic phospho-profiling in human early erythropoiesis. <i>British Journal of Haematology</i> , 0, , .	1.2	1
28713	Expressing OsiSAP8, a Zinc-Finger Associated Protein Gene, Mitigates Stress Dynamics in Existing Elite Rice Varieties of the "Green Revolution"™. <i>Sustainability</i> , 2022, 14, 10174.	1.6	1
28714	Pancancer Analysis of the Oncogenic and Prognostic Role of NOL7: A Potential Target for Carcinogenesis and Survival. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9611.	1.8	0
28715	Abiotic stress rather than biotic interactions drives contrasting trends in chemical richness and variation in alpine willows. <i>Functional Ecology</i> , 2022, 36, 2701-2712.	1.7	6
28716	<i>Mycobacterium abscessus</i> pathogenesis identified by phenogenomic analyses. <i>Nature Microbiology</i> , 2022, 7, 1431-1441.	5.9	14
28717	Identification of Pseudo-R genes in <i>Vitis vinifera</i> and characterization of their role as immunomodulators in host-pathogen interactions. <i>Journal of Advanced Research</i> , 2022, 42, 17-28.	4.4	1
28718	<i>N</i> -glycosylation induced changes in tau protein dynamics reveal its role in tau misfolding and aggregation: A microsecond long molecular dynamics study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 147-160.	1.5	5
28719	Risperidone-induced changes in DNA methylation in peripheral blood from first-episode schizophrenia patients parallel changes in neuroimaging and cognitive phenotypes. <i>Psychiatry Research</i> , 2022, 317, 114789.	1.7	4
28720	Concentration-response gene expression analysis in zebrafish reveals phenotypically-anchored transcriptional responses to retene. <i>Frontiers in Toxicology</i> , 0, 4, .	1.6	3
28721	Distinct microglia alternative splicing in Alzheimer's disease. <i>Aging</i> , 2022, 14, 6554-6566.	1.4	3
28722	Weighted gene co-expression identification of CDKN1A as a hub inflammation gene following cardiopulmonary bypass in children with congenital heart disease. <i>Frontiers in Surgery</i> , 0, 9, .	0.6	3
28723	Interactive bioinformatics analysis for the screening of hub genes and molecular docking of phytochemicals present in kitchen spices to inhibit CDK1 in cervical cancer. <i>Computers in Biology and Medicine</i> , 2022, 149, 105994.	3.9	5
28724	Integrated Analysis of the microRNA-mRNA Network Predicts Potential Regulators of Atrial Fibrillation in Humans. <i>Cells</i> , 2022, 11, 2629.	1.8	3
28725	Analysis of gene expression changes in wheat in response to <i>Rhizoctonia cerealis</i> infection using RNA-Seq. , 0, , .		0



#	ARTICLE	IF	CITATIONS
28727	Meta-analysis of fungal plant pathogen <i>Fusarium oxysporum</i> infection-related gene profiles using transcriptome datasets. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
28728	scRNA-seq of gastric tumor shows complex intercellular interaction with an alternative T cell exhaustion trajectory. <i>Nature Communications</i> , 2022, 13, .	5.8	32
28729	Ab initio modelling of an essential mammalian protein: Transcription Termination Factor 1 (TTF1). <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 6581-6590.	2.0	4
28730	Co-expression network analysis of human tau-transgenic mice reveals protein modules associated with tau-induced pathologies. <i>iScience</i> , 2022, 25, 104832.	1.9	9
28731	FE UPTAKE-INDUCING PEPTIDE1 maintains Fe translocation by controlling Fe deficiency response genes in the vascular tissue of <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2022, 45, 3322-3337.	2.8	7
28732	RNA-Seq Analyzing Reveals the Key Role of SVR3 Gene in Tolerating the Freezing Stress in <i>Saccharum spontaneum</i> . <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
28733	A systematic study of traditional Chinese medicine treating hepatitis B virus-related hepatocellular carcinoma based on target-driven reverse network pharmacology. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
28734	Downregulation of growth plate genes involved with the onset of femoral head separation in young broilers. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	2
28735	Functional Portrait of Irf1 (Orf19.217), a Regulator of Morphogenesis and Iron Homeostasis in <i>Candida albicans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
28736	Ezrin deficiency triggers glial fibrillary acidic protein upregulation and a distinct reactive astrocyte phenotype. <i>Glia</i> , 2022, 70, 2309-2329.	2.5	12
28737	Identification of sex-biased and neurodevelopment genes via brain transcriptome in <i>Ostrinia furnacalis</i> . <i>Frontiers in Physiology</i> , 0, 13, .	1.3	0
28738	Small non-coding RNA landscape of extracellular vesicles from a post-traumatic model of equine osteoarthritis. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	11
28739	Integrated physiological and transcriptomic analyses reveal the molecular mechanism behind the response to cultivation in <i>Quercus mongolica</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
28740	Wenshenyang recipe treats infertility through hormonal regulation and inflammatory responses revealed by transcriptome analysis and network pharmacology. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
28741	SbTT8, a New Sorghum bHLH Transcription Factor that Rescues Brown Seed Coat Phenotype in <i>Arabidopsis tt8</i> Mutant Plants. <i>Journal of Plant Biology</i> , 2022, 65, 473-485.	0.9	1
28743	Major transcriptomic, epigenetic and metabolic changes underlie the pluripotency continuum in rabbit preimplantation embryos. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	7
28744	A Long Noncoding RNA Derived from lncRNA-mRNA Networks Modulates Seed Vigor. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9472.	1.8	3
28745	T cell activation and B cell interaction signatures in rectal tissues are associated with HIV replication in ex vivo model of infection. <i>Aids</i> , 0, Publish Ahead of Print, .	1.0	2

#	ARTICLE	IF	CITATIONS
28746	Functional Prediction of trans-Prenyltransferases Reveals the Distribution of GFPPs in Species beyond the Brassicaceae Clade. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9471.	1.8	1
28747	Potential Mechanisms of Biejiajian Pill in the Treatment of Diabetic Atherosclerosis Based on Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	5
28748	Identification and analysis of circRNAs in the prefrontal cortices of wild boar and domestic pig. <i>Animal Biotechnology</i> , 2023, 34, 2596-2607.	0.7	0
28749	Prognostic Gene Expression-Based Signature in Clear-Cell Renal Cell Carcinoma. <i>Cancers</i> , 2022, 14, 3754.	1.7	10
28750	Global proteome analyses of phosphorylation and succinylation of barley root proteins in response to phosphate starvation and recovery. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
28752	Graph Theory Analysis of Semantic Fluency in Russian-English Bilinguals. <i>Cognitive and Behavioral Neurology</i> , 2022, 35, 179-187.	0.5	1
28753	Relationships between genome-wide R-loop distribution and classes of recurrent DNA breaks in neural stem/progenitor cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
28754	CHAC1 as a novel biomarker for distinguishing alopecia from other dermatological diseases and determining its severity. <i>IET Systems Biology</i> , 2022, 16, 173-185.	0.8	2
28755	Integrating UPLC-HR-MS/MS, Network Pharmacology, and Experimental Validation to Uncover the Mechanisms of Jinâ€™gan Capsules against Breast Cancer. <i>ACS Omega</i> , 2022, 7, 28003-28015.	1.6	1
28758	Comparative de novo transcriptome analysis of flower and root of <i>Oliveria decumbens</i> Vent. to identify putative genes in terpenes biosynthesis pathway. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28759	Exploration of the relationship between hippocampus and immune system in schizophrenia based on immune infiltration analysis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
28760	CoVM2: Molecular Biological Data Integration of SARS-CoV-2 Proteins in a Macro-to-Micro Method. <i>Biomolecules</i> , 2022, 12, 1067.	1.8	1
28761	Comparative transcriptome analysis, unfolding the pathways regulating the seed-size trait in cultivated lentil ( <i>Lens culinaris</i> Medik.). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
28762	Association of FLG mutation with tumor mutation load and clinical outcomes in patients with gastric cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
28763	Anti-Inflammatory Diet Prevents Subclinical Colonic Inflammation and Alters Metabolomic Profile of Ulcerative Colitis Patients in Clinical Remission. <i>Nutrients</i> , 2022, 14, 3294.	1.7	26
28764	Assessing the Global Impact on the Mouse Kidney After Traumatic Brain Injury: A Transcriptomic Study. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4833-4851.	1.6	1
28766	Transplantation of IGF-1-induced BMSC-derived NPCs promotes tissue repair and motor recovery in a rat spinal cord injury model. <i>Heliyon</i> , 2022, 8, e10384.	1.4	0
28767	Ubiquitome profiling reveals a regulatory pattern of UPL3 with UBP12 on metabolic-leaf senescence. <i>Life Science Alliance</i> , 2022, 5, e202201492.	1.3	3

#	ARTICLE	IF	CITATIONS
28768	Untargeted metabolomics analysis based on HS-SPME-GC-MS and UPLC-Q-TOF/MS reveals the contribution of stem to the flavor of <i>Cyclocarya paliurus</i> herbal extract. <i>LWT - Food Science and Technology</i> , 2022, 167, 113819.	2.5	5
28769	Identification of key candidate genes for IgA nephropathy using machine learning and statistics based bioinformatics models. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
28770	Exploring the pathogenesis of diabetic kidney disease by microarray data analysis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
28771	A pipeline of integrating transcriptome and interactome to elucidate central nodes in host-pathogens interactions. <i>STAR Protocols</i> , 2022, 3, 101608.	0.5	9
28772	Gene expression pattern of microbes associated with large cyanobacterial colonies for a whole year in Lake Taihu. <i>Water Research</i> , 2022, 223, 118958.	5.3	7
28773	A novel multi-class classification model for schizophrenia, bipolar disorder and healthy controls using comprehensive transcriptomic data. <i>Computers in Biology and Medicine</i> , 2022, 148, 105956.	3.9	16
28774	Large extracellular vesicles do not mitigate the harmful effect of hyperglycemia on endothelial cell mobility. <i>European Journal of Cell Biology</i> , 2022, 101, 151266.	1.6	3
28775	Integrated analysis of long-noncoding RNA and circular RNA expression in Peste-des-Petits-Ruminants Virus (PPRV) infected marmoset B lymphocyte (B95a) cells. <i>Microbial Pathogenesis</i> , 2022, 170, 105702.	1.3	3
28776	Pan-genomic, transcriptomic, and miRNA analyses to decipher genetic diversity and anthocyanin pathway genes among the traditional rice landraces. <i>Genomics</i> , 2022, 114, 110436.	1.3	1
28777	The microRNAs in the antennae of <i>Apolygus lucorum</i> (Hemiptera: Miridae): Expression properties and targets prediction. <i>Genomics</i> , 2022, 114, 110447.	1.3	0
28778	Comparative transcriptomic analysis reveals different host cell responses to Singapore grouper iridovirus and red-spotted grouper nervous necrosis virus. <i>Fish and Shellfish Immunology</i> , 2022, 128, 136-147.	1.6	7
28779	Integrated transcriptome and regulatory network analyses identify candidate genes and pathways modulating ewe fertility. <i>Gene Reports</i> , 2022, 28, 101659.	0.4	2
28780	Phylogenic analysis of new viral cluster of large phages with unusual DNA genomes containing uracil in place of thymine in gene-sharing network, using phages S6 and PBS1 and relevant uncultured phages derived from sewage metagenomics. <i>Virus Research</i> , 2022, 319, 198881.	1.1	1
28781	Comprehensive analysis of shared genetic loci between hippocampal volume and schizophrenia. <i>Psychiatry Research</i> , 2022, 316, 114795.	1.7	0
28782	Effect of polystyrene nanoplastics on cell apoptosis, glucose metabolism, and antibacterial immunity of <i>Eriocheir sinensis</i> . <i>Environmental Pollution</i> , 2022, 311, 119960.	3.7	14
28783	Characterizing intrinsic molecular features of the immune subtypes of salivary mucoepidermoid carcinoma. <i>Translational Oncology</i> , 2022, 24, 101496.	1.7	7
28784	Chloroplast proteomics reveals transgenerational cross-stress priming in <i>Pinus radiata</i> . <i>Environmental and Experimental Botany</i> , 2022, 202, 105009.	2.0	7
28785	Novel insights into host responses to Japanese Encephalitis Virus infection: Reanalysis of public transcriptome and microRNAome datasets. <i>Virus Research</i> , 2022, 320, 198887.	1.1	1

#	ARTICLE	IF	CITATIONS
28786	MCEMP1 is a potential therapeutic biomarker associated with immune infiltration in advanced gastric cancer microenvironment. <i>Gene</i> , 2022, 840, 146760.	1.0	6
28787	Integrated genomics, QTL mapping, and co-expression analyses identifying candidates of low-temperature tolerance in <i>Brassica napus</i> L. <i>Industrial Crops and Products</i> , 2022, 187, 115437.	2.5	3
28788	Investigation of the mechanism of action of Shengxuexiaoban Capsules against primary immune thrombocytopenia using network pharmacology and experimental validation. <i>Phytomedicine</i> , 2022, 106, 154413.	2.3	3
28789	Integrative analysis of the metabolome and transcriptome provides insights into the mechanisms of anthocyanins and proanthocyanidins biosynthesis in <i>Trifolium repens</i> . <i>Industrial Crops and Products</i> , 2022, 187, 115529.	2.5	10
28790	Revealing the impacts on shaping scutate scales in goose skin. <i>Gene</i> , 2022, 844, 146840.	1.0	0
28791	Bioactive molecular network-guided discovery of dihydro- $\hat{1}^2$ -agarofurans from the fruits of <i>Celastrus orbiculatus</i> . <i>Phytochemistry</i> , 2022, 203, 113349.	1.4	0
28792	Construction and validation of a novel ten miRNA-pair based signature for the prognosis of clear cell renal cell carcinoma. <i>Translational Oncology</i> , 2022, 25, 101519.	1.7	0
28793	Structural variability and niche differentiation of <i>Paeonia lactiflora</i> 's root-associated microbiomes. <i>Applied Soil Ecology</i> , 2022, 180, 104632.	2.1	2
28794	Whole blood transcriptome profiling identifies gene expression subnetworks and a key gene characteristic of the rare type of osteomyelitis. <i>Biochemistry and Biophysics Reports</i> , 2022, 32, 101328.	0.7	0
28795	Genomic, metabonomic and transcriptomic analyses of sweet osmanthus varieties provide insights into floral aroma formation. <i>Scientia Horticulturae</i> , 2022, 306, 111442.	1.7	7
28796	Biological treatment of ironworks wastewater with high-concentration nitrate using a nitrogen gas aerated anaerobic membrane bioreactor. <i>Chemical Engineering Journal</i> , 2022, 450, 138366.	6.6	5
28797	Bioinformatics analysis of ferroptosis in spinal cord injury. <i>Neural Regeneration Research</i> , 2023, 18, 626.	1.6	12
28798	Proteomics of serum exosomes identified fibulin-1 as a novel biomarker for mild cognitive impairment. <i>Neural Regeneration Research</i> , 2023, 18, 587.	1.6	5
28799	BET inhibition induces vulnerability to MCL1 targeting through upregulation of fatty acid synthesis pathway in breast cancer. <i>Cell Reports</i> , 2022, 40, 111304.	2.9	1
28800	3,5-Dinitrobenzoate and 3,5-Dinitrobenzamide Derivatives: Mechanistic, Antifungal, and In Silico Studies. <i>Journal of Chemistry</i> , 2022, 2022, 1-17.	0.9	3
28801	Integrated single-cell transcriptomic analyses reveal that GPNMB-high macrophages promote PN-MES transition and impede T cell activation in GBM. <i>EBioMedicine</i> , 2022, 83, 104239.	2.7	11
28802	Fucosyltransferase 4 Predicts Patient Outcome in Rectal Cancer through an Immune Microenvironment-Mediated Multi-Mechanism. <i>Journal of Oncology</i> , 2022, 2022, 1-38.	0.6	0
28803	Use of heparin to rescue immunosuppressive monocyte reprogramming by glioblastoma-derived extracellular vesicles. <i>Journal of Neurosurgery</i> , 2022, , 1-11.	0.9	1

#	ARTICLE	IF	CITATIONS
28804	Mitochondrial Aldehyde Dehydrogenase 2 Represents a Potential Biomarker of Biochemical Recurrence in Prostate Cancer Patients. <i>Molecules</i> , 2022, 27, 6000.	1.7	4
28805	The mechanism of Lingze tablets in the treatment of benign prostatic hyperplasia based on network pharmacology and molecular docking technology. <i>Andrologia</i> , 2022, 54, .	1.0	3
28806	Identification and Verification of Key MiRNAs Associated with Intervertebral Disc Degeneration. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 1766-1774.	0.6	1
28807	Exploration of shared TF-miRNA-mRNA and mRNA-RBP-pseudogene networks in type 2 diabetes mellitus and breast cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
28808	Genome-Wide Identification and Expression Patterns of the F-box Family in Poplar under Salt Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10934.	1.8	4
28809	Study on the effect of Pogostemon cablin Benth on skin aging based on network pharmacology. <i>Current Computer-Aided Drug Design</i> , 2022, 18, .	0.8	0
28810	Integrative analysis of synovial sarcoma transcriptome reveals different types of transcriptomic changes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
28811	Expression pattern of non-coding RNAs in non-functioning pituitary adenoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	5
28812	Identification of potential key genes for immune infiltration in childhood asthma by data mining and biological validation. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
28813	PIM1 promotes hepatic conversion by suppressing reprogramming-induced ferroptosis and cell cycle arrest. <i>Nature Communications</i> , 2022, 13, .	5.8	4
28814	Immune features of the peritumoral stroma in pancreatic ductal adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
28816	Association of Cytotoxic T-Lymphocyte Antigen-4 Gene Polymorphism with Type 1 Diabetes Mellitus: In silico Analysis of Biological Features of CTLA-4 Protein on Ethiopian Population. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 0, Volume 15, 2733-2751.	1.1	3
28817	Infection by the Parasite <i>Myxobolus bejeranoi</i> (Cnidaria: Myxozoa) Suppresses the Immune System of Hybrid Tilapia. <i>Microorganisms</i> , 2022, 10, 1893.	1.6	1
28818	Viruses Ubiquity and Diversity in Atacama Desert Endolithic Communities. <i>Viruses</i> , 2022, 14, 1983.	1.5	3
28820	Systems analysis of de novo mutations in congenital heart diseases identified a protein network in the hypoplastic left heart syndrome. <i>Cell Systems</i> , 2022, 13, 895-910.e4.	2.9	3
28822	The Role of <i>Medicago lupulina</i> Interaction with <i>Rhizophagus irregularis</i> in the Determination of Root Metabolome at Early Stages of AM Symbiosis. <i>Plants</i> , 2022, 11, 2338.	1.6	4
28823	AntiVIRmiR: A repository of host antiviral miRNAs and their expression along with experimentally validated viral miRNAs and their targets. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28825	Mechanistic Wound Healing and Antioxidant Potential of <i>Moringa oleifera</i> Seeds Extract Supported by Metabolic Profiling, In Silico Network Design, Molecular Docking, and In Vivo Studies. <i>Antioxidants</i> , 2022, 11, 1743.	2.2	13

#	ARTICLE	IF	CITATIONS
28826	Carbofuran self-poisoning: forensic and analytic investigations in twins and literature review. <i>International Journal of Legal Medicine</i> , 2022, 136, 1585-1596.	1.2	6
28828	A small proportion of X-linked genes contribute to X chromosome upregulation in early embryos via BRD4-mediated transcriptional activation. <i>Current Biology</i> , 2022, 32, 4397-4410.e5.	1.8	6
28829	Network-Based Data Analysis Reveals Ion Channel-Related Gene Features in COVID-19: A Bioinformatic Approach. <i>Biochemical Genetics</i> , 0, , .	0.8	1
28830	The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences. <i>Nature Plants</i> , 2022, 8, 1024-1037.	4.7	27
28831	RedB, a Member of the CRP/FNR Family, Functions as a Transcriptional Redox Brake. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
28832	Integrated mRNA and microRNA expression analysis of root response to phosphate deficiency in <i>Medicago sativa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
28833	Profile analysis and functional modeling identify circular RNAs in nonalcoholic fatty liver disease as regulators of hepatic lipid metabolism. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28834	Combined Proteomic and Metabolomic Analysis of the Molecular Mechanism Underlying the Response to Salt Stress during Seed Germination in Barley. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10515.	1.8	7
28835	Medical aid to war victims in Syria in 2019: a report of organized healthcare support from a charity organization. <i>BMC Health Services Research</i> , 2022, 22, .	0.9	1
28836	Comparative transcriptomics analysis of developing peanut ( <i>Arachis hypogaea</i> L.) pods reveals candidate genes affecting peanut seed size. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
28837	Morphological and transcriptome analyses reveal mechanism for efficient regeneration of adventitious buds from in vitro leaves of <i>Rhododendron delavayi</i> regulated by exogenous TDZ. In <i>Vitro Cellular and Developmental Biology - Plant</i> , 2022, 58, 1025-1037.	0.9	5
28838	Loss of Pleckstrin homology like domain, family A, member 1 promotes type $\alpha$ alveolar epithelial cell apoptosis in chronic obstructive pulmonary disease emphysematous phenotype via interaction with tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon. <i>International Journal of Biochemistry and Cell Biology</i> , 2022, 151, 106297.	1.2	0
28839	Toxicological and transcriptomic-based analysis of monensin and sulfamethazine co-exposure on male SD rats. <i>Ecotoxicology and Environmental Safety</i> , 2022, 245, 114110.	2.9	1
28840	The mitochondrial RNA granule modulates manganese-dependent cell toxicity. <i>Molecular Biology of the Cell</i> , 2022, 33, .	0.9	1
28841	Inhibition of $\alpha$ -synuclein aggregation by MT101-5 is neuroprotective in mouse models of Parkinson's disease. <i>Biomedicine and Pharmacotherapy</i> , 2022, 154, 113637.	2.5	0
28842	Functional insights of antibiotic resistance mechanism in <i>Helicobacter pylori</i> : Driven by gene interaction network and centrality-based nodes essentiality analysis. <i>Microbial Pathogenesis</i> , 2022, 171, 105737.	1.3	1
28843	LONP1 downregulation with ageing contributes to osteoarthritis via mitochondrial dysfunction. <i>Free Radical Biology and Medicine</i> , 2022, 191, 176-190.	1.3	8
28844	Mori fructus aqueous extracts attenuate carbon tetrachloride-induced renal injury via the Nrf2 pathway and intestinal flora. <i>Ecotoxicology and Environmental Safety</i> , 2022, 245, 114118.	2.9	5



#	ARTICLE	IF	CITATIONS
28845	Plasma proteomic signature of major depressive episode in the elderly. <i>Journal of Proteomics</i> , 2022, 269, 104713.	1.2	5
28846	Characterization of chicken p53 transcriptional function via parallel genome-wide chromatin occupancy and gene expression analysis. <i>Poultry Science</i> , 2022, 101, 102164.	1.5	1
28847	Patterns and Crucial Regulation of Alternative Splicing During Early Development in Zebrafish. <i>Journal of Molecular Biology</i> , 2022, 434, 167821.	2.0	0
28848	KIF20A promotes the development of fibrosarcoma via PI3K-Akt signaling pathway. <i>Experimental Cell Research</i> , 2022, 420, 113322.	1.2	4
28849	A mechanism of microbial sensitivity regulation on interventional remediation by nanozyme manganese oxide in soil heavy metal pollution. <i>Journal of Cleaner Production</i> , 2022, 373, 133825.	4.6	4
28850	Identification of BRIP1, NSMCE2, ANAPC7, RAD18 and TTL from chromosome segregation gene set associated with hepatocellular carcinoma. <i>Cancer Genetics</i> , 2022, 268-269, 28-36.	0.2	1
28851	Peritoneal effluent MicroRNA profile for detection of encapsulating peritoneal sclerosis. <i>Clinica Chimica Acta</i> , 2022, 536, 45-55.	0.5	1
28852	iCancer-Pred: A tool for identifying cancer and its type using DNA methylation. <i>Genomics</i> , 2022, 114, 110486.	1.3	4
28853	Comprehensive analysis to identify the RP11-478C19.2/ E2F7 axis as a novel biomarker for treatment decisions in clear cell renal cell carcinoma. <i>Translational Oncology</i> , 2022, 25, 101525.	1.7	4
28854	Identification of the novel natural product inhibitors of SHP2 from the plant <i>Toona sinensis</i> : In vitro and in silico study. <i>International Journal of Biological Macromolecules</i> , 2022, 221, 679-690.	3.6	6
28855	Mechanical stress elicits kiwifruit ripening changes in gene expression and metabolic status. <i>Postharvest Biology and Technology</i> , 2022, 194, 112102.	2.9	8
28856	Genome-wide identification and transcriptome analysis of the heavy metal-associated (HMA) gene family in Tartary buckwheat and their regulatory roles under cadmium stress. <i>Gene</i> , 2022, 847, 146884.	1.0	10
28857	Effect of fumigants and non-fumigants on nematode and weed control, crop yield, and soil microbial diversity and predicted functionality in a strawberry production system. <i>Science of the Total Environment</i> , 2022, 852, 158285.	3.9	8
28858	Contrasting archaeal and bacterial community assembly processes and the importance of rare taxa along a depth gradient in shallow coastal sediments. <i>Science of the Total Environment</i> , 2022, 852, 158411.	3.9	11
28859	Methanogenic communities and methane emissions from enrichments of Brazilian Amazonia soils under land-use change. <i>Microbiological Research</i> , 2022, 265, 127178.	2.5	8
28860	Malonylome analysis uncovers the association of lysine malonylation with metabolism and acidic stress in pathogenic <i>Mycobacterium tuberculosis</i> . <i>Microbiological Research</i> , 2022, 265, 127209.	2.5	1
28861	Trace metal complexation with dissolved organic matter stresses microbial metabolisms and triggers community shifts: The intercorrelations. <i>Environmental Pollution</i> , 2022, 314, 120221.	3.7	8
28862	Microbiome structure in biofilms from a volcanic island in Maritime Antarctica investigated by genome-centric metagenomics and metatranscriptomics. <i>Microbiological Research</i> , 2022, 265, 127197.	2.5	3

#	ARTICLE	IF	CITATIONS
28863	Application of network composite module analysis and verification to explore the bidirectional immunomodulatory effect of Zukamu granules on Th1 / Th2 cytokines in lung injury. <i>Journal of Ethnopharmacology</i> , 2022, 299, 115674.	2.0	3
28864	Differential co-expression networks of the gut microbiota are associated with depression and anxiety treatment resistance among psychiatric inpatients. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2023, 120, 110638.	2.5	10
28865	Changes in rhizosphere phosphorus fractions and phosphate-mineralizing microbial populations in acid soil as influenced by organic acid exudation. <i>Soil and Tillage Research</i> , 2023, 225, 105543.	2.6	16
28866	The fecal arsenic excretion, tissue arsenic accumulation, and metabolomics analysis in sub-chronic arsenic-exposed mice after in situ arsenic-induced fecal microbiota transplantation. <i>Science of the Total Environment</i> , 2023, 854, 158583.	3.9	3
28867	Multiomics techniques for plant secondary metabolism engineering: Pathways to shape the bioeconomy. , 2023, , 205-252.		0
28868	Cell wall lignification may be necessary for somatic embryogenesis of areca palm ( <i>Areca catechu</i> ). <i>Scientia Horticulturae</i> , 2023, 307, 111538.	1.7	5
28869	Combining LC-MS/MS profiles with network pharmacology to predict molecular mechanisms of the hyperlipidemic activity of <i>Lagenaria siceraria</i> stand. <i>Journal of Ethnopharmacology</i> , 2023, 300, 115633.	2.0	4
28870	Modular structure of complex II: An evolutionary perspective. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2023, 1864, 148916.	0.5	5
28871	Identification of upregulated genes in glioblastoma and glioblastoma cancer stem cells using bioinformatics analysis. <i>Gene</i> , 2023, 848, 146895.	1.0	4
28872	Residue interaction network and molecular dynamics simulation study on the binding of S239D/I332E Fc variant with enhanced affinity to Fcγ3R1IIa receptor. <i>Journal of Molecular Graphics and Modelling</i> , 2023, 118, 108327.	1.3	2
28873	Investigation of the chemical composition of antibacterial <i>Psidium guajava</i> extract and partitions against foodborne pathogens. <i>Food Chemistry</i> , 2023, 403, 134400.	4.2	1
28874	Mapping the Mutual Transcriptional Responses During <i>Candida Albicans</i> and Human Macrophage Interactions by Dual Rna-Sequencing. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28875	Genomics and morphometrics reveal the adaptive evolution of pikas. <i>Zoological Research</i> , 2022, 43, 813-826.	0.9	5
28876	Comparison of Soil and Grass Microbiomes and Resistomes Reveals Grass as a Greater Antimicrobial Resistance Reservoir than Soil. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28877	Transient upregulation of EGR1 signaling enhances kidney repair by activating SOX9 <sup>+</sup> renal tubular cells. <i>Theranostics</i> , 2022, 12, 5434-5450.	4.6	24
28878	Polypharmacology in Predicting Drug Toxicity: Drug Promiscuity. , 2022, , 593-623.		0
28879	Succinyl-CoA Synthetase Deficiency in Mouse Forebrain Results in Hyper-Succinylation With Perturbed Neuronal Transcriptional Regulation and Metabolism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
28880	Chemical Networks: A Methodology to Rapidly Assess the Environmental Impact of Chemical Processes. <i>Johnson Matthey Technology Review</i> , 2022, 66, 466-478.	0.5	1

#	ARTICLE	IF	CITATIONS
28881	An explorative study for leveraging transcriptomic data of embryonic stem cells in mining cancer stemness genes, regulators, and networks. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 13949-13966.	1.0	0
28882	Modeling Biological Information Processing Networks. <i>Graduate Texts in Physics</i> , 2022, , 213-236.	0.1	1
28883	Sex differences in hepatocellular carcinoma indicated BEX4 as a potential target to improve efficacy of lenvatinib plus immune checkpoint inhibitors. <i>Journal of Cancer</i> , 2022, 13, 3221-3233.	1.2	0
28884	Virus-host interaction analysis in colorectal cancer identifies core virus network signature and small molecules. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4025-4039.	1.9	2
28885	Computational Analyses Reveal Fundamental Properties of the Hemophilia Literature in the Last 6 Decades. <i>Bioinformatics and Biology Insights</i> , 2022, 16, 117793222211256.	1.0	1
28886	Effect of a methanolic extract of <i>Salvadora oleoides</i> Decne. on LPS-activated J774 macrophages, its in vitro and in vivo toxicity study and dereplication of its chemical constituents. <i>Toxicology Reports</i> , 2022, 9, 1742-1753.	1.6	0
28887	Association of glioma CD44 expression with glial dynamics in the tumour microenvironment and patient prognosis. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5203-5217.	1.9	6
28888	Screening and Identification of Potential Hub Genes and Immune Cell Infiltration in the Synovial Tissue of Rheumatoid Arthritis by Bioinformatic Approach. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28889	Univ-flu: A structure-based model of influenza A virus hemagglutinin for universal antigenic prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4656-4666.	1.9	1
28890	The synergistic interaction landscape of chromatin regulators reveals their epigenetic regulation mechanisms across five cancer cell lines. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5028-5039.	1.9	1
28891	An intramodular thioesterase domain catalyses chain release in the biosynthesis of a cytotoxic virulence factor. <i>RSC Chemical Biology</i> , 2022, 3, 1121-1128.	2.0	3
28892	Characterizing Basal and Feed Media Effects on Mammalian Cell Cultures by Systems Engineering Approaches. <i>IFAC-PapersOnLine</i> , 2022, 55, 31-36.	0.5	2
28893	Network metrics, structural dynamics and density functional theory calculations identified a novel Ursodeoxycholic Acid derivative against therapeutic target Parkin for Parkinson's disease. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4271-4287.	1.9	18
28894	Systems biology models to identify the influence of SARS-CoV-2 infections to the progression of human autoimmune diseases. <i>Informatics in Medicine Unlocked</i> , 2022, 32, 101003.	1.9	2
28895	Deciphering potential biomarkers for celiac disease by using an integrated bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2022, 32, 101040.	1.9	0
28896	Metagenomic Approaches for the Discovery of Pollutant-Remediating Enzymes: Recent Trends and Challenges. , 2022, , 571-604.		0
28897	MicroRNA expression profile of cholesterol metabolism analysis mediated by <i>Thelenota ananas</i> desulfated holothurin A saponin in RAW264.7 macrophage-foam cells. <i>Food and Function</i> , 2022, 13, 11049-11060.	2.1	2
28898	Temporal and spatial auxin responsive networks in maize primary roots. <i>Quantitative Plant Biology</i> , 2022, 3, .	0.8	4

#	ARTICLE	IF	CITATIONS
28899	Functional Annotation of Hypothetical Proteins From the <i>Enterobacter cloacae</i> B13 Strain and Its Association With Pathogenicity. <i>Bioinformatics and Biology Insights</i> , 2022, 16, 117793222211155.	1.0	1
28900	Notch Pathway Defines an Aggressive and Immune-Suppressive Phenotype Associated with Checkpoint Inhibitor Resistance in Pan-Gastrointestinal Adenocarcinomas. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28901	Identification of differentially expressed genes and their major pathways among the patient with COVID-19, cystic fibrosis, and chronic kidney disease. <i>Informatics in Medicine Unlocked</i> , 2022, 32, 101038.	1.9	4
28902	Cell Wall Lignification May Be Necessary for Somatic Embryogenesis of Areca Palm ( <i>Areca Catechu</i> ). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28903	Comparative maternal protein profiling of mouse biparental and uniparental embryos. <i>GigaScience</i> , 2022, 11, .	3.3	3
28904	TCM Preparation Network Pharmacology Analysis. <i>Translational Bioinformatics</i> , 2022, , 81-98.	0.0	0
28905	Treatment with silica-gold nanostructures decreases inflammation-related gene expression in collagen-induced arthritis. <i>Biomaterials Science</i> , 2022, 10, 5216-5229.	2.6	4
28906	Microbial profiling of peri-implantitis compared to the periodontal microbiota in health and disease using 16S rRNA sequencing. <i>Journal of Periodontal and Implant Science</i> , 2023, 53, 69.	0.9	8
28907	Multiple time-series expression trajectories imply dynamic functional changes during cellular senescence. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4131-4137.	1.9	1
28908	Exploring SARS-CoV2 host-pathogen interactions and associated fungal infections cross-talk: Screening of targets and understanding pathogenesis. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4351-4359.	1.9	4
28909	Characterization of chemical components and the potential anti-influenza mechanism of <i>Fructus Arctii</i> by a strategy integrating pharmacological evaluations, chemical profiling, serum pharmacochemistry, and network pharmacology. <i>New Journal of Chemistry</i> , 2022, 46, 18426-18446.	1.4	0
28910	Discovering surface reaction pathways using accelerated molecular dynamics and network analysis tools. <i>RSC Advances</i> , 2022, 12, 23274-23283.	1.7	1
28911	The multiple roles of lipid metabolism in yeast physiology during beer fermentation. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	0
28912	TFLink: an integrated gateway to access transcription factor-target gene interactions for multiple species. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	22
28913	Humoral Immunity and Transcriptome Differences of COVID-19 Inactivated Vaccine and Protein Subunit Vaccine as Third Booster Dose in Human. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28914	Analysis of the Human Pineal Proteome by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2022, , 123-132.	0.4	0
28915	<i>In vivo</i> and <i>in silico</i> approaches to assess surface water genotoxicity from Tocantins River, in the cities of Porto Nacional and Palmas, Brazil. <i>Journal of Environmental Science and Health, Part C: Toxicology and Carcinogenesis</i> , 2022, 40, 27-45.	0.4	0
28916	( $\hat{\alpha}$ )-Epicatechin exerts positive effects on anxiety in high fat diet-induced obese mice through multi-genomic modifications in the hippocampus. <i>Food and Function</i> , 2022, 13, 10623-10641.	2.1	1

#	ARTICLE	IF	CITATIONS
28917	Prioritization of Candidate Genes Through Boolean Networks. <i>Lecture Notes in Computer Science</i> , 2022, , 89-121.	1.0	2
28918	Advancements in antimicrobial nanoscale materials and self-assembling systems. <i>Chemical Society Reviews</i> , 2022, 51, 8696-8755.	18.7	23
28919	Rational computational approaches to predict novel drug candidates against leishmaniasis. <i>Annual Reports in Medicinal Chemistry</i> , 2022, , .	0.5	0
28920	Proteomic Landscape of Primary and Metastatic Brain Tumors for Heterogeneity Discovery. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28921	Bioinformatics Analysis Identifies Potential Related Genes in the Pathogenesis of Intrauterine Fetal Growth Retardation. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432211127.	0.6	0
28922	An approach to nearest neighbor analysis of pigment-protein complexes using chemical cross-linking in combination with mass spectrometry. <i>Methods in Enzymology</i> , 2023, , 139-162.	0.4	1
28923	Warmer Ambient Air Temperatures Reduce Nasal Turbinate and Brain Infection, But Increase Lung Inflammation in the K18-hACE2 Mouse Model of COVID-19. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
28924	LargeNetVis: Visual Exploration of Large Temporal Networks Based On Community Taxonomies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2022, , 1-11.	2.9	0
28925	Classification for psychiatric disorders including schizophrenia, bipolar disorder, and major depressive disorder using machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5054-5064.	1.9	6
28926	Combining confocal microscopy, dSTORM, and mass spectroscopy to unveil the evolution of the protein corona associated with nanostructured lipid carriers during blood-brain barrier crossing. <i>Nanoscale</i> , 2022, 14, 13292-13307.	2.8	3
28927	Comprehensive bioinformatic analysis of key genes and signaling pathways in glioma. , 2022, 52, 3.		0
28928	TCM Analysis Data Resources, Web Services and Visualizations. <i>Translational Bioinformatics</i> , 2022, , 99-110.	0.0	0
28937	Cross-biome soil viruses as an important reservoir of virulence genes. <i>Journal of Hazardous Materials</i> , 2023, 442, 130111.	6.5	5
28938	Transformation of dissolved organic matter in landfill leachate during a membrane bioreactor treatment. <i>Science of the Total Environment</i> , 2023, 856, 159066.	3.9	15
28939	Reciprocal effect and heterosis for tomato fruit metabolites revealed by whole transcriptomic analysis of two cultivars and their reciprocal hybrids. <i>Scientia Horticulturae</i> , 2023, 308, 111583.	1.7	0
28940	Genome-wide identification reveals the DcMADS-box family transcription factors involved in flowering of carrot. <i>Scientia Horticulturae</i> , 2023, 308, 111558.	1.7	2
28941	The Long Non-coding RNA AC148477.2 Is a Novel Therapeutic Target Associated With Vascular Smooth Muscle Cells Proliferation of Femoral Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	0
28943	Employ machine learning methods in combination with bioinformatic analysis of the gene structure of polygenic diseases to develop effective methods for early diagnosis and prognosis of their developmentaper. , 2022, , .		0

#	ARTICLE	IF	CITATIONS
28944	Mechanism of Astragali Radix for the treatment of osteoarthritis: A study based on network pharmacology and molecular docking. <i>Medicine (United States)</i> , 2022, 101, e29885.	0.4	3
28945	Dysbiotic Oral and Gut Viromes in Untreated and Treated Rheumatoid Arthritis Patients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12
28946	Integrated relationship of nasopharyngeal airway host response and microbiome associates with bronchiolitis severity. <i>Nature Communications</i> , 2022, 13, .	5.8	12
28947	Classification and biomarker gene selection of pyroptosis-related gene expression in psoriasis using a random forest algorithm. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
28948	Integrated analysis and identification of hub genes as novel biomarkers for Alzheimer's disease. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	5
28949	Prognostic model based on m6A-associated lncRNAs in esophageal cancer. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
28950	Dysregulation of Pseudogenes/lncRNA-Hsa-miR-1-3p-PAICS Pathway Promotes the Development of NSCLC. <i>Journal of Oncology</i> , 2022, 2022, 1-22.	0.6	4
28951	Identification of Src Family Kinases as Potential Therapeutic Targets for Chemotherapy-Resistant Triple Negative Breast Cancer. <i>Cancers</i> , 2022, 14, 4220.	1.7	6
28952	Mechanism of Key Ingredient of Astragalus membranaceus on Lung Adenocarcinoma via PI3K/AKT Signaling Clarified by Utilizing Network Pharmacology Approach and Experimental Validation. <i>Chinese Journal of Integrative Medicine</i> , 0, , .	0.7	0
28953	Integrative Investigation of Root-Related mRNAs, lncRNAs and circRNAs of "Muscat Hamburg" (Vitis TJ ETQq1 1 0.784314 rgBT 13, 1547.	1.0	1
28954	Modeling exercise using optogenetically contractible Drosophila larvae. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
28955	Molecular programs associated with glomerular hyperfiltration in early diabetic kidney disease. <i>Kidney International</i> , 2022, 102, 1345-1358.	2.6	10
28956	Increased expression of MMP17 predicts poor clinical outcomes in epithelial ovarian cancer patients. <i>Medicine (United States)</i> , 2022, 101, e30279.	0.4	5
28957	Exploring the bioactive compounds derived from Plumula Nelumbinis and potential targets for the treatment of non-small cell lung cancer: A network pharmacology study. , 0, , 30-48.		2
28958	Mechanisms and network pharmacological analysis of Yangyin Fuzheng Jiedu prescription in the treatment of hepatocellular carcinoma. <i>Cancer Medicine</i> , 2023, 12, 3237-3259.	1.3	3
28959	Transcriptomic analysis shows that surgical treatment is likely to influence the endometrial receptivity of patients with stage III/IV endometriosis. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
28960	Prognostic risk assessment model for alternative splicing events and splicing factors in malignant pleural mesothelioma. <i>Cancer Medicine</i> , 2023, 12, 4895-4906.	1.3	4
28961	Absence of Gut Microbiota Is Associated with RPE/Choroid Transcriptomic Changes Related to Age-Related Macular Degeneration Pathobiology and Decreased Choroidal Neovascularization. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9676.	1.8	12



#	ARTICLE	IF	CITATIONS
28962	Impact of Visceral Leishmaniasis on Local Organ Metabolism in Hamsters. <i>Metabolites</i> , 2022, 12, 802.	1.3	5
28963	Pharmacological Mechanism of Zuojin Pill for Gastroesophageal Reflux Disease: A Network Pharmacology Study. <i>Journal of Food Quality</i> , 2022, 2022, 1-13.	1.4	1
28964	Wolbachia infection and genetic diversity of Italian populations of <i>Philaenus spumarius</i> , the main vector of <i>Xylella fastidiosa</i> in Europe. <i>PLoS ONE</i> , 2022, 17, e0272028.	1.1	5
28966	Transcriptomic signatures responding to PKM2 activator TEPP-46 in the hyperglycemic human renal proximal epithelial tubular cells. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
28967	Extra benefit of microalgae in raw piggery wastewater treatment: pathogen reduction. <i>Microbiome</i> , 2022, 10, .	4.9	12
28969	Identification of a Signature for Predicting Prognosis and Immunotherapy Response in Patients with Glioma. <i>Journal of Oncology</i> , 2022, 2022, 1-13.	0.6	1
28970	Identification and functional analysis of LncRNA-XIST ceRNA network in prostate cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	2
28971	Therapeutic Effects of Retinoic Acid in Lipopolysaccharide-Induced Cardiac Dysfunction: Network Pharmacology and Experimental Validation. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4963-4979.	1.6	2
28972	Monoamine Oxidase-Dependent Pro-Survival Signaling in Diabetic Hearts Is Mediated by miRNAs. <i>Cells</i> , 2022, 11, 2697.	1.8	10
28973	Downregulation of S100A9 Reverses Cisplatin-Resistance and Inhibits Proliferation and Migration in Hypopharyngeal Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	1
28974	Glutamine synthetase gene <i>PpGS1.1</i> negatively regulates the powdery mildew resistance in Kentucky bluegrass. <i>Horticulture Research</i> , 2022, 9, .	2.9	6
28975	Longitudinal Study of Fecal Microbiota in Calves with or without Diarrhea Episodes before Weaning. <i>Veterinary Sciences</i> , 2022, 9, 463.	0.6	3
28976	Genome-Wide Identification and Characterization of Circular RNAs during Skeletal Muscle Development in Meat Rabbits. <i>Animals</i> , 2022, 12, 2208.	1.0	2
28977	Differential Oral Microbial Input Determines Two Microbiota Pneumotypes Associated with Health Status. <i>Advanced Science</i> , 2022, 9, .	5.6	8
28978	Effect of Ningxin-Yishen Formula on D-galactose-induced Premature Ovarian Insufficiency Mice by Inhibiting p53. <i>Clinical Complementary Medicine and Pharmacology</i> , 2023, 3, 100068.	0.9	0
28979	Methylation Drives SLC2A1 Transcription and Ferroptosis Process Decreasing Autophagy Pressure in Colon Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-14.	0.6	7
28980	Exploring the mechanism of action of dapansutride in the treatment of gouty arthritis based on molecular docking and molecular dynamics. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	7
28981	E2F1 as a potential prognostic and therapeutic biomarker by affecting tumor development and immune microenvironment in hepatocellular carcinoma. <i>Translational Cancer Research</i> , 2022, 11, 2713-2732.	0.4	1

#	ARTICLE	IF	CITATIONS
28983	Methamphetamine signals transcription of IL1 $\beta$ and TNF $\alpha$ in a reactive oxygen species-dependent manner and interacts with HIV-1 Tat to decrease antioxidant defense mechanisms. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	1.8	1
28984	Identification of Novel Multi-Omics Expression Landscapes and Meta-Analysis of Landscape-Based Competitive Endogenous RNA Networks in ALDH+ Lung Adenocarcinoma Stem Cells. <i>BioMed Research International</i> , 2022, 2022, 1-20.	0.9	1
28985	Integrated Analysis of the lncRNA-Associated ceRNA Network in Wilms Tumor via TARGET and GEO Databases. <i>Genetical Research</i> , 2022, 2022, 1-12.	0.3	0
28986	Identification of EZH2 as Cancer Stem Cell Marker in Clear Cell Renal Cell Carcinoma and the Anti-Tumor Effect of Epigallocatechin-3-Gallate (EGCG). <i>Cancers</i> , 2022, 14, 4200.	1.7	9
28987	Undiagnosed HIV Infections May Drive HIV Transmission in the Era of “Treat All”: A Deep-Sampling Molecular Network Study in Northeast China during 2016 to 2019. <i>Viruses</i> , 2022, 14, 1895.	1.5	5
28988	Network Pharmacology-Based Exploration of the Therapeutic Mechanisms of <i>Cordyceps cicadae</i> in Renal Ischemia/Reperfusion. <i>Annals of Transplantation</i> , 0, 27, .	0.5	0
28989	A Preliminary Study for Identifying Genes Associated with Pellicle Development in Xinjiang Walnut ( <i>Juglans regia</i> L.). <i>Horticulturae</i> , 2022, 8, 784.	1.2	1
28990	The identification of hub biomarkers and pathways in lung cancer and prognostic evaluation. <i>Translational Cancer Research</i> , 2022, 11, 2622-2635.	0.4	1
28991	Identification of key genes and pathways associated with diabetes of the exocrine pancreas. <i>Medicine (United States)</i> , 2022, 101, e29781.	0.4	0
28992	Identification of candidate biomarkers associated with gastric cancer prognosis based on an integrated bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 1690-1700.	0.6	2
28993	The ETV1/ER81 transcription factor coordinates myelination-related genes to regulate Schwann cell differentiation and myelination. <i>Annals of Translational Medicine</i> , 2022, 10, 875-875.	0.7	3
28994	Identification of molecular subtypes in lung adenocarcinoma based on DNA methylation and gene expression profiling—a bioinformatic analysis. <i>Annals of Translational Medicine</i> , 2022, 10, 882-882.	0.7	3
28995	Systematic identification of aberrant non-coding RNAs and their mediated modules in rotator cuff tears. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
28996	The Specific microRNA Profile and Functional Networks for Children with Allergic Asthma. <i>Journal of Asthma and Allergy</i> , 0, Volume 15, 1179-1194.	1.5	2
28997	Cellular transcriptional alterations of peripheral blood in Alzheimer’s disease. <i>BMC Medicine</i> , 2022, 20, .	2.3	15
28998	Disease-related protein co-expression networks are associated with the prognosis of resectable node-positive pancreatic ductal adenocarcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
28999	Insights into the Metabolomic Capacity of <i>Podaxis</i> and Isolation of Podaxisterols A–D, Ergosterol Derivatives Carrying Nitrosyl Cyanide-Derived Modifications. <i>Journal of Natural Products</i> , 2022, 85, 2159-2167.	1.5	2
29000	Lactic acid from vaginal microbiota enhances cervicovaginal epithelial barrier integrity by promoting tight junction protein expression. <i>Microbiome</i> , 2022, 10, .	4.9	25

#	ARTICLE	IF	CITATIONS
29002	A Review on Computational Analysis of Big Data in Breast Cancer for Predicting Potential Biomarkers. <i>Current Topics in Medicinal Chemistry</i> , 2022, 22, 1793-1810.	1.0	3
29004	Different MicroRNA profiles in Peripheral Blood mononuclear cells from patients with initial-onset and recurrent vogtâ€™Koyanagiâ€™Harada Disease. <i>Molecular Biology Reports</i> , 2022, 49, 11421-11431.	1.0	1
29005	Integrated Analysis of Transcriptome and Metabolome Reveals the Regulation of Chitooligosaccharide on Drought Tolerance in Sugarcane ( <i>Saccharum</i> spp. Hybrid) under Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9737.	1.8	8
29006	Acesulfame Anoxic Biodegradation Coupled to Nitrate Reduction by Enriched Consortia and Isolated <i>Shinella</i> spp.. <i>Environmental Science &amp; Technology</i> , 2022, 56, 13096-13106.	4.6	10
29007	Chromosomal Instability Characterizes Pediatric Medulloblastoma but Is Not Tolerated in the Developing Cerebellum. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9852.	1.8	1
29008	Antibacterial Activity from <i>Momordica charantia</i> L. Leaves and Flavones Enriched Phase. <i>Pharmaceutics</i> , 2022, 14, 1796.	2.0	4
29009	Cell Division Cycle-Associated Protein 3 (CDCA3) Is a Potential Biomarker for Clinical Prognosis and Immunotherapy in Pan-Cancer. <i>BioMed Research International</i> , 2022, 2022, 1-28.	0.9	4
29010	A TCF7L2-responsive suppression of both homeostatic and compensatory remyelination in Huntington disease mice. <i>Cell Reports</i> , 2022, 40, 111291.	2.9	11
29011	Construction of miRNA-mRNA network and a nomogram model of prognostic analysis for prostate cancer. <i>Translational Cancer Research</i> , 2022, 11, 2562-2571.	0.4	1
29012	Deep mutational learning predicts ACE2 binding and antibody escape to combinatorial mutations in the SARS-CoV-2 receptor-binding domain. <i>Cell</i> , 2022, 185, 4008-4022.e14.	13.5	55
29013	Interaction between <i>HER2</i> and <i>ATM</i> predicts poor survival in bladder cancer patients. <i>Journal of Cellular and Molecular Medicine</i> , 0, , .	1.6	2
29014	Molecular subtype identification and predictive power of N6-methyladenosine regulator in unexplained recurrent pregnancy loss. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29015	Metabolomic analysis of halotolerant endophytic bacterium <i>Salinivibrio costicola</i> isolated from <i>Suaeda maritima</i> (L.) dumort. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
29016	Basic helix-loop-helix transcription factor <i>PxbHLH02</i> enhances drought tolerance in <i>Populus</i> ( <i>Populus simonii</i> Å— <i>P. nigra</i> ). <i>Tree Physiology</i> , 2023, 43, 185-202.	1.4	8
29017	scAllele: A versatile tool for the detection and analysis of variants in scRNA-seq. <i>Science Advances</i> , 2022, 8, .	4.7	2
29018	The genus <i>Serratia</i> revisited by genomics. <i>Nature Communications</i> , 2022, 13, .	5.8	21
29019	Failure of human rhombic lip differentiation underlies medulloblastoma formation. <i>Nature</i> , 2022, 609, 1021-1028.	13.7	52
29021	Genome-wide identification of three-amino-acid-loop-extension gene family and their expression profile under hormone and abiotic stress treatments during stem development of <i>Prunus mume</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4

#	ARTICLE	IF	CITATIONS
29022	Analysis of body color formation of leopard coral grouper <i>Plectropomus leopardus</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
29023	Anti-asthmatic fraction screening and mechanisms prediction of <i>Schisandrae Sphenantherae Fructus</i> based on a combined approach. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
29024	Construction and validation model of necroptosis-related gene signature associates with immunity for osteosarcoma patients. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
29025	Feature importance network reveals novel functional relationships between biological features in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
29026	<i>SrpK1</i> Regulates Asexual Blood Stage Schizogony and Is Essential for Male Gamete Formation. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
29027	Decreased TCF1 and BCL11B expression predicts poor prognosis for patients with chronic lymphocytic leukemia. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
29028	A common vesicle proteome drives fungal biofilm development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	14
29029	miR-378 associated with proliferation, migration and apoptosis properties in A549 cells and targeted NPNT in COPD. <i>PeerJ</i> , 0, 10, e14062.	0.9	1
29030	Cross-Talk of Protein Expression and Lysine Acetylation in Response to TMV Infection in <i>Nicotiana benthamiana</i> . <i>ACS Omega</i> , 2022, 7, 32496-32511.	1.6	0
29031	Quercetin attenuates viral infections by interacting with target proteins and linked genes in chemico-biological models. <i>In Silico Pharmacology</i> , 2022, 10, .	1.8	10
29032	Multi-omics analysis to characterize molecular adaptation of <i>Entamoeba histolytica</i> during serum stress. <i>Proteomics</i> , 2022, 22, .	1.3	0
29033	Association of Metabolic Signatures with Nonalcoholic Fatty Liver Disease in Pediatric Population. <i>Metabolites</i> , 2022, 12, 881.	1.3	3
29035	A stem cell roadmap of ribosome heterogeneity reveals a function for RPL10A in mesoderm production. <i>Nature Communications</i> , 2022, 13, .	5.8	15
29036	Transcriptomic and methylation analysis of susceptible and tolerant grapevine genotypes following <i>Plasmopara viticola</i> infection. <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	5
29037	Unraveling axonal mechanisms of traumatic brain injury. <i>Acta Neuropathologica Communications</i> , 2022, 10, .	2.4	5
29038	DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in glioma. <i>Aging</i> , 2022, 14, 7824-7850.	1.4	1
29039	Histidine kinase inhibitors impair shoot regeneration in <i>Arabidopsis thaliana</i> via cytokinin signaling and SAM patterning determinants. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
29040	Mechanistic Prediction of Chinese Herb Compound (Zhi Zhu Ma Ren Pill) in the Treatment of Constipation Using Network Pharmacology and Molecular Docking. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211247.	0.2	1

#	ARTICLE	IF	CITATIONS
29041	Bioinformatics and systems biology approach to identify the pathogenetic link of Long COVID and Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
29042	Potential Biomarkers and Signaling Pathways Associated with the Pathogenesis of Primary Ameloblastoma: A Systems Biology Approach. <i>International Journal of Dentistry</i> , 2022, 2022, 1-14.	0.5	5
29043	Genome-wide CRISPR screens identify ferroptosis as a novel therapeutic vulnerability in acute lymphoblastic leukemia. <i>Haematologica</i> , 2023, 108, 382-393.	1.7	5
29044	Guanmaitong Granule Attenuates Atherosclerosis by Inhibiting Inflammatory Immune Response in ApoE <sup>-/-</sup> Mice Fed High-Fat Diet. <i>Drug Design, Development and Therapy</i> , 0, Volume 16, 3145-3168.	2.0	1
29045	Differential expression of circRNAs of testes with high and low sperm motility in Yili geese. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
29046	Analysis of Tumor-Infiltrating T-Cell Transcriptomes Reveal a Unique Genetic Signature across Different Types of Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11065.	1.8	4
29047	Comparative physiological and coexpression network analyses reveal the potential drought tolerance mechanism of peanut. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
29048	Bacterial Membrane Vesicles as a Novel Strategy for Extrusion of Antimicrobial Bismuth Drug in <i>Helicobacter pylori</i> . <i>MBio</i> , 2022, 13, .	1.8	7
29049	Genome-Wide Identification of Membrane-Bound Fatty Acid Desaturase Genes in Three Peanut Species and Their Expression in <i>Arachis hypogaea</i> during Drought Stress. <i>Genes</i> , 2022, 13, 1718.	1.0	3
29050	Identification of the effects of COVID-19 on patients with pulmonary fibrosis and lung cancer: a bioinformatics analysis and literature review. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
29051	Metabolization and sequestration of plant specialized metabolites in insect herbivores: Current and emerging approaches. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	4
29052	Improved biomarker discovery through a plot twist in transcriptomic data analysis. <i>BMC Biology</i> , 2022, 20, .	1.7	9
29054	Proteomic characterisation of prostate cancer intercellular communication reveals cell type-selective signalling and TMSB4X-dependent fibroblast reprogramming. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 1311-1328.	2.1	1
29055	RTN2, a new member of circadian clock genes identified by database mining and bioinformatics prediction, is highly expressed in ovarian cancer. <i>Molecular Medicine Reports</i> , 2022, 26, .	1.1	0
29056	Integration of three machine learning algorithms identifies characteristic RNA binding proteins linked with diagnosis, immunity and pyroptosis of IgA nephropathy. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29057	Validation of the application of gel beads-based single-cell genome sequencing platform to soil and seawater. <i>ISME Communications</i> , 2022, 2, .	1.7	15
29058	Screening and verification of prognostic lncRNA markers related to immune infiltration in the metastasis of osteosarcoma. <i>Translational Cancer Research</i> , 2022, 11, 3235-3249.	0.4	0
29059	The Differential Paracrine Role of the Endothelium in Prostate Cancer Cells. <i>Cancers</i> , 2022, 14, 4750.	1.7	1

#	ARTICLE	IF	CITATIONS
29060	Meta-Analytic Comparison of Global RNA Transcriptomes of Acute and Chronic Myeloid Leukemia Cells Reveals Novel Gene Candidates Governing Myeloid Malignancies. <i>Cancers</i> , 2022, 14, 4681.	1.7	1
29061	Proteomic analysis of the regulatory networks of ClpX in a model cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29063	The SPARC complex defines RNAPII promoters in <i>Trypanosoma brucei</i> . <i>ELife</i> , 0, 11, .	2.8	7
29064	Understanding the Function and Mechanism of Zebrafish <i>Tmem39b</i> in Regulating Cold Resistance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11442.	1.8	6
29065	The Molecular Network behind Volatile Aroma Formation in Pear ( <i>Pyrus</i> spp. <i>Panguxiang</i> ) Revealed by Transcriptome Profiling via Fatty Acid Metabolic Pathways. <i>Life</i> , 2022, 12, 1494.	1.1	1
29066	Dereplication of Cytochalasans and Octaketides in Cytotoxic Extracts of Endophytic Fungi from <i>Casearia arborea</i> (Salicaceae). <i>Metabolites</i> , 2022, 12, 903.	1.3	1
29067	Metabolomics-based investigation of SARS-CoV-2 vaccination (Sinovac) reveals an immune-dependent metabolite biomarker. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
29068	Arbovirus-vector protein interactomics identifies Loquacious as a co-factor for dengue virus replication in <i>Aedes</i> mosquitoes. <i>PLoS Pathogens</i> , 2022, 18, e1010329.	2.1	6
29071	Multifaceted investigation underlies diverse mechanisms contributing to the downregulation of Hedgehog pathway-associated genes <i>INTU</i> and <i>IFT88</i> in lung adenocarcinoma and uterine corpus endometrial carcinoma. <i>Aging</i> , 0, , .	1.4	0
29072	An Integrated Approach to Identify Intrinsically Disordered Regions in Osteopontin with its Interacting Network in Rheumatoid Arthritis. <i>Recent Advances in Anti-Infective Drug Discovery</i> , 2023, 18, 69-86.	0.4	1
29073	Antagonism Between <i>DUX4</i> and <i>DUX4c</i> Highlights a Pathomechanism Operating Through $\beta$ -Catenin in Facioscapulohumeral Muscular Dystrophy. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	9
29074	Network pharmacology study of Yishen capsules in the treatment of diabetic nephropathy. <i>PLoS ONE</i> , 2022, 17, e0273498.	1.1	7
29075	MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. <i>MSystems</i> , 2022, 7, .	1.7	15
29076	Identification of signaling pathways associated with <i>achaete-scute</i> homolog 1 in glioblastomas through ChIP-seq data bioinformatics. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
29077	Comprehensive analysis and validation of novel immune and vascular remodeling related genes signature associated with drug interactions in pulmonary arterial hypertension. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
29078	Apatinib enhances chemosensitivity of <i>ABT-199</i> in diffuse large B-cell lymphoma. <i>Molecular Oncology</i> , 2022, 16, 3735-3753.	2.1	1
29079	Clinical significance and potential mechanism of heat shock factor 1 in acute myeloid leukemia. <i>Aging</i> , 2022, 14, 7026-7037.	1.4	0
29082	Identifying potential therapeutic targets for ischemic stroke through immune infiltration analysis and construction of a programmed cell death-related ceRNA network. <i>Experimental and Therapeutic Medicine</i> , 2022, 24, .	0.8	2



#	ARTICLE	IF	CITATIONS
29084	CDC20 May Serve as a Potential Biomarker-Based Risk Score System in Predicting the Prognosis of Patients with Hepatocellular Carcinoma. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-21.	1.9	2
29085	An integrative bioinformatics investigation and experimental validation of critically involved genes in high-grade gliomas. <i>Diagnostic Pathology</i> , 2022, 17, .	0.9	2
29086	Multi-Omics Analysis of GNL3L Expression, Prognosis, and Immune Value in Pan-Cancer. <i>Cancers</i> , 2022, 14, 4595.	1.7	1
29087	Transcriptomic and metabolic signatures of diatom plasticity to light fluctuations. <i>Plant Physiology</i> , 2022, 190, 2295-2314.	2.3	5
29088	Data Processing and Analysis in Mass Spectrometry-Based Metabolomics. <i>Methods in Molecular Biology</i> , 2023, , 207-239.	0.4	0
29089	An Integrative Transcriptional Network Revealed Spatial Molecular Interplay Underlying Alantolactone and Inulin Biosynthesis in <i>Inula racemosa</i> Hook f.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11213.	1.8	1
29090	Identification of kaempferol as an OSX upregulator by network pharmacology-based analysis of qianggu Capsule for osteoporosis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
29093	Network analysis approach to Likert-style surveys. <i>Physical Review Physics Education Research</i> , 2022, 18, .	1.4	2
29094	An immune-related microRNA signature prognostic model for pancreatic carcinoma and association with immune microenvironment. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
29095	Low expression of isocitrate dehydrogenase 1 (IDH1) R132H is associated with advanced pathological features in laryngeal squamous cell carcinoma. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 4253-4267.	1.2	3
29096	Identification of WRKY transcription factor family genes in <i>Pinus massoniana</i> Lamb. and their expression patterns and functions in response to drought stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
29097	Olive- and Coconut-Oil-Enriched Diets Decreased Secondary Bile Acids and Regulated Metabolic and Transcriptomic Markers of Brain Injury in the Frontal Cortexes of NAFLD Pigs. <i>Brain Sciences</i> , 2022, 12, 1193.	1.1	3
29098	Time-course RNA-seq analysis provides an improved understanding of genetic regulation in response to cold stress from white clover ( <i>Trifolium repens</i> L.). <i>Biotechnology and Biotechnological Equipment</i> , 2022, 36, 745-752.	0.5	6
29100	A Study on the Mechanism of Herbal Drug FDY003 for Colorectal Cancer Treatment by Employing Network Pharmacology. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211269.	0.2	0
29101	Later Growth Cessation and Increased Freezing Tolerance Potentially Result in Later Dormancy in Evergreen Iris Compared with Deciduous Iris. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11123.	1.8	2
29102	Dissecting genetic links between Alzheimer's disease and type 2 diabetes mellitus in a systems biology way. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29103	Ayka, a Novel Curtobacterium Bacteriophage, Provides Protection against Soybean Bacterial Wilt and Tan Spot. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10913.	1.8	8
29104	In Vitro Induction of Apoptosis in Isolated Acute Myeloid Leukemia Cells: The Role of <i>Anastatica hierochuntica</i> Methanolic Extract. <i>Metabolites</i> , 2022, 12, 878.	1.3	3

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29105	Comparative transcriptome analysis reveals molecular adaptations underlying distinct immunity and inverted resting posture in bats. <i>Integrative Zoology</i> , 2023, 18, 493-505.	1.3	2
29106	miR-145, miR-92a and miR-375 Show Differential Expression in Serum from Patients with Diabetic Retinopathies. <i>Diagnostics</i> , 2022, 12, 2275.	1.3	4
29107	Transcriptomic profiles of muscular dystrophy with myositis (mdm) in extensor digitorum longus, psoas, and soleus muscles from mice. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
29108	Transcriptomic heterochrony and completely cleistogamous flower development in the mycoheterotrophic orchid <i>Gastrodia</i> . <i>New Phytologist</i> , 2023, 237, 323-338.	3.5	7
29109	Integrated bioinformatics analysis for novel miRNAs markers and ceRNA network in diabetic retinopathy. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29110	Steroidogenic Effects of Salinity Change on the Hypothalamusâ€Pituitaryâ€Gonad (HPG) Axis of Male Chinese Sea Bass ( <i>Lateolabrax maculatus</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 10905.	1.8	1
29112	Visceral Adipose Tissue Molecular Networks and Regulatory microRNA in Pediatric Obesity: An In Silico Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11036.	1.8	5
29113	Transcriptome Analysis of Berries of Spine Grape ( <i>Vitis davidii</i> FÃ¶r ex) Infected by <i>Colletotrichum viniferum</i> during Symptom Development. <i>Horticulturae</i> , 2022, 8, 843.	1.2	4
29114	Bioinformatics analysis reveals the changes of peroxisome proliferator-activated receptor (PPAR) pathway in the development of Marjolin ulcers. <i>International Journal of Transgender Health</i> , 2022, 15, 960-969.	1.1	0
29115	Effects of Let-7c on the processing of hepatitis B virus associated liver diseases. <i>Infectious Agents and Cancer</i> , 2022, 17, .	1.2	0
29116	Integrated network pharmacology analysis, molecular docking, LC-MS analysis and bioassays revealed the potential active ingredients and underlying mechanism of <i>Scutellariae radix</i> for COVID-19. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
29117	Transcriptome and metabolome integration in sugarcane through culm development. <i>Food and Energy Security</i> , 0, , .	2.0	1
29118	Comparative transcriptome meta-analysis reveals a set of genes involved in the responses to multiple pathogens in maize. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
29119	Systematic analysis of MCM3 in pediatric medulloblastoma via multi-omics analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
29120	Protein interactions network of goat innate immune signalling pathway proteins and <i>Haemonchus contortus</i> excretoryâ€secretory proteins. <i>Parasite Immunology</i> , 2022, 44, .	0.7	0
29121	Transcriptomics, Cheminformatics, and Systems Pharmacology Strategies Unveil the Potential Bioactives to Combat COVID-19. <i>Molecules</i> , 2022, 27, 5955.	1.7	5
29122	Tissue-specific pathway activities: A retrospective analysis in COVID-19 patients. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
29123	CAR-T cell therapy-related cytokine release syndrome and therapeutic response is modulated by the gut microbiome in hematologic malignancies. <i>Nature Communications</i> , 2022, 13, .	5.8	35

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29124	The non-glycosylated protein of <i>Toxocara canis</i> MUC-1 interacts with proteins of murine macrophages. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010734.	1.3	2
29125	Lipid metabolism patterns and relevant clinical and molecular features of coronary artery disease patients: an integrated bioinformatic analysis. <i>Lipids in Health and Disease</i> , 2022, 21, .	1.2	3
29126	Proteomic Analysis Identifies Molecular Players and Biological Processes Specific to SARS-CoV-2 Exposure in Endothelial Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10452.	1.8	5
29128	Proteomic changes associated with maternal dietary low n-6:n-3 ratio in piglets supplemented with seaweed. Part I: Serum proteomes. <i>Journal of Proteomics</i> , 2023, 270, 104740.	1.2	0
29129	Irradiation potentiates p53 phosphorylation and p53 binding to the promoter and coding region of the TP53 gene. <i>Biochimie</i> , 2023, 204, 154-168.	1.3	2
29132	Diverse selection pressures shaping the genetic architecture of behaviour disease susceptibility. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29133	An in-silico approach to studying a very rare neurodegenerative disease using a disease with higher prevalence with shared pathways and genes: Cerebral adrenoleukodystrophy and Alzheimer's disease. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	3
29134	Landscape of immune infiltration in entorhinal cortex of patients with Alzheimer's disease. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
29135	Revealing bacteria-phage interactions in human microbiome through the CRISPR-Cas immune systems. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
29136	The Potential Connection between Molecular Changes and Biomarkers Related to ALS and the Development and Regeneration of CNS. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11360.	1.8	3
29137	Autonomous Innovations in Rural Communities of Developing Countries II—Causal Network and Leverage Point Analyses of Transformations. <i>Sustainability</i> , 2022, 14, 12054.	1.6	2
29138	Proteome Analysis of Swine Macrophages after Infection with Two Genotype II African Swine Fever Isolates of Different Pathogenicity. <i>Viruses</i> , 2022, 14, 2140.	1.5	2
29139	Transcriptome Analysis of Immune Response against <i>Streptococcus agalactiae</i> Infection in the Nile Tilapia GIFT Strain. <i>Fishes</i> , 2022, 7, 246.	0.7	0
29140	Long-term excessive application of K <sub>2</sub> SO <sub>4</sub> fertilizer alters bacterial community and functional pathway of tobacco-planting soil. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
29142	On the Tracks of the Aggregation Mechanism of the PHF6 Peptide from Tau Protein: Molecular Dynamics, Energy, and Interaction Network Investigations. <i>ACS Chemical Neuroscience</i> , 2022, 13, 2874-2887.	1.7	4
29143	The protein-protein interaction landscape of transcription factors during gynoecium development in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2023, 16, 260-278.	3.9	8
29144	Prenatal immune stress blunts microglia reactivity, impairing neurocircuitry. <i>Nature</i> , 2022, 610, 327-334.	13.7	30
29145	Product Specificity of C4-Reductases in the Biosynthesis of GDP-6-Deoxy-Heptoses during Capsular Polysaccharide Formation in <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2022, 61, 2138-2147.	1.2	6

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29146	Specialised chemistry affects insect abundance but not overall community similarity in three rare shrub willows: <i>Salix myrtilloides</i> , <i>S. repens</i> and <i>S. rosmarinifolia</i> . <i>European Journal of Entomology</i> , 0, 119, 368-378.	1.2	2
29147	KCTD9 inhibits the Wnt/ $\beta$ -catenin pathway by decreasing the level of $\beta$ -catenin in colorectal cancer. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	7
29148	Individualized Diagnosis and Prescription in Traditional Medicine: Decision-Making Process Analysis and Machine Learning-Based Analysis Tool Development. <i>The American Journal of Chinese Medicine</i> , 2022, 50, 1827-1844.	1.5	1
29149	Impacts of Japanese Larch Invasion on Soil Bacterial Communities of the Giant Panda Habitat in the Qinling Mountains. <i>Microorganisms</i> , 2022, 10, 1807.	1.6	2
29151	Combined Evaluation of mRNA and Protein Expression, Promoter Methylation, and Immune Infiltration of UBE2I in Pan-Digestive System Tumors. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-20.	1.9	1
29152	Ferroptosis is involved in corpus cavernosum smooth muscle cells impairment in diabetes mellitus-induced erectile dysfunction. <i>Andrology</i> , 2023, 11, 332-343.	1.9	8
29153	Estuarine microbial networks and relationships vary between environmentally distinct communities. <i>PeerJ</i> , 0, 10, e14005.	0.9	1
29154	Bioinformatics analysis identifies potential biomarkers involved in the metastasis of locoregionally advanced nasopharyngeal carcinoma. <i>Medicine (United States)</i> , 2022, 101, e30126.	0.4	3
29156	Integrated PPI- and WGCNA-retrieval of hub gene signatures for soft substrates inhibition of human fibroblasts proliferation and differentiation. <i>Aging</i> , 2022, 14, 6957-6974.	1.4	1
29158	Insight into the Fecal Microbiota Signature Associated with Growth Specificity in Korean Jindo Dogs Using 16S rRNA Sequencing. <i>Animals</i> , 2022, 12, 2499.	1.0	1
29159	Analysis of the Function of LncRNA-MSTRG.16919.1 in BHV-1-infected Bovine Kidney Subculture Cells by Transcriptome Sequencing. <i>Viruses</i> , 2022, 14, 2104.	1.5	0
29160	RNF4-RGMB-BMP6 axis required for osteogenic differentiation and cancer cell survival. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	5
29162	A variable gene family encoding nodule-specific cysteine-rich peptides in pea ( <i>Pisum sativum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
29163	Integrative Bioinformatics Analysis Reveals That miR-524-5p/MEF2C Regulates Bone Metastasis in Prostate Cancer and Breast Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	2
29164	Characterization of chromatin regulators identified prognosis and heterogeneity in hepatocellular carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
29165	4D genetic networks reveal the genetic basis of metabolites and seed oil-related traits in 398 soybean RILs. , 2022, 15, .		7
29167	Deciphering the Global Proteomic Profile Involved in Methylmercury-Induced Cerebellar Neurodegeneration and Motor Dysfunction in Adult Rats. <i>Toxics</i> , 2022, 10, 531.	1.6	1
29168	COVID-19 Salivary Protein Profile: Unravelling Molecular Aspects of SARS-CoV-2 Infection. <i>Journal of Clinical Medicine</i> , 2022, 11, 5571.	1.0	0

#	ARTICLE	IF	CITATIONS
29169	Analysis of <i>Camellia oleifera</i> transcriptome reveals key pathways and hub genes involved during different photoperiods. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
29170	Functional genomics uncovers the transcription factor BNC2 as required for myofibroblastic activation in fibrosis. <i>Nature Communications</i> , 2022, 13, .	5.8	11
29171	Characteristics of soil microbiota and organic carbon distribution in jackfruit plantation under different fertilization regimes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
29173	Blood-based protein biomarkers for the diagnosis of acute stroke: A discovery-based SWATH-MS proteomic approach. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	5
29174	Microbial co-occurrence network in the rhizosphere microbiome: its association with physicochemical properties and soybean yield at a regional scale. <i>Journal of Microbiology</i> , 2022, 60, 986-997.	1.3	3
29175	A novel prognostic biomarker CD3G that correlates with the tumor microenvironment in cervical cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	5
29176	Comparative transcriptomics of <i>Pinus massoniana</i> organs provides insights on terpene biosynthesis regulation. <i>Physiologia Plantarum</i> , 0, , .	2.6	2
29177	Loss of SNAI1 induces cellular plasticity in invasive triple-negative breast cancer cells. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	4
29178	Bioinformatics analysis of inflammation and oncology in pulmonary lymphangiomyomatosis. <i>Medicine (United States)</i> , 2022, 101, e30593.	0.4	0
29179	SARS-CoV-2 infects adipose tissue in a fat depot- and viral lineage-dependent manner. <i>Nature Communications</i> , 2022, 13, .	5.8	27
29181	Identification of key pathways and genes that regulate cashmere development in cashmere goats mediated by exogenous melatonin. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
29182	Investigating the cardioprotective effects of Fuzheng Yangxin recipe based on network pharmacology and experimental evaluation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
29183	Hippocampal cells segregate positive and negative engrams. <i>Communications Biology</i> , 2022, 5, .	2.0	19
29184	Transcriptomic and proteomic analyses provide insights into the adaptive responses to the combined impact of salinity and alkalinity in <i>Gymnocypris przewalskii</i> . <i>Bioresources and Bioprocessing</i> , 2022, 9, .	2.0	3
29185	Comprehensive analysis of immune-related biomarkers and pathways in intracerebral hemorrhage using weighted gene co-expression network analysis and competing endogenous ribonucleic acid. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	3
29186	Gene activation of metazoan Fox transcription factors at the onset of metamorphosis in the marine demosponge <i>Amphimedon queenslandica</i> . <i>Development Growth and Differentiation</i> , 2022, 64, 455-468.	0.6	2
29187	Sugarcane Rhizosphere Bacteria Community Migration Correlates with Growth Stages and Soil Nutrient. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10303.	1.8	1
29188	Genome-Wide Identification and Characterization of Heat Shock Protein 20 Genes in Maize. <i>Life</i> , 2022, 12, 1397.	1.1	3

#	ARTICLE	IF	CITATIONS
29190	Overview of methods for characterization and visualization of a proteinâ€“protein interaction network in a multi-omics integration context. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
29191	Protein Interaction Networks of Catalytically Active and Catalytically Inactive PqsE in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2022, 13, .	1.8	1
29192	Indole and p-cresol in feces of healthy subjects: Concentration, kinetics, and correlation with microbiome. <i>Frontiers in Molecular Medicine</i> , 0, 2, .	0.6	5
29193	Integrated Bioinformatics and Validation of lncRNA-Mediated ceRNA Network in Myocardial Ischemia/Reperfusion Injury. <i>Journal of Immunology Research</i> , 2022, 2022, 1-13.	0.9	7
29194	Integrated identification of key immune related genes and patterns of immune infiltration in calcified aortic valvular disease: A network based meta-analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
29195	Deciphering the lncRNA and mRNA profiles of Min pig backfat after acute cold stress. <i>Journal of Applied Animal Research</i> , 2022, 50, 620-628.	0.4	0
29197	H19 may regulate the immune cell infiltration in carcinogenesis of gastric cancer through miR-378a-5p/SERPINH1 signaling. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	3
29198	Comparison of allosteric signaling in <scp>DnaK</scp> and <scp>BiP</scp> using mutual information between simulated residue conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 237-255.	1.5	2
29199	Mechanisms of Banxia Xiexin Decoction Underlying Chronic Atrophic Gastritis via Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulations. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	1
29200	Key factors for differential drought tolerance in two contrasting wild materials of <i>Artemisia wellbyi</i> identified using comparative transcriptomics. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
29201	Nonsense-Mediated Decay Targeted RNA (ntRNA): Proposal of a ntRNAâ€“miRNAâ€“lncRNA Triple Regulatory Network Usable as Biomarker of Prognostic Risk in Patients with Kidney Cancer. <i>Genes</i> , 2022, 13, 1656.	1.0	0
29202	Co-overexpression of AtSAT1 and EcPAPR improves seed nutritional value in maize. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
29203	Biopsy and blood-based molecular biomarker of inflammation in IBD. <i>Gut</i> , 2023, 72, 1271-1287.	6.1	18
29204	Identification of Inflammation-Related Genes and Exploration of Regulatory Mechanisms in Patients with Osteonecrosis of the Femoral Head. <i>BioMed Research International</i> , 2022, 2022, 1-21.	0.9	2
29205	Metabolome genomeâ€“wide association study provides biochemical and genetic insights into natural variation of primary metabolites in sesame. <i>Plant Journal</i> , 2022, 112, 1051-1069.	2.8	2
29207	Network pharmacology-based screening of the active ingredients and mechanisms of <i>evodiae fructus</i> anti-glioblastoma multiforme. <i>Medicine (United States)</i> , 2022, 101, e30853.	0.4	1
29208	The RPN12a proteasome subunit is essential for the multiple hormonal homeostasis controlling the progression of leaf senescence. <i>Communications Biology</i> , 2022, 5, .	2.0	2
29209	Age-Associated Different Transcriptome Profiling in Zebrafish and Rats: an Insight into the Diversity of Vertebrate Aging. <i>Marine Biotechnology</i> , 2022, 24, 895-910.	1.1	4



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29213	An Integrated Proteomic Strategy to Identify SHP2 Substrates. <i>Journal of Proteome Research</i> , 2022, 21, 2515-2525.	1.8	4
29214	Temporal Proteomic and Phosphoproteomic Analysis of EV-A71-Infected Human Cells. <i>Journal of Proteome Research</i> , 2022, 21, 2367-2384.	1.8	2
29215	Bioinformatics and network-based screening and discovery of potential molecular targets and small molecular drugs for breast cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	6
29216	Most reactions leading to neuropathic pain at dorsal root ganglion of rats with spinal nerve ligation have occurred in the early phase. <i>Animal Gene</i> , 2022, 26, 200138.	0.2	0
29217	CASK loss of function differentially regulates neuronal maturation and synaptic function in human induced cortical excitatory neurons. <i>IScience</i> , 2022, 25, 105187.	1.9	6
29218	The general law of plasma proteome alterations occurring in the lifetime of Chinese individuals reveals the importance of immunity. <i>Aging</i> , 2022, 14, 7065-7092.	1.4	0
29220	T cell proliferation-related genes: Predicting prognosis, identifying the cold and hot tumors, and guiding treatment in clear cell renal cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
29221	Proper acquisition of cell class identity in organoids allows definition of fate specification programs of the human cerebral cortex. <i>Cell</i> , 2022, 185, 3770-3788.e27.	13.5	56
29223	GBP2 acts as a member of the interferon signalling pathway in lupus nephritis. <i>BMC Immunology</i> , 2022, 23, .	0.9	1
29224	Genetic analyses of the electrocardiographic QT interval and its components identify additional loci and pathways. <i>Nature Communications</i> , 2022, 13, .	5.8	15
29225	Candidates for drug repurposing to address the cognitive symptoms in schizophrenia. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2023, 120, 110637.	2.5	0
29226	Root and shoot biology of <i>Arabidopsis halleri</i> dissected by WGCNA: an insight into the organ pivotal pathways and genes of an hyperaccumulator. <i>Functional and Integrative Genomics</i> , 2022, 22, 1159-1172.	1.4	3
29227	Whole-exome Sequencing of Nigerian Prostate Tumors from the Prostate Cancer Transatlantic Consortium (CaPTC) Reveals DNA Repair Genes Associated with African Ancestry. <i>Cancer Research Communications</i> , 2022, 2, 1005-1016.	0.7	8
29230	Gut and Gill-Associated Microbiota of the Flatfish European Plaice ( <i>Pleuronectes platessa</i> ): Diversity, Metabolome and Bioactivity against Human and Aquaculture Pathogens. <i>Marine Drugs</i> , 2022, 20, 573.	2.2	6
29231	In-Silico Drug Toxicity and Interaction Prediction for Plant Complexes Based on Virtual Screening and Text Mining. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10056.	1.8	0
29232	IRF7 expression correlates with HIV latency reversal upon specific blockade of immune activation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
29233	C3- and C3/C5-Epimerases Required for the Biosynthesis of the Capsular Polysaccharides from <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2022, 61, 2036-2048.	1.2	8
29234	Oncohistone interactome profiling uncovers contrasting oncogenic mechanisms and identifies potential therapeutic targets in high grade glioma. <i>Acta Neuropathologica</i> , 2022, 144, 1027-1048.	3.9	10

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29235	Identification and Analysis of MADS-box, WRKY, NAC, and SBP-box Transcription Factor Families in <i>Diospyros oleifera</i> Cheng and Their Associations with Sex Differentiation. <i>Agronomy</i> , 2022, 12, 2100.	1.3	1
29236	Genetic Mechanism Study of Auditory Phoenix Spheres and Transcription Factors Prediction for Direct Reprogramming by Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10287.	1.8	2
29237	Pan-cancer analyses reveal cancer-type-specific fungal ecologies and bacteriome interactions. <i>Cell</i> , 2022, 185, 3789-3806.e17.	13.5	163
29238	MVsim is a toolset for quantifying and designing multivalent interactions. <i>Nature Communications</i> , 2022, 13, .	5.8	1
29239	Whole-Genome Sequence Analysis of an Endophytic Fungus <i>Alternaria</i> sp. SPS-2 and Its Biosynthetic Potential of Bioactive Secondary Metabolites. <i>Microorganisms</i> , 2022, 10, 1789.	1.6	6
29240	Spatial Genomic Resource Reveals Molecular Insights into Key Bioactive-Metabolite Biosynthesis in Endangered <i>Angelica glauca</i> Edgew. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11064.	1.8	1
29241	Decoding the Mechanism of CheReCunjin Formula in Treating Sjögren's Syndrome Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	0
29242	Identification of Hub Genes and Potential Biomarkers for Childhood Asthma by Utilizing an Established Bioinformatic Analysis Approach. <i>Biomedicines</i> , 2022, 10, 2311.	1.4	2
29243	Mechanism of Shizi Sanhua Decoction on Male Oligospermia Revealed by Herbs-Ingredients and Disease Co-Target Genes Sub-Network. <i>Current Bioinformatics</i> , 2022, 17, 937-945.	0.7	1
29244	Comprehensive In Silico Analysis of RNA Silencing-Related Genes and Their Regulatory Elements in Wheat ( <i>Triticum aestivum</i> L.). <i>BioMed Research International</i> , 2022, 2022, 1-26.	0.9	5
29245	Hub Genes and Long Noncoding RNAs That Regulates It Associated with the Prognosis of Esophageal Squamous Cell Carcinoma Based on Bioinformatics Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	1
29246	Identification of Potential miRNA-mRNA Regulatory Network Contributing to Parkinson's Disease. <i>Parkinson's Disease</i> , 2022, 2022, 1-12.	0.6	4
29247	Peripheral Blood circRNA Microarray Profiling Identifies hsa_circ_0001831 and hsa_circ_0000867 as Two Novel circRNA Biomarkers for Early Type 2 Diabetic Nephropathy. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 0, Volume 15, 2789-2801.	1.1	7
29248	Activation of CCL21-GPR174/CCR7 on cardiac fibroblasts underlies myocardial ischemia/reperfusion injury. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
29249	Prognostic Value, Immune Signature, and Molecular Mechanisms of the PHLDA Family in Pancreatic Adenocarcinoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10316.	1.8	4
29250	Identification of key genes and mechanisms of epicardial adipose tissue in patients with diabetes through bioinformatic analysis. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	3
29251	Comparative transcriptome analysis of longissimus dorsi tissues with different intramuscular fat contents from Guangling donkeys. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
29252	Biological Assay-Guided Fractionation and Mass Spectrometry-Based Metabolite Profiling of <i>Annona muricata</i> L. Cytotoxic Compounds against Lung Cancer A549 Cell Line. <i>Plants</i> , 2022, 11, 2380.	1.6	3

#	ARTICLE	IF	CITATIONS
29253	Single-cell transcriptomics reveals skewed cellular communication and phenotypic shift in pulmonary artery remodeling. <i>JCI Insight</i> , 2022, 7, .	2.3	13
29254	Expression profiling suggests the involvement of hormone-related, metabolic, and Wnt signaling pathways in pterygium progression. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	0
29255	Identification, characterization, and expression profiling of the putative U-box E3 ubiquitin ligase gene family in <i>Sorghum bicolor</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
29256	Identification of Putative Neuropeptides That Alter the Behaviour of <i>Schistosoma mansoni</i> Cercariae. <i>Biology</i> , 2022, 11, 1344.	1.3	1
29257	Transcriptional regulation of proanthocyanidin biosynthesis pathway genes and transcription factors in <i>Indigofera stachyodes</i> Lindl. roots. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
29258	Pregestational diabetes alters cardiac structure and function of neonatal rats through developmental plasticity. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	6
29259	The coral <i>Acropora loripes</i> genome reveals an alternative pathway for cysteine biosynthesis in animals. <i>Science Advances</i> , 2022, 8, .	4.7	10
29260	Screening of potential key ferroptosis-related genes in sepsis. <i>PeerJ</i> , 0, 10, e13983.	0.9	5
29262	Construction and validation of a prognostic model with RNA binding protein-related mRNAs for the HBV-related hepatocellular carcinoma patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
29264	Integrating diverse layers of omic data to identify novel drug targets in <i>Listeria monocytogenes</i> . <i>Frontiers in Drug Discovery</i> , 0, 2, .	1.1	4
29266	Exploring the Ferroptosis Mechanism of Zhilong Huoxue Tongyu Capsule for the Treatment of Intracerebral Hemorrhage Based on Network Pharmacology and In Vivo Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	0
29268	Molecular Classification of Hepatocellular Carcinoma Using Wnt/Hippo Signaling Pathway-Related Genes. <i>Cancers</i> , 2022, 14, 4580.	1.7	3
29269	A regulatory network comprising <i>let-7</i> miRNA and SMUG1 is associated with good prognosis in ER+ breast tumours. <i>Nucleic Acids Research</i> , 2022, 50, 10449-10468.	6.5	3
29274	Genetic analysis of GEFs and GDIs in rice reveals the roles of OsGEF5, OsGDI1, and OsGEF3 in the regulation of grain size and plant height. <i>Crop Journal</i> , 2023, 11, 345-360.	2.3	1
29275	JAZF1: A Metabolic Regulator of Sensitivity to a Polyamine-Targeted Therapy. <i>Molecular Cancer Research</i> , 2023, 21, 24-35.	1.5	0
29276	circGPA: circRNA functional annotation based on probability-generating functions. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
29277	Targeting the succinate receptor effectively inhibits periodontitis. <i>Cell Reports</i> , 2022, 40, 111389.	2.9	10
29278	A Bioinformatic Approach Based on Systems Biology to Determine the Effects of SARS-CoV-2 Infection in Patients with Hypertrophic Cardiomyopathy. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	1

#	ARTICLE	IF	CITATIONS
29279	Cell-type identity of the avian utricle. <i>Cell Reports</i> , 2022, 40, 111432.	2.9	4
29280	Genome-wide Mendelian randomization identifies actionable novel drug targets for psychiatric disorders. <i>Neuropsychopharmacology</i> , 2023, 48, 270-280.	2.8	12
29281	Single-cell transcriptome reveals cellular hierarchies and guides p-EMT-targeted trial in skull base chordoma. <i>Cell Discovery</i> , 2022, 8, .	3.1	12
29282	Deciphering the Role of Aquaporins Under Different Abiotic Stress Conditions in Watermelon ( <i>Citrullus lanatus</i> ). <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	3
29283	Characterization of glucose metabolism in breast cancer to guide clinical therapy. <i>Frontiers in Surgery</i> , 0, 9, .	0.6	3
29284	Network Analysis of the Herbâ€™Drug Interactions of Citrus Herbs Inspired by the â€™Grapefruit Juice Effectâ€™. <i>ACS Omega</i> , 2022, 7, 35911-35923.	1.6	5
29285	Bioinformatic Atlas of Radical SAM Enzyme-Modified RiPP Natural Products Reveals an Isoleucineâ€™Tryptophan Crosslink. <i>Journal of the American Chemical Society</i> , 2022, 144, 17876-17888.	6.6	26
29286	Multi-omic integration by machine learning (MIMaL). <i>Bioinformatics</i> , 2022, 38, 4908-4918.	1.8	5
29287	Identification of potential biomarkers and pathogenesis in neutrophil-predominant severe asthma: A comprehensive bioinformatics analysis. <i>Medicine (United States)</i> , 2022, 101, e30661.	0.4	4
29288	Dynamic transcriptome and network-based analysis of yellow leaf mutant <i>Ginkgo biloba</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
29289	Comprehensive phylogenetic analysis of the ribonucleotide reductase family reveals an ancestral clade. <i>ELife</i> , 0, 11, .	2.8	9
29290	Identification of the 14-3-3 Gene Family in Bamboo and Characterization of Pe14-3-3b Reveals Its Potential Role in Promoting Growth. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11221.	1.8	5
29291	Meta-Analysis of SNPs Determining Litter Traits in Pigs. <i>Genes</i> , 2022, 13, 1730.	1.0	5
29292	Combining NMR and MS to Describe Pyrrole-2-Carbaldehydes in Wheat Bran of Radiation. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 13002-13014.	2.4	2
29293	What Drives the Assembly of Plant-associated Protist Microbiomes? Investigating the Effects of Crop Species, Soil Type and Bacterial Microbiomes. <i>Protist</i> , 2022, 173, 125913.	0.6	5
29294	Colonization characteristics of fungi in <i>Polygonum hydropiper</i> L. and <i>Polygonum lapathifolium</i> L. and its effect on the content of active ingredients. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
29295	Silicon fertilizer mediated structural variation and niche differentiation in the rhizosphere and endosphere bacterial microbiome and metabolites of sugarcane. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
29296	Identification of hub genes for early detection of bone metastasis in breast cancer. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4

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29297	Network analysis reveals microbe-mediated impacts of aeration on deep sediment layer microbial communities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
29299	Metformin regulates multiple signaling pathways within castration-resistant human prostate cancer cells. <i>BMC Cancer</i> , 2022, 22, .	1.1	5
29300	Autologous Protein Solution processing alters lymphoid and myeloid cell populations and modulates gene expression dependent on cell type. <i>Arthritis Research and Therapy</i> , 2022, 24, .	1.6	1
29301	Mouse models of COVID-19 recapitulate inflammatory pathways rather than gene expression. <i>PLoS Pathogens</i> , 2022, 18, e1010867.	2.1	17
29302	The roles of divergent and parallel molecular evolution contributing to thermal adaptive strategies in trees. <i>Plant, Cell and Environment</i> , 0, , .	2.8	1
29303	Lead-exposure associated miRNAs in humans and Alzheimer's disease as potential biomarkers of the disease and disease processes. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
29304	A Comparative Cross-Platform Analysis to Identify Potential Biomarker Genes for Evaluation of Teratozoospermia and Azoospermia. <i>Genes</i> , 2022, 13, 1721.	1.0	1
29305	Role of the Gut Microbiota in the Increased Infant Body Mass Index Induced by Gestational Diabetes Mellitus. <i>MSystems</i> , 2022, 7, .	1.7	10
29306	Exploration of Biomarkers of Psoriasis through Combined Multiomics Analysis. <i>Mediators of Inflammation</i> , 2022, 2022, 1-25.	1.4	7
29307	Genome-Wide Identification and Expression Analysis of the Zinc Finger Protein Gene Subfamilies under Drought Stress in <i>Triticum aestivum</i> . <i>Plants</i> , 2022, 11, 2511.	1.6	5
29308	Microarray and Bioinformatics Analysis of Differential Gene and lncRNA Expression during Erythropoietin Treatment of Acute Spinal Cord Injury in Rats. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	1
29313	The transcriptome expression levels related to ovulation induction and acupuncture protection therapy in rats through gene microarray. <i>International Journal of Transgender Health</i> , 2022, 15, 1013-1024.	1.1	0
29314	Molecular Mechanisms Underlying Qi-Invigorating Effects in Traditional Medicine: Network Pharmacology-Based Study on the Unique Functions of Qi-Invigorating Herb Group. <i>Plants</i> , 2022, 11, 2470.	1.6	2
29315	Identification of stage-associated exosome miRNAs in colorectal cancer by improved robust and corroborative approach embedded miRNA-target network. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	1
29316	Comparative transcriptome analysis reveals key pathways and genes involved in trichome development in tea plant ( <i>Camellia sinensis</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29317	Microarray meta-analysis reveals IL6 and p38 <sup>β</sup> /MAPK11 as potential targets of hsa-miR-124 in endothelial progenitor cells: Implications for stent re-endothelization in diabetic patients. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	1
29318	Noncoding RNAs responsive to nitric oxide and their protein-coding gene targets shed light on root hair formation in <i>Arabidopsis thaliana</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29320	Transcriptome Analysis of Human Endogenous Retroviruses at Locus-Specific Resolution in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2022, 14, 4433.	1.7	3

#	ARTICLE	IF	CITATIONS
29321	Integrating Text Mining into the Curation of Disease Maps. <i>Biomolecules</i> , 2022, 12, 1278.	1.8	1
29323	An Integrative Multi-Omics Analysis Based on Nomogram for Predicting Prostate Cancer Bone Metastasis Incidence. <i>Genetical Research</i> , 2022, 2022, 1-17.	0.3	1
29324	Transcriptomic analysis of mRNA expression in giant congenital melanocytic nevi. <i>Gene</i> , 2023, 850, 146894.	1.0	0
29325	A transcriptome-wide association study of uterine fibroids to identify potential genetic markers and toxic chemicals. <i>PLoS ONE</i> , 2022, 17, e0274879.	1.1	3
29326	Bioinformatics algorithm for lung adenocarcinoma based on macropinocytosis-related long noncoding RNAs as a reliable indicator for predicting survival outcomes and selecting suitable anti-tumor drugs. <i>Medicine (United States)</i> , 2022, 101, e30543.	0.4	0
29329	Identification of hub genes associated with acute kidney injury induced by renal ischemia–reperfusion injury in mice. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	6
29330	Systems Network Pharmacology-Based Prediction and Analysis of Potential Targets and Pharmacological Mechanism of <i>Actinidia chinensis</i> Planch. Root Extract for Application in Hepatocellular Carcinoma. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-17.	0.5	1
29331	WGCNA Identifies a Comprehensive and Dynamic Gene Co-Expression Network That Associates with Smut Resistance in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10770.	1.8	18
29332	Genome-Wide Identification, Evolution, and Expression Analysis of GASA Gene Family in <i>Prunus mume</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 10923.	1.8	8
29333	Comprehensive analysis of m6A/m5C/m1A-related gene expression, immune infiltration, and sensitivity of antineoplastic drugs in glioma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
29334	The global integrative network: integration of signaling and metabolic pathways. <i>ABIOTECH</i> , 2022, 3, 281-291.	1.8	3
29335	Gene Regulation during Carapacial Ridge Development of <i>Mauremys reevesii</i> : The Development of Carapacial Ridge, Ribs and Scutes. <i>Genes</i> , 2022, 13, 1676.	1.0	0
29337	Proteomic Investigation over the Antimicrobial Photodynamic Therapy Mediated by Rose Bengal Against <i>Staphylococcus aureus</i> . <i>Photochemistry and Photobiology</i> , 0, , .	1.3	1
29338	The microbiome-derived metabolite TMAO drives immune activation and boosts responses to immune checkpoint blockade in pancreatic cancer. <i>Science Immunology</i> , 2022, 7, .	5.6	74
29339	Drug repurposing candidates to treat core symptoms in autism spectrum disorder. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
29340	Mechanism of <i>Salvia miltiorrhiza</i> Bge. for the Treatment of Ischemic Stroke Based on Bioinformatics and Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	1
29341	TRAF3IP3 promotes glioma progression through the ERK signaling pathway. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
29342	Identification of potential biomarkers and pathways associated with carotid atherosclerotic plaques in type 2 diabetes mellitus: A transcriptomics study. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	19



#	ARTICLE	IF	CITATIONS
29343	Characterization of differentially expressed and lipid metabolism-related lncRNA-mRNA interaction networks during the growth of liver tissue through rabbit models. <i>Frontiers in Veterinary Science</i> , 2022, 9, .	0.9	0
29344	Identification and Characterization of Circular RNAs Involved in the Flower Development and Senescence of <i>Rhododendron delavayi</i> Franch. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11214.	1.8	1
29345	Proteomic features of skeletal muscle adaptation to resistance exercise training as a function of age. <i>GeroScience</i> , 2023, 45, 1271-1287.	2.1	9
29346	Identifying celiac disease-related chemicals by transcriptome-wide association study and chemical-gene interaction analyses. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
29347	The Molecular Mechanisms of <i>Panax ginseng</i> in Treating Type 2 Diabetes Mellitus: Network Pharmacology Analysis and Molecular Docking Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	3
29348	Unveiling the Mechanism of the Traditional Korean Medicinal Formula FDY003 on Glioblastoma Through a Computational Network Pharmacology Approach. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211263.	0.2	0
29349	Neddylation pattern indicates tumor microenvironment characterization and predicts prognosis in lung adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	3
29350	Temporal dysregulation of genes in lamb testis cell during sheeppox virus infection. <i>Letters in Applied Microbiology</i> , 2022, .	1.0	0
29351	Unveiling the molecular features, relevant immune and clinical characteristics of SIGLEC15 in thyroid cancer. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	3
29353	Identification of AP2/ERF Transcription Factor Family Genes and Expression Patterns in Response to Drought Stress in <i>Pinus massoniana</i> . <i>Forests</i> , 2022, 13, 1430.	0.9	2
29354	Transcription analysis of chicken embryo fibroblast cells infected with the recombinant avian leukosis virus isolate GX14FF03. <i>Archives of Virology</i> , 2022, 167, 2613-2621.	0.9	1
29355	Decoding the formation of diverse petal colors of <i>Lagerstroemia indica</i> by integrating the data from transcriptome and metabolome. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
29356	Proteotype coevolution and quantitative diversity across 11 mammalian species. <i>Science Advances</i> , 2022, 8, .	4.7	10
29357	Investigation of Anti-Liver Cancer Activity of the Herbal Drug FDY003 Using Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	0
29358	Identification of Novel Loci Involved in Adalimumab Response in Crohn's Disease Patients Using Integration of Genome Profiling and Isoform-Level Immune-Cell Deconvoluted Transcriptome Profiling of Colon Tissue. <i>Pharmaceutics</i> , 2022, 14, 1893.	2.0	2
29359	Calcium dobesilate efficiency in the treatment of diabetic kidney disease through suppressing MAPK and chemokine signaling pathways based on clinical evaluation and network pharmacology. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	2
29360	Rad54L promotes bladder cancer progression by regulating cell cycle and cell senescence. <i>Cell Death and Disease</i> , 2022, 39, .		4
29361	IFI44 is an immune evasion biomarker for SARS-CoV-2 and <i>Staphylococcus aureus</i> infection in patients with RA. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	12

#	ARTICLE	IF	CITATIONS
29362	Transcriptome analysis of Homo sapiens and Mus musculus reveals mechanisms of CD8+ T cell exhaustion caused by different factors. PLoS ONE, 2022, 17, e0274494.	1.1	3
29363	NOX4 has the potential to be a biomarker associated with colon cancer ferroptosis and immune infiltration based on bioinformatics analysis. Frontiers in Oncology, 0, 12, .	1.3	4
29364	Genetic regulation of RNA splicing in human pancreatic islets. Genome Biology, 2022, 23, .	3.8	10
29365	Whole-transcriptome sequencing data reveals a disparate cognitive and immune signature in COVID-19 patients with and without dementia. Journal of Medical Virology, 2023, 95, .	2.5	1
29367	Mining Potential Drug Targets and Constructing Diagnostic Models for Heart Failure Based on miRNA-mRNA Networks. Mediators of Inflammation, 2022, 2022, 1-21.	1.4	0
29369	Potential biomarkers and immune characteristics of small bowel adenocarcinoma. Scientific Reports, 2022, 12, .	1.6	5
29370	HSPA1A, HSPA2, and HSPA8 Are Potential Molecular Biomarkers for Prognosis among HSP70 Family in Alzheimer's Disease. Disease Markers, 2022, 2022, 1-16.	0.6	9
29371	Muscle atrophy phenotype gene expression during spaceflight is linked to a metabolic crosstalk in both the liver and the muscle in mice. IScience, 2022, 25, 105213.	1.9	6
29372	Overexpression of cotton GhNAC072 gene enhances drought and salt stress tolerance in transgenic Arabidopsis. BMC Genomics, 2022, 23, .	1.2	8
29373	Cytokine responsive networks in human colonic epithelial organoids unveil a molecular classification of inflammatory bowel disease. Cell Reports, 2022, 40, 111439.	2.9	10
29374	Survival-based bioinformatics analysis to identify hub long non-coding RNAs along with lncRNA-miRNA-mRNA network for potential diagnosis/prognosis of thyroid cancer. Journal of Cell Communication and Signaling, 2023, 17, 639-655.	1.8	6
29375	Single-cell transcriptome landscape and antigen receptor dynamic during SARS-CoV-2 vaccination. Genes and Diseases, 2022, , .	1.5	0
29377	Icariin: A Potential Lipid Metabolism Regulator in Osteoarthritis. Natural Product Communications, 2022, 17, 1934578X2211260.	0.2	0
29378	Insulin-like growth factor binding protein 7 (IGFBP7), a link between heart failure and senescence. ESC Heart Failure, 2022, 9, 4167-4176.	1.4	17
29379	Proteomic changes associated with maternal dietary low n-6:n-3 ratio in piglets supplemented with seaweed part II: ileum proteomes. Journal of Proteomics, 2022, , 104739.	1.2	1
29380	Metabarcoding of mycetangia from the Dendroctonus frontalis species complex (Curculionidae: Tj ETQq1 1 0.784314 rgBT /Overlock Microbiology, 0, 13, .	1.5	3
29381	Molecular Insights on Bioactive Compounds against Covid-19: A Network Pharmacological and Computational Study. Current Computer-Aided Drug Design, 2022, 18, 425-439.	0.8	1
29382	Transformer for Gene Expression Modeling (T-GEM): An Interpretable Deep Learning Model for Gene Expression-Based Phenotype Predictions. Cancers, 2022, 14, 4763.	1.7	8

#	ARTICLE	IF	CITATIONS
29383	â€œOmicsâ€•data unveil early molecular response underlying limb regeneration in the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Science Advances</i> , 2022, 8, .	4.7	9
29384	Alternative ANKHD1 transcript promotes proliferation and inhibits migration in uterine corpus endometrial carcinoma. <i>Npj Genomic Medicine</i> , 2022, 7, .	1.7	1
29385	Accurate detection of benign and malignant renal tumor subtypes with MethylBoostER: An epigenetic markerâ€•driven learning framework. <i>Science Advances</i> , 2022, 8, .	4.7	1
29386	Organic Anion Transporters (OAT) and Other SLC22 Transporters in Progression of Renal Cell Carcinoma. <i>Cancers</i> , 2022, 14, 4772.	1.7	4
29387	TIMP-1 Dependent Modulation of Metabolic Profiles Impacts Chemoresistance in NSCLC. <i>Cells</i> , 2022, 11, 3036.	1.8	2
29388	Drug genetic associations with COVID-19 manifestations: a data mining and network biology approach. <i>Pharmacogenomics Journal</i> , 2022, 22, 294-302.	0.9	2
29389	Genome Sequencing and Transcriptome Profiling in Twins Discordant for Mayer-Rokitansky-KÅ¼ster-Hauser Syndrome. <i>Journal of Clinical Medicine</i> , 2022, 11, 5598.	1.0	4
29390	Effects of RAGE Deletion on the Cardiac Transcriptome during Aging. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11130.	1.8	4
29391	The transcriptional coactivator RUVBL2 regulates Pol II clustering with diverse transcription factors. <i>Nature Communications</i> , 2022, 13, .	5.8	11
29392	Multitissue Integrative Analysis Identifies Susceptibility Genes for Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2023, 143, 602-611.e14.	0.3	0
29393	Intestinal microbiome-mediated resistance against vibriosis for <i>Cynoglossus semilaevis</i> . <i>Microbiome</i> , 2022, 10, .	4.9	13
29394	Integration of mRNA and miRNA analysis reveals the differentially regulatory network in two different <i>Camellia oleifera</i> cultivars under drought stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
29396	Progeria and Agingâ€•Omics Based Comparative Analysis. <i>Biomedicines</i> , 2022, 10, 2440.	1.4	3
29397	Integrative Analysis of Motor Neuron and Microglial Transcriptomes from SOD1G93A Mice Models Uncover Potential Drug Treatments for ALS. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 2360-2376.	1.1	5
29398	Transcriptomic analysis of uterine receptivity in Guinea pigs. <i>Biochemical and Biophysical Research Communications</i> , 2022, 634, 145-151.	1.0	0
29399	CRABP2 â€• A novel biomarker for high-risk endometrial cancer. <i>Gynecologic Oncology</i> , 2022, 167, 314-322.	0.6	2
29400	Warming Accelerates the Onset of the Molecular Stress Response and Increases Mortality of Larval Atlantic Cod. <i>Integrative and Comparative Biology</i> , 2022, 62, 1784-1801.	0.9	2
29401	Spatiotemporal dynamics of the tomato fruit transcriptome under prolonged water stress. <i>Plant Physiology</i> , 2022, 190, 2557-2578.	2.3	6

#	ARTICLE	IF	CITATIONS
29402	A review of causal discovery methods for molecular network analysis. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2022, 10, .	0.6	3
29403	Independent phenotypic plasticity axes define distinct obesity sub-types. <i>Nature Metabolism</i> , 2022, 4, 1150-1165.	5.1	12
29404	SUBATOMIC: a SUBgraph BAsed mulTi-OMics clustering framework to analyze integrated multi-edge networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	5
29405	Transcriptome meta-analysis of abiotic stresses-responsive genes and identification of candidate transcription factors for broad stress tolerance in wheat. <i>Protoplasma</i> , 2023, 260, 707-721.	1.0	6
29406	Molecular Mechanisms of Cassia fistula against Epithelial Ovarian Cancer Using Network Pharmacology and Molecular Docking Approaches. <i>Pharmaceutics</i> , 2022, 14, 1970.	2.0	1
29407	Anti-Postmenopausal osteoporosis effects of Isoporsolen: A bioinformatics-integrated experimental study. <i>Phytotherapy Research</i> , 2023, 37, 231-251.	2.8	3
29409	Long-term stimulation with alternating electric fields modulates the differentiation and mineralization of human pre-osteoblasts. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	5
29410	Genome-wide characterization and identification of cyclophilin genes associated with leaf rust resistance in bread wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29411	Characterization of exogenous $\pm$ SN response genes and their relation to Parkinson's disease using network analyses. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
29412	Data Mining and Network Pharmacology Analysis of Kidney-Tonifying Herbs on the Treatment of Renal Osteodystrophy Based on the Theory of "Kidney Governing Bones" in Traditional Chinese Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	2
29413	Deciphering the chemical composition of <i>Ganoderma lucidum</i> from different geographical origins by mass spectrometry molecular networking coupled with multivariate analysis. <i>Biomedical Chromatography</i> , 0, .	0.8	1
29414	Identification of a functional circRNA-miRNA-mRNA regulatory network in infantile hemangioma by bioinformatics analysis. <i>Medicine (United States)</i> , 2022, 101, e30791.	0.4	2
29415	Low expression of the metabolism-related gene SLC25A21 predicts unfavourable prognosis in patients with acute myeloid leukaemia. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
29416	Identification of a novel m5C/m6A-related gene signature for predicting prognosis and immunotherapy efficacy in lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
29417	Visualizing novel connections and genetic similarities across diseases using a network-medicine based approach. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
29418	Expression profile of long non-coding RNA in inner Mongolian cashmere goat with putative roles in hair follicles development. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
29419	Disease- and headache-specific microRNA signatures and their predicted mRNA targets in peripheral blood mononuclear cells in migraineurs: role of inflammatory signalling and oxidative stress. <i>Journal of Headache and Pain</i> , 2022, 23, .	2.5	11
29420	Microbial community structure and niche differentiation under different health statuses of <i>Pinus bungeana</i> in the Xiong'an New Area in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4

#	ARTICLE	IF	CITATIONS
29421	Aberrant mitochondrial homeostasis at the crossroad of musculoskeletal ageing and non-small cell lung cancer. <i>PLoS ONE</i> , 2022, 17, e0273766.	1.1	4
29422	Systematic analysis of prognostic and immunologic characteristics associated with coronavirus disease 2019 regulators in acute myeloid leukemia. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
29423	OpNAC1 transcription factor regulates the biosynthesis of the anticancer drug camptothecin by targeting loganic acid <i>O</i> -methyltransferase in <i>Ophiorrhiza pumila</i> . <i>Journal of Integrative Plant Biology</i> , 2023, 65, 133-149.	4.1	9
29424	Identification of neoplasm-specific signatures of miRNA interactions by employing a systems biology approach. <i>PeerJ</i> , 0, 10, e14149.	0.9	1
29425	Conservation of Allosteric Ligand Binding Sites in G-Protein Coupled Receptors. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 4937-4954.	2.5	12
29426	Protective Mechanisms of Nootropic Herb Shankhpushpi ( <i>Convolvulus pluricaulis</i> ) against Dementia: Network Pharmacology and Computational Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	3
29427	Comparative genomic analysis of N6-methyladenosine regulators in nine rosaceae species and functional characterization in response to drought stress in pear. <i>Horticultural Plant Journal</i> , 2023, 9, 693-704.	2.3	2
29429	Characterization of serum protein expression profiles in the early sarcopenia older adults with low grip strength: a cross-sectional study. <i>BMC Musculoskeletal Disorders</i> , 2022, 23, .	0.8	3
29430	Quantitative phosphoproteomics analyses reveal the regulatory mechanisms related to frozen-thawed sperm capacitation and acrosome reaction in yak ( <i>Bos grunniens</i> ). <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
29431	DNA methylation regulator-mediated modification pattern defines tumor microenvironment immune infiltration landscape in colon cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29432	The mechanism of the Nfe2l2/Hmox1 signaling pathway in ferroptosis regulation in acute compartment syndrome. <i>Journal of Biochemical and Molecular Toxicology</i> , 2023, 37, .	1.4	2
29434	Comprehensive analysis of key m5C modification-related genes in type 2 diabetes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29435	Tissue-resident glial cells associate with tumoral vasculature and promote cancer progression. <i>Angiogenesis</i> , 0, , .	3.7	2
29436	RNA-Sequencing Analysis Identifies Etiology Specific Transcriptional Signatures in Neonatal Acute Liver Failure. <i>Journal of Pediatrics</i> , 2022, , .	0.9	1
29437	Interleukin-22 regulates neutrophil recruitment in ulcerative colitis and is associated with resistance to ustekinumab therapy. <i>Nature Communications</i> , 2022, 13, .	5.8	38
29438	Label-free quantitative SWATH-MS proteomic analysis of adult myocardial slices in vitro after biomimetic electromechanical stimulation. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
29439	Systematic analysis of cancer-specific synthetic lethal interactions provides insight into personalized anticancer therapy. <i>FEBS Journal</i> , 2023, 290, 1531-1548.	2.2	2
29440	Dual effects of zearalenone on aflatoxin B1-induced liver and mammary gland toxicity in pregnant and lactating rats. <i>Ecotoxicology and Environmental Safety</i> , 2022, 245, 114115.	2.9	9

#	ARTICLE	IF	CITATIONS
29441	BIONIC: biological network integration using convolutions. <i>Nature Methods</i> , 2022, 19, 1250-1261.	9.0	17
29442	Identification of the bZIP gene family and regulation of metabolites under salt stress in <i>isatis indigotica</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
29443	Machine learning-assisted elucidation of CD81â€“CD44 interactions in promoting cancer stemness and extracellular vesicle integrity. <i>ELife</i> , 0, 11, .	2.8	12
29444	Effective data filtering is prerequisite for robust microbial association network construction. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
29445	Improvement in heat stress-induced multiple organ dysfunction and intestinal damage through protection of intestinal goblet cells from prostaglandin E1 analogue misoprostol. <i>Life Sciences</i> , 2022, 310, 121039.	2.0	4
29446	Network Pharmacology-Based Analysis on the Potential Biological Mechanisms of Yinzhihuang Oral Liquid in Treating Neonatal Hyperbilirubinemia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-9.	0.5	4
29447	A genome-wide landscape of mRNAs, lncRNAs, circRNAs and miRNAs during intramuscular adipogenesis in cattle. <i>BMC Genomics</i> , 2022, 23, .	1.2	8
29448	Mode and Tempo of 3D Genome Evolution in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
29449	Explainable machine learning-assisted origin identification: Chemical profiling of five lotus ( <i>Nelumbo</i> ) Tj ETQq0 0 0 rBT /Overlock 10 Tf	4.2	4
29450	Physiological insight into the conserved properties of <i>Caenorhabditis elegans</i> acidâ€“sensing degenerin/epithelial sodium channels. <i>Journal of Physiology</i> , 2023, 601, 1625-1653.	1.3	7
29451	Integrative analysis of macrophage ribo-Seq and RNA-Seq data define glucocorticoid receptor regulated inflammatory response genes into distinct regulatory classes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5622-5638.	1.9	2
29452	Recognition of driver genes with potential prognostic implications in lung adenocarcinoma based on H3K79me2. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5535-5546.	1.9	1
29455	Therapeutic potential of metal ions for COVID-19: insights from the papain-like protease of SARS-CoV-2. <i>Biochemical Journal</i> , 2022, 479, 2175-2193.	1.7	4
29457	Photoactive Yellow Protein Represents a Distinct, Evolutionarily Novel Family of PAS Domains. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	4
29458	Single-cell dissection of the obesity-exercise axis in adipose-muscle tissues implies a critical role for mesenchymal stem cells. <i>Cell Metabolism</i> , 2022, 34, 1578-1593.e6.	7.2	35
29459	Identification of neurotoxic compounds in cyanobacteria exudate mixtures. <i>Science of the Total Environment</i> , 2023, 857, 159257.	3.9	2
29460	Inhibition of mTOR signaling protects human glioma cells from hypoxia-induced cell death in an autophagy-independent manner. <i>Cell Death Discovery</i> , 2022, 8, .	2.0	5
29461	Multi-omic phenotyping reveals host-microbe responses to bariatric surgery, glycaemic control and obesity. <i>Communications Medicine</i> , 2022, 2, .	1.9	2



#	ARTICLE	IF	CITATIONS
29462	Comparative genomic and biochemical analyses identify a collagen galactosylhydroxylsyl glucosyltransferase from <i>Acanthamoeba polyphaga</i> mimivirus. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
29463	A novel prognostic model based on three integrin subunit genes-related signature for bladder cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
29464	Comprehensive ceRNA network for MACF1 regulates osteoblast proliferation. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
29465	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of <i>Citrus grandis</i> "Tomentosa". <i>Plant Science</i> , 2022, 325, 111489.	1.7	7
29466	Genome-wide identification and expression of TIFY family in cassava ( <i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
29467	Dynamics of the gut microbiota in rats after hypobaric hypoxia exposure. <i>PeerJ</i> , 0, 10, e14090.	0.9	5
29468	Peripheral Blood Gene Expression Profile of Infants with Atopic Dermatitis. <i>JID Innovations</i> , 2023, 3, 100165.	1.2	4
29469	Metabolite alterations in zebrafish embryos exposed to hydroxylated polybrominated diphenyl ethers. <i>Science of the Total Environment</i> , 2023, 857, 159269.	3.9	2
29470	SARS-CoV-2 variants impact RBD conformational dynamics and ACE2 accessibility. <i>Frontiers in Medical Technology</i> , 0, 4, .	1.3	6
29471	miR2Trait: an integrated resource for investigating miRNA-disease associations. <i>PeerJ</i> , 0, 10, e14146.	0.9	3
29472	Prophage-encoded immune evasion factors are critical for <i>Staphylococcus aureus</i> host infection, switching, and adaptation. <i>Cell Genomics</i> , 2022, , 100194.	3.0	11
29473	Integrated Bioinformatics and Experimental Analysis Identified TRIM28 a Potential Prognostic Biomarker and Correlated with Immune Infiltrates in Liver Hepatocellular Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-17.	0.7	3
29474	DDX17 is required for efficient DSB repair at DNA:RNA hybrid deficient loci. <i>Nucleic Acids Research</i> , 2022, 50, 10487-10502.	6.5	6
29475	Common and species-specific molecular signatures, networks, and regulators of influenza virus infection in mice, ferrets, and humans. <i>Science Advances</i> , 2022, 8, .	4.7	6
29476	The inÂvivo Interaction Landscape of Histones H3.1 and H3.3. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100411.	2.5	6
29477	The oncogenic role of SNRPB in human tumors: A pan-cancer analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
29478	Integrated Analysis and Validation of Autophagy-Related Genes and Immune Infiltration in Acute Myocardial Infarction. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-14.	0.7	1
29479	Immune infiltration landscape on prognosis and therapeutic response and relevant epigenetic and transcriptomic mechanisms in lung adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2

#	ARTICLE	IF	CITATIONS
29480	Coadministration of Compound Danshen dripping pills and bezafibrate has a protective effect against diabetic retinopathy. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
29481	Connectivity and divergence of symbiotic bacteria of deep-sea hydrothermal vent mussels in relation to the structure and dynamics of mid-ocean ridges. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
29483	Insight into co-hosts of nitrate reduction genes and antibiotic resistance genes in an urban river of the qinghai-tibet plateau. <i>Water Research</i> , 2022, 225, 119189.	5.3	12
29484	Comparison of soil and grass microbiomes and resistomes reveals grass as a greater antimicrobial resistance reservoir than soil. <i>Science of the Total Environment</i> , 2023, 857, 159179.	3.9	7
29485	Prognostic Significance of ANGPTL4 in Lung Adenocarcinoma: A Meta-Analysis Based on Integrated TCGA and GEO Databases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	2
29486	Discrimination of <i>Fritillariae cirrhosae</i> bulbus from multi-source by potential Q-marker based on metabolomics and network pharmacology. <i>Rapid Communications in Mass Spectrometry</i> , 0, , .	0.7	1
29487	Omics profiling identifies the regulatory functions of the MAPK/ERK pathway in nephron progenitor metabolism. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	1
29488	Meta-analysis of fecal viromes demonstrates high diagnostic potential of the gut viral signatures for colorectal cancer and adenoma risk assessment. <i>Journal of Advanced Research</i> , 2023, 49, 103-114.	4.4	16
29489	DNA Methylation Profiling in a Cigarette Smoke-Exposed Mouse Model of Airway Inflammation. <i>International Journal of COPD</i> , 0, Volume 17, 2443-2450.	0.9	4
29490	Mechanisms of Xiaochaihu Decoction on Treating Hepatic Fibrosis Explored by Network Pharmacology. <i>Disease Markers</i> , 2022, 2022, 1-15.	0.6	1
29491	Network Analysis for Signal Detection in Spontaneous Adverse Event Reporting Database: Application of Network Weighting Normalization to Characterize Cardiovascular Drug Safety. <i>Drug Safety</i> , 2022, 45, 1423-1438.	1.4	4
29492	Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes, and normal tissues. <i>Cell Reports Medicine</i> , 2022, 3, 100763.	3.3	10
29493	Moderate salinity improves the availability of soil P by regulating P-cycling microbial communities in coastal wetlands. <i>Global Change Biology</i> , 2023, 29, 276-288.	4.2	16
29494	Identification of an 11 immune-related gene signature as the novel biomarker for acute myocardial infarction diagnosis. <i>Genes and Immunity</i> , 2022, 23, 209-217.	2.2	3
29495	The Effect of Coumestrol on Hub Genes in Lung Squamous Cell Carcinoma Based on Bioinformatic Strategy. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211279.	0.2	0
29496	Identifying the genes impacted by cell proliferation in proteomics and transcriptomics studies. <i>PLoS Computational Biology</i> , 2022, 18, e1010604.	1.5	3
29497	Single cell clonal analysis identifies an AID-dependent pathway of plasma cell differentiation. <i>EMBO Reports</i> , 2022, 23, .	2.0	4
29498	MICAL1 activation by PAK1 mediates actin filament disassembly. <i>Cell Reports</i> , 2022, 41, 111442.	2.9	8

#	ARTICLE	IF	CITATIONS
29499	p73 is required for vessel integrity controlling endothelial junctional dynamics through Angiotenin. Cellular and Molecular Life Sciences, 2022, 79, .	2.4	0
29500	Advanced database mining of efficient haloalkane dehalogenases by sequence and structure bioinformatics and microfluidics. Chem Catalysis, 2022, 2, 2704-2725.	2.9	15
29501	Drug Value of Drynariae Rhizoma Root-Derived Extracellular Vesicles for Neurodegenerative Diseases Based on Proteomics and Bioinformatics. Plant Signaling and Behavior, 2022, 17, .	1.2	3
29502	Identification of the Key Genes Involved in the Tumorigenesis and Prognosis of Prostate Cancer. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-17.	0.7	0
29503	A systems biology investigation of curcumin potency against TGF- $\beta$ -induced EMT signaling in lung cancer. 3 Biotech, 2022, 12, .	1.1	2
29504	Identification of differentially expressed genes based on antennae RNA-seq analyses in Culex quinquefasciatus and Culex pipiens molestus. Parasites and Vectors, 2022, 15, .	1.0	1
29505	Expression pattern and clinical value of Key RNA methylation modification regulators in ischemic stroke. Frontiers in Genetics, 0, 13, .	1.1	0
29506	Identification of Cyclic-di-GMP-Modulating Protein Residues by Bidirectionally Evolving a Social Behavior in Pseudomonas fluorescens. MSystems, 2022, 7, .	1.7	1
29507	Transcriptomic analysis of paternal behaviors in prairie voles. BMC Genomics, 2022, 23, .	1.2	2
29508	Metabolic, physiological and anatomical responses of soybean plants under water deficit and high temperature condition. Scientific Reports, 2022, 12, .	1.6	9
29510	Tanshinone IIA alleviates the mitochondrial toxicity of Salvia miltiorrhiza Bunge seedlings by regulating the transport capacity of ATP-binding cassette transporter to doxycycline. Environmental and Experimental Botany, 2022, 204, 105091.	2.0	3
29511	Deciphering Spatial Protein-Protein Interactions in Brain Using Proximity Labeling. Molecular and Cellular Proteomics, 2022, 21, 100422.	2.5	12
29512	Predicted COVID-19 molecular effects on endometrium reveal key dysregulated genes and functions. Molecular Human Reproduction, 2022, 28, .	1.3	5
29513	Bacterial community shifts in a di-(2-ethylhexyl) phthalate-degrading enriched consortium and the isolation and characterization of degraders predicted through network analyses. Chemosphere, 2023, 310, 136730.	4.2	6
29517	A novel strategy integrating gas phase fractionation with staggered mass range and LC-MS/MS molecular network for comprehensive metabolites profiling of Gui Ling Ji in rats. Journal of Pharmaceutical and Biomedical Analysis, 2023, 222, 115092.	1.4	5
29518	Analysis and identification of potential type II helper T cell (Th2)-Related key genes and therapeutic agents for COVID-19. Computers in Biology and Medicine, 2022, 150, 106134.	3.9	6
29519	Functional analysis of litter size and number of teats in pigs: From GWAS to post-GWAS. Theriogenology, 2022, 193, 157-166.	0.9	4
29520	Inductive database to support iterative data mining: Application to biomarker analysis on patient data in the Fight-HF project. Journal of Biomedical Informatics, 2022, 135, 104212.	2.5	0

#	ARTICLE	IF	CITATIONS
29521	Transcriptome analysis reveals the molecular regulatory network of muscle development and meat quality in Sunit lamb supplemented with dietary probiotic. <i>Meat Science</i> , 2022, 194, 108996.	2.7	7
29522	Metabolomics and molecular networking analyses in <i>Arabidopsis thaliana</i> show that extracellular self-DNA affects nucleoside/nucleotide cycles with accumulation of cAMP, cGMP and N6-methyl-AMP. <i>Phytochemistry</i> , 2022, 204, 113453.	1.4	8
29523	Molecular mechanisms regulating mesophyll conductance under severe water stress for water-saving drought-resistant rice in wetting-drying alternate irrigation. <i>Environmental and Experimental Botany</i> , 2022, 204, 105090.	2.0	1
29524	Colchicine increases intestinal toxic load by disturbing fecal metabolome homeostasis in mice. <i>Chemico-Biological Interactions</i> , 2022, 368, 110193.	1.7	3
29526	Prognostic biomarkers of pancreatic cancer identified based on a competing endogenous RNA regulatory network. <i>Translational Cancer Research</i> , 2022, 11, 4019-4036.	0.4	1
29527	Structure, Function, and Genetics of the Cerebellum in Autism. <i>Journal of Psychiatry and Brain Science</i> , 0, , .	0.3	6
29528	âŸ°ä°Žă...âŸ°ă>ç>,ă...3è*âˆ†æžžèšfæžžŽ%oç±³ç±½ç²'âšâ°çš,,é-ă¼ç>“æž,,. <i>Acta Agronomica Sinica(China)</i> , 2022, 48, 304-309.		
29529	Statistical Analysis of Post-Translational Modifications Quantified by Label-Free Proteomics Across Multiple Biological Conditions with R: Illustration from SARS-CoV-2 Infected Cells. <i>Methods in Molecular Biology</i> , 2023, , 267-302.	0.4	4
29530	Influence of different sample preparation strategies on hypothesis-driven shotgun proteomic analysis of human saliva. <i>Open Chemistry</i> , 2022, 20, 1000-1018.	1.0	1
29531	A study of the therapeutic mechanism of Jakyakgamcho-Tang about functional dyspepsia through network pharmacology research. <i>International Journal of Medical Sciences</i> , 2022, 19, 1824-1834.	1.1	0
29532	Linking microbial body size to community co-occurrences and stability at multiple geographical scales in agricultural soils. <i>Advances in Ecological Research</i> , 2022, , 1-26.	1.4	1
29533	Dynamic alternative polyadenylation during iPSC differentiation into cardiomyocytes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5859-5869.	1.9	4
29534	Vitamin D receptor (<i>VDR</i>) mRNA overexpression is associated with poor prognosis in breast carcinoma. <i>Annals of Surgical Treatment and Research</i> , 2022, 103, 183.	0.4	3
29535	Mining of the CULLIN E3 ubiquitin ligase genes in the whole genome of <i>Salvia miltiorrhiza</i> . <i>Current Research in Food Science</i> , 2022, 5, 1760-1768.	2.7	3
29536	Proteomics-based molecular and functional characteristic profiling of muscle tissue in Triploid crucian carp. <i>Molecular Omics</i> , 0, , .	1.4	0
29537	Local Community Detection: A Survey. <i>IEEE Access</i> , 2022, 10, 110701-110726.	2.6	5
29538	<i>N</i>-6-Methyladenosine-related alternative splicing events play a role in bladder cancer. <i>Open Life Sciences</i> , 2022, 17, 1371-1382.	0.6	0
29539	Identifying common signatures and potential therapeutic biomarkers in COPD and lung cancer using miRNA-mRNA co-expression networks. <i>Informatics in Medicine Unlocked</i> , 2022, 34, 101115.	1.9	1

#	ARTICLE	IF	CITATIONS
29540	Prognostic Value of Tumor-microenvironment-associated Genes in Ovarian Cancer. <i>BIO Integration</i> , 2023, 4, .	0.9	0
29541	Hsa_Circ_0066351 Acts as a Prognostic and Immunotherapeutic Biomarker in Colorectal Cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
29542	Duck CD8+ T Cell Response to H5N1 Highly Pathogenic Avian Influenza Virus Infection In Vivo and In Vitro. <i>Journal of Immunology</i> , 2022, 209, 979-990.	0.4	4
29543	An integrative approach toward identification and analysis of therapeutic targets involved in HPV pathogenesis with a focus on carcinomas. <i>Cancer Biomarkers</i> , 2022, , 1-22.	0.8	2
29544	Prognostic value of Talin-1 in renal cell carcinoma and its association with B7-H3. <i>Cancer Biomarkers</i> , 2022, 35, 269-292.	0.8	3
29545	ML-DTD: Machine Learning-Based Drug Target Discovery for the Potential Treatment of COVID-19. <i>Vaccines</i> , 2022, 10, 1643.	2.1	5
29546	Exploring Precise Medication Strategies for OSCC Based on Single-Cell Transcriptome Analysis from a Dynamic Perspective. <i>Cancers</i> , 2022, 14, 4801.	1.7	0
29547	The Structure and Function of the <i>Sargassum fusiforme</i> Microbiome under Different Conditions. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1401.	1.2	1
29548	Comparative Metagenomics and Metabolomes Reveals Abnormal Metabolism Activity Is Associated with Gut Microbiota in Alzheimer's Disease Mice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11560.	1.8	9
29549	Gene Signatures Associated with Temporal Rhythm as Diagnostic Markers of Major Depressive Disorder and Their Role in Immune Infiltration. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11558.	1.8	0
29550	Pivotal interplays between fecal metabolome and gut microbiome reveal functional signatures in cerebral ischemic stroke. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	9
29551	Computational Metabolomics Tools Reveal Subarmigerides, Unprecedented Linear Peptides from the Marine Sponge Holobiont <i>Callyspongia subarmigera</i> . <i>Marine Drugs</i> , 2022, 20, 673.	2.2	2
29552	Enrofloxacin-induced transfer of multiple-antibiotic resistance genes and emergence of novel resistant bacteria in red swamp crayfish guts and pond sediments. <i>Journal of Hazardous Materials</i> , 2023, 443, 130261.	6.5	14
29553	Machine Learning-Based Co-Expression Network Analysis Unravels Potential Fertility-Related Genes in Beef Cows. <i>Animals</i> , 2022, 12, 2715.	1.0	4
29554	Ecological insights into the resilience of marine plastisphere throughout a storm disturbance. <i>Science of the Total Environment</i> , 2022, , 159775.	3.9	4
29555	Pan-cancer analysis of oncogenic TNFAIP2 identifying its prognostic value and immunological function in acute myeloid leukemia. <i>BMC Cancer</i> , 2022, 22, .	1.1	5
29556	Computational models of neurotransmission at cerebellar synapses unveil the impact on network computation. <i>Frontiers in Computational Neuroscience</i> , 0, 16, .	1.2	3
29557	Construction and Transcriptomic Study of Chicken IFNAR1-Knockout Cell Line Reveals the Essential Roles of Cell Growth- and Apoptosis-Related Pathways in Duck Tembusu Virus Infection. <i>Viruses</i> , 2022, 14, 2225.	1.5	4

#	ARTICLE	IF	CITATIONS
29558	Agathis robusta Bark Extract Protects from Renal Ischemia-Reperfusion Injury: Phytochemical, In Silico and In Vivo Studies. <i>Pharmaceuticals</i> , 2022, 15, 1270.	1.7	8
29560	Developmental defects and behavioral changes in a diet-induced inflammation model of zebrafish. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
29561	Metabolomic Aspects of Conservative and Resistance-Related Elements of Response to <i>Fusarium culmorum</i> in the Grass Family. <i>Cells</i> , 2022, 11, 3213.	1.8	2
29562	Comparative transcriptomic analysis of normal and abnormal in vitro flowers in <i>Cymbidium nanulum</i> Y. S. Wu et S. C. Chen identifies differentially expressed genes and candidate genes involved in flower formation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29563	Quantitative proteomics and biological activity of extracellular vesicles engineered to express SARS-CoV-2 spike protein. , 2022, 1, .		2
29564	Expression of AKT1 Related with Clinicopathological Parameters in Clear Cell Renal Cell Carcinoma. <i>Current Issues in Molecular Biology</i> , 2022, 44, 4921-4929.	1.0	2
29565	Analysis of exosomal competing endogenous RNA network response to paclitaxel treatment reveals key genes in advanced gastric cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
29566	Pro-Inflammatory Cytokines Promote the Transcription of Circular RNAs in Human Pancreatic Î² Cells. <i>Non-coding RNA</i> , 2022, 8, 69.	1.3	0
29567	Semantic Annotation of Experimental Methods in Analytical Chemistry. <i>Analytical Chemistry</i> , 0, , .	3.2	0
29568	The Construction and Analysis of a ceRNA Network Related to Salt-Sensitivity Hypertensives. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	2
29569	CCR7-mediated T follicular helper cell differentiation is associated with the pathogenesis and immune microenvironment of spinal cord injury-induced immune deficiency syndrome. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	1
29570	<i>In silico</i> analysis of metabolic effects of bipolar disorder on prefrontal cortex identified altered GABA, glutamate-glutamine cycle, energy metabolism and amino acid synthesis pathways. <i>Integrative Biology (United Kingdom)</i> , 0, , .	0.6	0
29571	Degradome-focused RNA interference screens to identify proteases important for breast cancer cell growth. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
29572	Branched-chain ketoacids derived from cancer cells modulate macrophage polarization and metabolic reprogramming. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
29573	The chromosome-level genome of female ginseng ( <i>Angelica sinensis</i> ) provides insights into molecular mechanisms and evolution of coumarin biosynthesis. <i>Plant Journal</i> , 2022, 112, 1224-1237.	2.8	19
29574	Identification of the common differentially expressed genes and pathogenesis between neuropathic pain and aging. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	3
29576	Flavin Mononucleotide-Dependent Lactate Dehydrogenases: Expanding the Toolbox of Enzymes for Lactate Biosensors. <i>ACS Omega</i> , 2022, 7, 41480-41492.	1.6	4
29577	Comparison of anther transcriptomes in response to cold stress at the reproductive stage between susceptible and resistant Japonica rice varieties. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3



#	ARTICLE	IF	CITATIONS
29578	Regulation of Bacterial Metabolic Activities and Community Composition by Temperature in a Fringing Coral Reef. <i>Journal of Geophysical Research: Oceans</i> , 2022, 127, .	1.0	1
29579	MIR retrotransposons link the epigenome and the transcriptome of coding genes in acute myeloid leukemia. <i>Nature Communications</i> , 2022, 13, .	5.8	1
29580	Graph-Based Conversation Analysis in Social Media. <i>Big Data and Cognitive Computing</i> , 2022, 6, 113.	2.9	4
29581	Well-being and relative deprivation in a digital era. <i>Heliyon</i> , 2022, 8, e11233.	1.4	1
29582	Elucidation of the mechanisms and molecular targets of Run-zao-zhi-yang capsule for itch based on network pharmacology, molecular docking and in vitro experiment. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 26, .	0.6	1
29583	MINI-EX: Integrative inference of single-cell gene regulatory networks in plants. <i>Molecular Plant</i> , 2022, 15, 1807-1824.	3.9	16
29584	The transcriptomic signature of responses to larval crowding in <i>Drosophila melanogaster</i> . <i>Insect Science</i> , 2023, 30, 539-554.	1.5	3
29585	Integrative Analysis of miRNA-mRNA in Ovarian Granulosa Cells Treated with Kisspeptin in Tan Sheep. <i>Animals</i> , 2022, 12, 2989.	1.0	2
29586	The Histone Methyltransferase SETD8 Regulates the Expression of Tumor Suppressor Genes via H4K20 Methylation and the p53 Signaling Pathway in Endometrial Cancer Cells. <i>Cancers</i> , 2022, 14, 5367.	1.7	8
29588	Integrative analysis of the immune-related ceRNA network in fetal growth restriction based on weighted gene co-expression network analysis. <i>Archives of Gynecology and Obstetrics</i> , 0, , .	0.8	0
29589	Imputation to whole-genome sequence and its use in genome-wide association studies for pork colour traits in crossbred and purebred pigs. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
29591	Niche differentiation modulates metabolites abundance and composition in silicon fertilizer amended soil during sugarcane growth. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
29592	A Comprehensive Gene Co-Expression Network Analysis Reveals a Role of GhWRKY46 in Responding to Drought and Salt Stresses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12181.	1.8	3
29593	Identification and Validation of Yak ( <i>Bos grunniens</i> ) Frozen-Thawed Sperm Proteins Associated with Capacitation and the Acrosome Reaction. <i>Journal of Proteome Research</i> , 2022, 21, 2754-2770.	1.8	5
29594	FunHoP analysis reveals upregulation of mitochondrial genes in prostate cancer. <i>PLoS ONE</i> , 2022, 17, e0275621.	1.1	1
29595	A comprehensive SARS-CoV-2 human protein-protein interactome reveals COVID-19 pathobiology and potential host therapeutic targets. <i>Nature Biotechnology</i> , 2023, 41, 128-139.	9.4	61
29596	Molecular Classification of Colorectal Cancer by microRNA Profiling: Correlation with the Consensus Molecular Subtypes (CMS) and Validation of miR-30b Targets. <i>Cancers</i> , 2022, 14, 5175.	1.7	3
29597	Deciphering the Mechanism of YuPingFeng Granules in Treating Pneumonia: A Network Pharmacology and Molecular Docking Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	1

#	ARTICLE	IF	CITATIONS
29598	Data-driven patient stratification of UK Biobank cohort suggests five endotypes of multimorbidity. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
29599	Phytoremediation of isoproturon-contaminated sites by transgenic soybean. <i>Plant Biotechnology Journal</i> , 2023, 21, 342-353.	4.1	0
29600	Genome-wide identification and expression analysis of BrAGC genes in <i>Brassica rapa</i> reveal their potential roles in sexual reproduction and abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29601	Network analysis-based strategy to investigate the protective effect of cepharanthine on rat acute respiratory distress syndrome. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
29602	Association of ScV-LA Virus with Host Protein Metabolism Determined by Proteomics Analysis and Cognate RNA Sequencing. <i>Viruses</i> , 2022, 14, 2345.	1.5	1
29603	Evaluation of the Heat Shock Protein 90 Inhibitor Ganetespib as a Sensitizer to Hyperthermia-Based Cancer Treatments. <i>Cancers</i> , 2022, 14, 5250.	1.7	3
29604	Transcriptome and metabolome analyses provide insights into the relevance of pericarp thickness variations in <i>Camellia drupifera</i> and <i>Camellia oleifera</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29608	Nucleotide-based genetic networks: Methods and applications. <i>Journal of Biosciences</i> , 2022, 47, .	0.5	0
29609	Integrated network pharmacology and experimental analysis unveil multi-targeted effect of 18 $\beta$ -glycyrrhetic acid against non-small cell lung cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
29610	Transcriptomics-metabolomics joint analysis: New highlight into the triterpenoid saponin biosynthesis in quinoa ( <i>Chenopodium quinoa</i> Willd.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
29611	Systems biology strategy and experimental validation to uncover the pharmacological mechanism of Xihuang Pill in treating non-small cell lung cancer. <i>Phytomedicine</i> , 2023, 108, 154491.	2.3	3
29612	Lipid and protein content profiling of isolated native autophagic vesicles. <i>EMBO Reports</i> , 2022, 23, .	2.0	15
29613	The Effect of Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> (Steiner and Buhner) Nickle on Intestinal Bacterial Community of Insect Vector <i>Monochamus saltuarius</i> (Coleoptera: Cerambycidae). <i>Forests</i> , 2022, 13, 1673.	0.9	0
29614	Transcriptome Remodeling in Response to Leaf Removal and Exogenous Abscisic Acid in Berries of Grapevine ( <i>Vitis vinifera</i> L.) Fruit Cuttings. <i>Horticulturae</i> , 2022, 8, 905.	1.2	1
29615	Optimizing Intermodal Transport and Hub Location Problem for ECOWAS in the Context of Improving Intra-African Trade. <i>Journal of Advanced Transportation</i> , 2022, 2022, 1-17.	0.9	0
29616	Integrated network pharmacology and serum metabolomics approach deciphers the anti-colon cancer mechanisms of Huangqi Guizhi Wuwu Decoction. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	6
29617	Prognostic analysis and validation of diagnostic marker genes in patients with osteoporosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
29618	Sex-based metabolic and microbiota differences in roots and rhizosphere soils of dioecious papaya ( <i>Carica papaya</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3

#	ARTICLE	IF	CITATIONS
29619	Proteomic Analysis Reveals Differential Protein Expression Induced by Inhibition of Prolyl Oligopeptidase in Filarial Parasites. <i>Protein Journal</i> , 2022, 41, 613-624.	0.7	1
29620	Circuit analysis of the <i>Drosophila</i> brain using connectivity-based neuronal classification reveals organization of key communication pathways. <i>Network Neuroscience</i> , 2023, 7, 269-298.	1.4	5
29621	Deciphering the action mechanism of paeoniflorin in suppressing pancreatic cancer: A network pharmacology study and experimental validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
29622	Optineurin links Hace1-dependent Rac ubiquitylation to integrin-mediated mechanotransduction to control bacterial invasion and cell division. <i>Nature Communications</i> , 2022, 13, .	5.8	7
29623	Histone methyltransferases SDG33 and SDG34 regulate organ-specific nitrogen responses in tomato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
29624	The salivary microbiome shows a high prevalence of core bacterial members yet variability across human populations. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	13
29625	High Expression of Fibronectin 1 Predicts a Poor Prognosis in Glioblastoma. <i>Current Medical Science</i> , 2022, 42, 1055-1065.	0.7	7
29629	Network-based methods for psychometric data of eating disorders: A systematic review. <i>PLoS ONE</i> , 2022, 17, e0276341.	1.1	4
29630	Computational genomics insights into cold acclimation in wheat. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
29631	Biosynthesis-guided discovery reveals enteropeptins as alternative sactipeptides containing N-methylornithine. <i>Nature Chemistry</i> , 2022, 14, 1390-1398.	6.6	8
29632	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. <i>Nature Ecology and Evolution</i> , 2022, 6, 1891-1906.	3.4	23
29633	Combined hepatoprotective pharmacotherapy for liver disease. <i>Eksperimental'naya I Klinicheskaya Gastroenterologiya</i> , 2022, , 5-20.	0.1	2
29634	Beneficial bacterial-Auricularia cornea interactions fostering growth enhancement identified from microbiota present in spent mushroom substrate. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
29635	Central gene transcriptional regulatory networks shaping monocyte development in bone marrow. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
29636	Integrated Multi-Omics Analysis Reveals Differential Effects of Fructo-Oligosaccharides (FOS) Supplementation on the Human Gut Ecosystem. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11728.	1.8	0
29637	Identification of Key Genes in the HBV-Related HCC Immune Microenvironment Using Integrated Bioinformatics Analysis. <i>Journal of Oncology</i> , 2022, 2022, 1-15.	0.6	0
29638	An Analysis of Transcriptomic Burden Identifies Biological Progression Roadmaps for Hematological Malignancies and Solid Tumors. <i>Biomedicines</i> , 2022, 10, 2720.	1.4	2
29639	Candidate genes screening based on phenotypic observation and transcriptome analysis for double flower of <i>Prunus mume</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2

#	ARTICLE	IF	CITATIONS
29640	Chemical Composition of Tagetes patula Flowers Essential Oil and Hepato-Therapeutic Effect against Carbon Tetrachloride-Induced Toxicity (In-Vivo). <i>Molecules</i> , 2022, 27, 7242.	1.7	3
29642	Tracking footprints of artificial and natural selection signatures in breeding and non-breeding cats. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
29643	System Biology Approaches Identified Novel Biomarkers and their Signaling Pathways Involved in Renal Cell Carcinoma (RCC) with Different Human Diseases. <i>Bioscience Reports</i> , 0, , .	1.1	1
29644	Molecular Mechanisms Underlying the Effects of Bimin Kang Mixture on Allergic Rhinitis: Network Pharmacology and RNA Sequencing Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-23.	0.9	1
29645	Characterization of the interactome profiling of Mycoplasma fermentans DnaK in cancer cells reveals interference with key cellular pathways. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
29646	Identification of Specific Cervical Cancer Subtypes and Prognostic Gene Sets in Tumor and Nontumor Tissues Based on GSVA Analysis. <i>Journal of Oncology</i> , 2022, 2022, 1-17.	0.6	2
29647	Basics on network theory to analyze biological systems: a hands-on outlook. <i>Functional and Integrative Genomics</i> , 2022, 22, 1433-1448.	1.4	4
29648	Identification of <scp>miR</scp>â€³182 and <scp>miR</scp>â€³143 target genes involved in the cell cycle as a novel approach in <scp>TNBC</scp> treatment: A systems biology approach. <i>Chemical Biology and Drug Design</i> , 2023, 101, 662-677.	1.5	3
29649	Shared 6mer Peptides of Human and Omicron (21K and 21L) at SARS-CoV-2 Mutation Sites. <i>Antibodies</i> , 2022, 11, 68.	1.2	2
29650	Tetrabromobisphenol A effects on differentiating mouse embryonic stem cells reveals unexpected impact on immune system. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29651	Dynamic Network Biomarker Analysis Reveals the Critical Phase Transition of Fruit Ripening in Grapevine. <i>Genes</i> , 2022, 13, 1851.	1.0	3
29652	Network toxicology and molecular docking analyses on strychnine indicate CHRM1 is a potential neurotoxic target. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	2
29653	Generation and maturation of human iPSC-derived 3D organotypic cardiac microtissues in long-term culture. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
29654	Immune system-wide Mendelian randomization and triangulation analyses support autoimmunity as a modifiable component in dementia-causing diseases. <i>Nature Aging</i> , 2022, 2, 956-972.	5.3	11
29655	Network Pharmacology-Based Dissection of the Mechanism of Drynariae Rhizoma for Low Back Pain. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	0
29656	Combinatorial analysis of transcription and metabolism reveals the regulatory network associated with antioxidant substances in waxy corn. <i>Food Quality and Safety</i> , 2022, 6, .	0.6	2
29658	Towards a hybrid user interface for the visual exploration of large biomolecular networks using virtual reality. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.0	2
29659	Studies on Chemical Composition of Pueraria lobata and Its Anti-Tumor Mechanism. <i>Molecules</i> , 2022, 27, 7253.	1.7	2

#	ARTICLE	IF	CITATIONS
29660	A network view of human immune system and virus-human interaction. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
29661	Transcriptional profiling of long non-coding RNAs regulating fruit cracking in <i>Punica granatum</i> L. under bagging. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29662	Shared Genetic Regulatory Networks Contribute to Neuropathic and Inflammatory Pain: Multi-Omics Systems Analysis. <i>Biomolecules</i> , 2022, 12, 1454.	1.8	3
29665	CircTCF4 Suppresses Proliferation and Differentiation of Goat Skeletal Muscle Satellite Cells Independent from AGO2 Binding. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12868.	1.8	5
29666	Combining Feature-Based Molecular Networking and Contextual Mass Spectral Libraries to Decipher Nutrimetabolomics Profiles. <i>Metabolites</i> , 2022, 12, 1005.	1.3	4
29667	Extracellular vesicles from pristane-treated CD38-deficient mice express an anti-inflammatory neutrophil protein signature, which reflects the mild lupus severity elicited in these mice. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
29670	Novel lncRNA <i>prader willi/angelman region RNA</i> , SNRPN neighbour <i>PWARSN</i> aggravates tubular epithelial cell pyroptosis by regulating <i>TXNIP</i> via dual way in diabetic kidney disease. <i>Cell Proliferation</i> , 2023, 56, .	2.4	4
29671	Characterization of interferon gamma gene in relation to immunological responses in <i>Haemonchus contortus</i> resistant and susceptible Garole sheep. <i>Veterinary Research Communications</i> , 2023, 47, 599-614.	0.6	3
29672	Alzheimer's disease large-scale gene expression portrait identifies exercise as the top theoretical treatment. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
29673	A transcriptomic analysis of the effects of macrophage polarization and endotoxin tolerance on the response to <i>Salmonella</i> . <i>PLoS ONE</i> , 2022, 17, e0276010.	1.1	1
29674	Proteomics Profiling of Stool Samples from Preterm Neonates with SWATH/DIA Mass Spectrometry for Predicting Necrotizing Enterocolitis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11601.	1.8	2
29675	Investigation of the hemostatic mechanism of <i>Gardeniae fructus Praeparatus</i> based on pharmacological evaluation and network pharmacology. <i>Annals of Translational Medicine</i> , 2022, 10, 1093-1093.	0.7	1
29677	Genome-Wide Identification, Expression Profiling, and Characterization of Cyclin-like Genes Reveal Their Role in the Fertility of the Diamondback Moth. <i>Biology</i> , 2022, 11, 1493.	1.3	4
29680	Single cell transcriptomic profiling of a neuron-astrocyte assembloid tauopathy model. <i>Nature Communications</i> , 2022, 13, .	5.8	14
29681	<i>ZmCCT10</i> -relayed photoperiod sensitivity regulates natural variation in the arithmetical formation of male germinal cells in maize. <i>New Phytologist</i> , 0, , .	3.5	1
29682	Landscape of epithelial-mesenchymal plasticity as an emergent property of coordinated teams in regulatory networks. <i>ELife</i> , 0, 11, .	2.8	31
29683	MicroRNA-92a-3p Regulates Retinal Angiogenesis by Targeting SGK3 in Vascular Endothelial Cells. , 2022, 63, 19.		4
29684	KCNQ1OT1 promotes genome-wide transposon repression by guiding RNA-DNA triplexes and HP1 binding. <i>Nature Cell Biology</i> , 2022, 24, 1617-1629.	4.6	20

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29685	Humoral immunity and transcriptome differences of COVID-19 inactivated vaccine and protein subunit vaccine as third booster dose in human. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
29686	Transcriptome-Wide lncRNA and mRNA Profiling of Spleens from Meishan Pigs at Different Development Stages. <i>Animals</i> , 2022, 12, 2676.	1.0	1
29687	Genome-Wide Identification and Expression Analysis of HSF Transcription Factors in Alfalfa ( <i>Medicago</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	6
29688	Modeling gene–environment interactions in PTSD using human neurons reveals diagnosis-specific glucocorticoid-induced gene expression. <i>Nature Neuroscience</i> , 2022, 25, 1434-1445.	7.1	19
29689	Global Proteomic Profile of Aluminum-Induced Hippocampal Impairments in Rats: Are Low Doses of Aluminum Really Safe?. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12523.	1.8	7
29690	A Plasma Circular RNA Profile Differentiates Subjects with Alzheimer’s Disease and Mild Cognitive Impairment from Healthy Controls. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13232.	1.8	7
29691	Contrasting sea ice conditions shape microbial food webs in Hudson Bay (Canadian Arctic). <i>ISME Communications</i> , 2022, 2, .	1.7	4
29692	Genome-Wide Identification of miRNAs and Its Downstream Transcriptional Regulatory Network during Seed Maturation in <i>Tilia tuan</i> . <i>Forests</i> , 2022, 13, 1750.	0.9	3
29693	Systematic molecular profiling of acute leukemia cancer stem cells allows identification of druggable targets. <i>Heliyon</i> , 2022, 8, e11093.	1.4	0
29694	Proteomics analysis of cancer tissues identifies IGF2R as a potential therapeutic target in laryngeal carcinoma. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
29695	Low-abundance populations distinguish microbiome performance in plant cell wall deconstruction. <i>Microbiome</i> , 2022, 10, .	4.9	10
29697	Metabolic, fibrotic and splicing pathways are all altered in Emery-Dreifuss muscular dystrophy spectrum patients to differing degrees. <i>Human Molecular Genetics</i> , 2023, 32, 1010-1031.	1.4	1
29698	A graph-based approach for the visualisation and analysis of bacterial pangenomes. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	7
29699	Portrait of Molecular Signaling and Putative Therapeutic Targets in Prostate Cancer with ETV4 Fusion. <i>Biomedicines</i> , 2022, 10, 2650.	1.4	0
29700	Induced pluripotent stem cell-derived astrocytes from patients with schizophrenia exhibit an inflammatory phenotype that affects vascularization. <i>Molecular Psychiatry</i> , 2023, 28, 871-882.	4.1	4
29701	Transcriptomic analysis of the human placenta reveals trophoblast dysfunction and augmented Wnt signalling associated with spontaneous preterm birth. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
29702	An immunogenetic investigation of 30 autoimmune and autoinflammatory diseases and their links to psychiatric disorders in a nationwide sample. <i>Immunology</i> , 2023, 168, 622-639.	2.0	5
29703	Alternation of heart microRNA–mRNA network by high-intensity interval training and proanthocyanidin in myocardial ischemia rats: Artificial intelligence and validation experimental. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	1



#	ARTICLE	IF	CITATIONS
29704	Current Insights into miRNA and lncRNA Dysregulation in Diabetes: Signal Transduction, Clinical Trials and Biomarker Discovery. <i>Pharmaceuticals</i> , 2022, 15, 1269.	1.7	8
29705	Proteomic Analysis of Decellularized Extracellular Matrix: Achieving a Competent Biomaterial for Osteogenesis. <i>BioMed Research International</i> , 2022, 2022, 1-18.	0.9	1
29706	Identification of Candidate Genes and Regulatory Competitive Endogenous RNA (ceRNA) Networks Underlying Intramuscular Fat Content in Yorkshire Pigs with Extreme Fat Deposition Phenotypes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12596.	1.8	3
29708	Structural impact of pathogenic SNPs on $\beta$ -tubulin using molecular dynamics study. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-11.	2.0	0
29709	Transcriptomic, cytological, and physiological analyses reveal the potential regulatory mechanism in Tartary buckwheat under cadmium stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
29711	The transcriptional characteristics of NADC34-like PRRSV in porcine alveolar macrophages. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
29712	Network analysis for the identification of hub genes and related molecules as potential biomarkers associated with the differentiation of bone marrow-derived stem cells into hepatocytes. <i>Aging</i> , 0, , .	1.4	0
29713	Identification of potential crucial genes and mechanisms associated with metastasis of medulloblastoma based on gene expression profile. <i>Neurological Research</i> , 0, , 1-8.	0.6	0
29714	Natural Products as a Major Source of Candidates for Potential Senolytic Compounds obtained by in silico Screening. <i>Medicinal Chemistry</i> , 2023, 19, 653-668.	0.7	3
29715	Investigating the effects and mechanisms of Erchen Decoction in the treatment of colorectal cancer by network pharmacology and experimental validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
29716	Fine-Tuned Immune Antagonism and Nodule-Specific Cysteine-Rich Peptides Govern the Symbiotic Specificity Between Alfalfa Cultivars and <i>Ensifer meliloti</i> . <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
29717	Expression Profiles of Differentially Expressed Circular RNAs and circRNA-miRNA-mRNA Regulatory Networks in SH-SY5Y Cells Infected with Coxsackievirus B5. <i>International Journal of Genomics</i> , 2022, 2022, 1-15.	0.8	1
29718	Identification of the Anti-Inflammatory Compound, Paeoniflorigenone, in <i>Radix Paeoniae Alba</i> for the Treatment of Polycystic Ovary Syndrome Through Network Pharmacology and Molecular Docking. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211291.	0.2	0
29720	A workflow for the creation of regulatory networks integrating miRNAs and lncRNAs associated with exposure to ionizing radiation using open source data and tools. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	0
29721	Identification and Investigation of the Genetic Variations and Candidate Genes Responsible for Seed Weight via GWAS in Paper Mulberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12520.	1.8	2
29722	Systematic analysis of circRNA biomarkers for diagnosis, prognosis and therapy in colorectal cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
29723	A genomic and transcriptomic study toward breast cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
29724	In silico characterization of competing endogenous RNA network in glioblastoma multiforme with a systems biology approach. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0

#	ARTICLE	IF	CITATIONS
29725	High-throughput data on circular RNA reveal novel insights into chronic glomerulonephritis. <i>Genes and Genomics</i> , 2023, 45, 475-490.	0.5	3
29726	Definition of a Novel Cuproptosis-Relevant lncRNA Signature for Uncovering Distinct Survival, Genomic Alterations, and Treatment Implications in Lung Adenocarcinoma. <i>Journal of Immunology Research</i> , 2022, 2022, 1-40.	0.9	8
29727	A system pharmacology Boolean network model for the TLR4-mediated inflammatory response in early sepsis. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2022, 49, 645-655.	0.8	2
29728	Identification of Candidate Genes in Breast Cancer Induced by Estrogen Plus Progestogens Using Bioinformatic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11892.	1.8	1
29729	Protein network and pathway analysis in a pharmacogenetic study of cyclosporine treatment response in Greek patients with psoriasis. <i>Pharmacogenomics Journal</i> , 2023, 23, 8-13.	0.9	4
29731	Identifying Key Lysosome-Related Genes Associated with Drug-Resistant Breast Cancer Using Computational and Systems Biology Approach. <i>Iranian Journal of Pharmaceutical Research</i> , 2022, 21, .	0.3	2
29732	Using Network Pharmacology and Animal Experiment to Investigate the Therapeutic Mechanisms of Polydatin against Vincristine-Induced Neuropathic Pain. <i>Mediators of Inflammation</i> , 2022, 2022, 1-13.	1.4	2
29733	Development and assessment of diabetic nephropathy prediction model using hub genes identified by weighted correlation network analysis. <i>Aging</i> , 2022, 14, 8095-8109.	1.4	0
29734	Integrated proteomic and metabolomic profile analyses of cardiac valves revealed molecular mechanisms and targets in calcific aortic valve disease. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	4
29735	Fasulyede Tuz ve Kuraklık Stresi Altında PIF Gen Ailesinin Genomunda Analizi ve Karakterizasyonu. <i>Türkiye Tarımsal Araştırmalar Dergisi</i> , 0, , .	0.5	0
29736	Structural basis of colibactin activation by the ClbP peptidase. <i>Nature Chemical Biology</i> , 2023, 19, 151-158.	3.9	12
29737	Identification of potential regulatory long non-coding RNA-associated competing endogenous RNA axes in periplaque regions in multiple sclerosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29738	Distinct molecular subtypes of papillary thyroid carcinoma and gene signature with diagnostic capability. <i>Oncogene</i> , 2022, 41, 5121-5132.	2.6	6
29739	Integrated analysis of miRNA and mRNA expression profiles in testes of Landrace and Hezuo boars. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	5
29740	Stability of a dominant sponge symbiont in spite of antibiotic-induced microbiome disturbance. <i>Environmental Microbiology</i> , 2022, 24, 6392-6410.	1.8	9
29743	Epigenomic and transcriptomic landscaping unraveled candidate repositioned therapeutics for non-functioning pituitary neuroendocrine tumors. <i>Journal of Endocrinological Investigation</i> , 2023, 46, 727-747.	1.8	2
29746	Transcriptome and Metabolome Analysis Provides Insights into the Heterosis of Yield and Quality Traits in Two Hybrid Rice Varieties ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 12934.	1.8	0
29747	Gapless genome assembly of azalea and multi-omics investigation into divergence between two species with distinct flower color. <i>Horticulture Research</i> , 2023, 10, .	2.9	11

#	ARTICLE	IF	CITATIONS
29748	Identification and characteristics of SnRK genes and cold stress-induced expression profiles in <i>Liriodendron chinense</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	5
29749	Scinderin Is a Novel Oncogene for Its Correlates with Poor Prognosis, Immune Infiltrates and Matrix Metalloproteinase-2/9 (MMP2/9) in Glioma. <i>Brain Sciences</i> , 2022, 12, 1415.	1.1	1
29750	Bibliometric analysis of research on gene expression in spinal cord injury. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	2
29751	Viral protein engagement of GBF1 induces host cell vulnerability through synthetic lethality. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	6
29752	Funneliformis mosseae Inoculation Enhances Cucurbita pepo L. Plant Growth and Fruit Yield by Reshaping Rhizosphere Microbial Community Structure. <i>Diversity</i> , 2022, 14, 932.	0.7	4
29753	Network-Based Analysis to Identify Hub Genes Involved in Spatial Root Response to Mechanical Constrains. <i>Cells</i> , 2022, 11, 3121.	1.8	2
29754	Progression of the pluripotent epiblast depends upon the NMD factor UPF2. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	3
29755	High-Throughput Metabolomics Integrated Network Pharmacology Reveals the Underlying Mechanism of <i>Paeoniae Radix Alba</i> Treating Rheumatoid Arthritis. <i>Molecules</i> , 2022, 27, 7014.	1.7	2
29757	Developing human olfactory network and exploring olfactory receptor-odorant interaction. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-20.	2.0	0
29758	Integrated single-cell and transcriptome sequencing analyses determines a chromatin regulator-based signature for evaluating prognosis in lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
29761	A Network Pharmacology Study on the Cervix Prescription for Treatment of Cervical Cancer. <i>Journal of Immunology Research</i> , 2022, 2022, 1-13.	0.9	3
29762	Prognostic value, immune signature and molecular mechanisms of the APOBEC family members APOBEC1, APOBEC3A, APOBEC3G and APOBEC3H in pancreatic adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
29763	A proteome-scale map of the SARS-CoV-2â€œhuman contactome. <i>Nature Biotechnology</i> , 2023, 41, 140-149.	9.4	29
29765	An Integrated Bioinformatics Approach to Identify Network-Derived Hub Genes in Starving Zebrafish. <i>Animals</i> , 2022, 12, 2724.	1.0	1
29766	Novel six-gene prognostic signature based on colon adenocarcinoma immune-related genes. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
29767	Constructed the ceRNA network and predicted a FEZF1-AS1/miR-92b-3p/ZIC5 axis in colon cancer. <i>Molecular and Cellular Biochemistry</i> , 0, , .	1.4	0
29768	Multi-Omics Reveals Mechanisms of Partial Modulation of COVID-19 Dysregulation by Glucocorticoid Treatment. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12079.	1.8	11
29769	Global ubiquitinome analysis reveals the role of E3 ubiquitin ligase FaBRIZ in strawberry fruit ripening. <i>Journal of Experimental Botany</i> , 2023, 74, 214-232.	2.4	2

#	ARTICLE	IF	CITATIONS
29770	The spatial transcriptomic landscape of non-small cell lung cancer brain metastasis. <i>Nature Communications</i> , 2022, 13, .	5.8	30
29771	A comprehensive survey of the approaches for pathway analysis using multi-omics data integration. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	13
29772	Age-associated changes in microglia activation and Sirtuin-1- chromatin binding patterns. <i>Aging</i> , 0, , .	1.4	0
29773	Discovery of Homogentisic Acid as a Precursor in Trimethoprim Metabolism and Natural Product Biosynthesis. <i>ACS Chemical Biology</i> , 0, , .	1.6	1
29774	Elucidation of Functional Genes Associated with Long Chain-Polyunsaturated Fatty Acids (LC-PUFAs) Metabolism in Oleaginous Diatom <i>Phaeodactylum tricornutum</i> . <i>Hydrobiology</i> , 2022, 1, 451-468.	0.9	2
29777	Integrative analyses of immune-related biomarkers and associated mechanisms in coronary heart disease. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	1
29778	Natural remedies medicine derived from flaxseed (secoisolariciresinol diglucoside, lignans, and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 51. computational chemistry techniques and pharmacophore modeling. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	16
29779	Identification and functional analysis of m6A in the mammary gland tissues of dairy goats at the early and peak lactation stages. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
29780	Integrated analyses of brain and platelet omics reveal their common altered and driven molecules in Alzheimer's disease. <i>MedComm</i> , 2022, 3, .	3.1	2
29781	Characterization of immune features and immunotherapy response in subtypes of hepatocellular carcinoma based on mitophagy. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
29784	<i>Glycine max</i> (L.) Merr. (Soybean) metabolome responses to potassium availability. <i>Phytochemistry</i> , 2023, 205, 113472.	1.4	4
29785	CTRR-ncRNA: A Knowledgebase for Cancer Therapy Resistance and Recurrence Associated Non-Coding RNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 292-299.	3.0	0
29786	Pangenome-wide analysis of cyclic nucleotide-gated channel (CNGC) gene family in citrus Spp. Revealed their intraspecies diversity and potential roles in abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
29787	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in <i>Ganoderma</i> . <i>Molecular Ecology Resources</i> , 0, , .	2.2	4
29788	Multi-Organ Transcriptome Response of Lumpfish ( <i>Cyclopterus lumpus</i> ) to <i>Aeromonas salmonicida</i> Subspecies <i>salmonicida</i> Systemic Infection. <i>Microorganisms</i> , 2022, 10, 2113.	1.6	6
29789	Expression of NMU, PPBP and GNG4 in colon cancer and their influences on prognosis. <i>Translational Cancer Research</i> , 2022, 11, 3572-3583.	0.4	3
29790	Methods of quantifying interactions among populations using Lotka-Volterra models. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	7
29791	Through network pharmacology and molecular docking to explore the underlying mechanism of <i>Artemisia annua</i> L. treating in abdominal aortic aneurysm. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	2

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29792	miR-31 from Mesenchymal Stem Cell-Derived Extracellular Vesicles Alleviates Intervertebral Disc Degeneration by Inhibiting NFAT5 and Upregulating the Wnt/ $\beta$ 2-Catenin Pathway. <i>Stem Cells International</i> , 2022, 2022, 1-16.	1.2	7
29793	Network pharmacology analysis reveals neuroprotective effects of the Qin-Zhi-Zhu-Dan Formula in Alzheimer's disease. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	3
29794	MbHY5-MbYSL7 mediates chlorophyll synthesis and iron transport under iron deficiency in <i>Malus baccata</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29795	Integrative Bioinformatics Analysis Revealed Mitochondrial Dysfunction-Related Genes Underlying Intervertebral Disc Degeneration. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-35.	1.9	6
29796	Identifying Hub Genes Associated with Neoadjuvant Chemotherapy Resistance in Breast Cancer and Potential Drug Repurposing for the Development of Precision Medicine. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12628.	1.8	4
29798	A systems biology approach for investigating significantly expressed genes among COVID-19, hepatocellular carcinoma, and chronic hepatitis B. <i>Egyptian Journal of Medical Human Genetics</i> , 2022, 23, .	0.5	1
29799	Computed cancer interactome explains the effects of somatic mutations in cancers. <i>Protein Science</i> , 2022, 31, .	3.1	8
29800	Hepatic urea, creatinine and uric acid metabolism in dairy cows with divergent milk urea concentrations. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
29801	Exploring Molecular Targets and Mechanisms of Apigenin in the Treatment of Papillary Thyroid Carcinoma Based on Network Pharmacology and Molecular Docking Analysis. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211354.	0.2	1
29802	Gene co-expression network analysis revealed novel biomarkers for ovarian cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
29803	Profiling ATM regulated genes in <i>Drosophila</i> at physiological condition and after ionizing radiation. <i>Hereditas</i> , 2022, 159, .	0.5	0
29806	Comprehensive analysis of endoplasmic reticulum stress and immune infiltration in major depressive disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	5
29807	Amino acid (acyl carrier protein) ligase-associated biosynthetic gene clusters reveal unexplored biosynthetic potential. <i>Molecular Genetics and Genomics</i> , 0, , .	1.0	0
29808	Neutrophil Extracellular Vesicles and Airway Smooth Muscle Proliferation in the Natural Model of Severe Asthma in Horses. <i>Cells</i> , 2022, 11, 3347.	1.8	2
29809	Using Computational Drug-Gene Analysis to Identify Novel Therapeutic Candidates for Retinal Neuroprotection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12648.	1.8	2
29810	Humic Lake Exhibits Higher Microbial Functional Gene Diversity and Weaker Gene Interaction Efficiency than a Common Alkaline Lake. <i>Biology</i> , 2022, 11, 1448.	1.3	1
29811	The development and validation of a m6A-lncRNAs based prognostic model for overall survival in lung squamous cell carcinoma. <i>Journal of Thoracic Disease</i> , 2022, 14, 4055-4072.	0.6	2
29814	CircRNAs Related to Breast Muscle Development and Their Interaction Regulatory Network in Gushi Chicken. <i>Genes</i> , 2022, 13, 1974.	1.0	4

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29815	Genome-Wide Analysis and Characterization of SABATH Gene Family in Phaseolus vulgaris Genotypes Subject to Melatonin under Drought and Salinity Stresses. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 242-259.	1.0	5
29816	Integrated analysis and exploration of potential shared gene signatures between carotid atherosclerosis and periodontitis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	4
29817	Visualization of patterns of lymph node metastases in nonâ€‘small cell lung cancer using network analysis. <i>JTCVS Open</i> , 2022, 12, 410-425.	0.2	0
29818	Network pharmacology-based and experimental identification of the effects of Renshen Yangrong decoction on myocardial infarction. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
29819	Metabolic and transcriptomic analyses elucidate a novel insight into the network for biosynthesis of carbohydrate and secondary metabolites in the stems of a medicinal orchid <i>Dendrobium nobile</i> . <i>Plant Diversity</i> , 2022, , .	1.8	1
29820	Transcriptome analysis reveals the proline metabolic pathway and its potential regulation TF-hub genes in salt-stressed potato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
29821	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
29823	Tools for analyzing protonation states and for tracing proton transfer pathways with examples from the <i>Rb. sphaeroides</i> photosynthetic reaction centers. <i>Photosynthesis Research</i> , 2023, 156, 101-112.	1.6	4
29824	Detection of new candidate genes controlling seed weight by integrating gene coexpression analysis and QTL mapping in <i>Brassica napus</i> L.. <i>Crop Journal</i> , 2023, 11, 842-851.	2.3	2
29827	The significance of glycolysis index and its correlations with immune infiltrates in Alzheimerâ€™s disease. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
29828	In silico investigations identified Butyl Xanalterate to competently target CK2Î± (CSNK2A1) for therapy of chronic lymphocytic leukemia. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
29831	Gene signature predicting recurrence in oral squamous cell carcinoma is characterized by increased oxidative phosphorylation. <i>Molecular Oncology</i> , 2023, 17, 134-149.	2.1	3
29832	Body weight changes and bipolar disorder: a molecular pathway analysis. <i>Pharmacogenetics and Genomics</i> , 2022, 32, 308-320.	0.7	0
29833	Spatial metabolomics reveals upregulation of several pyrophosphate-producing pathways in cortical bone of Hyp mice. <i>JCI Insight</i> , 2022, 7, .	2.3	4
29834	Circulating U13 Small Nucleolar RNA as a Potential Biomarker in Huntingtonâ€™s Disease: A Pilot Study. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12440.	1.8	1
29835	Uncovering the Fungal Diversity Colonizing Limestone Walls of a Forgotten Monument in the Central Region of Portugal by High-Throughput Sequencing and Culture-Based Methods. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 10650.	1.3	10
29836	Librarians and Bioinformatics Communities Working Together to Advance Research and Instruction. <i>Advances in Library and Information Science</i> , 2022, , 249-269.	0.2	0
29837	Nitrogen fertilization and CO <sub>2</sub> concentration synergistically affect the growth and protein content of <i>Agropyron mongolicum</i> . <i>PeerJ</i> , 0, 10, e14273.	0.9	2



#	ARTICLE	IF	CITATIONS
29838	Wnt-pathway inhibitors with selective activity against triple-negative breast cancer: From thienopyrimidine to quinazoline inhibitors. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
29839	Integrated network pharmacology approach shows a potential role of Ginseng catechins and ginsenosides in modulating protein aggregation in Amyotrophic Lateral Sclerosis. <i>3 Biotech</i> , 2022, 12, .	1.1	6
29840	Hedysarum multijugum Maxim treats ulcerative colitis through the PI3K-AKT and TNF signaling pathway according to network pharmacology and molecular docking. <i>Annals of Translational Medicine</i> , 2022, 10, 1132-1132.	0.7	2
29842	Severity of COVID-19 patients with coexistence of asthma and vitamin D deficiency. <i>Informatics in Medicine Unlocked</i> , 2022, 34, 101116.	1.9	6
29843	The Sphingolipids Metabolism Mechanism and Associated Molecular Biomarker Investigation in Keloid. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 2003-2012.	0.6	2
29844	CircRNA-Based Cervical Cancer Prognosis Model, Immunological Validation and Drug Prediction. <i>Current Oncology</i> , 2022, 29, 7994-8018.	0.9	2
29846	<scp>APE1</scp> interacts with the nuclear exosome complex protein <scp>MTR4</scp> and is involved in cisplatin and 5-fluorouracil induced <scp>RNA</scp> damage response. <i>FEBS Journal</i> , 2023, 290, 1740-1764.	2.2	5
29847	Immune-associated pivotal biomarkers identification and competing endogenous RNA network construction in post-operative atrial fibrillation by comprehensive bioinformatics and machine learning strategies. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
29848	Early suppression of antiviral host response and protocadherins by SARS-CoV-2 Spike protein in THP-1-derived macrophage-like cells. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
29849	Bio-Computational Evaluation of Compounds of Bacopa Monnieri as a Potential Treatment for Schizophrenia. <i>Molecules</i> , 2022, 27, 7050.	1.7	2
29851	In silico analysis of key regulatory networks related to microfibril angle in Populus trichocarpa Hook., 0, .		0
29852	Dysregulation of Circulatory Levels of lncRNAs in Parkinson's Disease. <i>Molecular Neurobiology</i> , 2023, 60, 317-328.	1.9	8
29853	Immune cells transcriptome-based drug repositioning for multiple sclerosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
29854	RNA-Sequencing approach for exploring the therapeutic effect of umbilical cord mesenchymal stem/stromal cells on lipopolysaccharide-induced acute lung injury. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
29855	Downregulation of hsa-miR-135b-5p Inhibits Cell Proliferation, Migration, and Invasion in Colon Adenocarcinoma. <i>Genetical Research</i> , 2022, 2022, 1-19.	0.3	0
29856	lluminating the dark metabolome of Pseudo-nitzschia "microbiome associations. <i>Environmental Microbiology</i> , 2022, 24, 5408-5424.	1.8	6
29857	Distributional Pattern of Bacteria, Protists, and Diatoms in Ocean according to Water Depth in the Northern South China Sea. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
29858	Contrasting transcriptomic patterns reveal a genomic basis for drought resilience in the relict fir Abies pinsapo Boiss. <i>Tree Physiology</i> , 2023, 43, 315-334.	1.4	2

#	ARTICLE	IF	CITATIONS
29859	<i>Bacteroides vulgatus</i> SNUG 40005 Restores Akkermansia Depletion by Metabolite Modulation. <i>Gastroenterology</i> , 2023, 164, 103-116.	0.6	25
29860	Development of Single Nucleotide Polymorphism and Association Analysis with Growth Traits for Black Porgy ( <i>Acanthopagrus schlegelii</i> ). <i>Genes</i> , 2022, 13, 1992.	1.0	3
29861	Molecular Mechanisms of <i>Notopterygii</i> Rhizoma Et Radix for Treating Arrhythmia Based on Network Pharmacology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 26, .	0.6	0
29862	The Ecological Differentiation of Particle-Attached and Free-Living Bacterial Communities in a Seasonal Flooding Lake—the Poyang Lake. <i>Microbial Ecology</i> , 0, .	1.4	0
29863	Tissue-wide genetic and cellular landscape shapes the execution of sequential PRC2 functions in neural stem cell lineage progression. <i>Science Advances</i> , 2022, 8, .	4.7	4
29864	Evaluation of Salivary KCNJ3 mRNA Levels in Breast Cancer: A Case–control Study and in silico Analysis. <i>Open Dentistry Journal</i> , 2022, 16, .	0.2	1
29865	Underlying genetic architecture of resistance to mastitis in dairy cattle: A systematic review and gene prioritization analysis of genome-wide association studies. <i>Journal of Dairy Science</i> , 2023, 106, 323-351.	1.4	5
29866	Single-cell RNA sequencing reveals different signatures of mesenchymal stromal cell pluripotent-like and multipotent populations. <i>IScience</i> , 2022, 25, 105395.	1.9	5
29867	Inulin fibre promotes microbiota-derived bile acids and type 2 inflammation. <i>Nature</i> , 2022, 611, 578-584.	13.7	50
29868	Seroprevalence and systemic immune biomarkers associated with <i>Toxoplasma gondii</i> infection in blood donors from Southern Brazil. <i>Immunobiology</i> , 2022, 227, 152294.	0.8	1
29870	Community Dynamics of Free-Living and Particle-Attached Bacteria over Sequential Blooms of Heterotrophic Dinoflagellate <i>Noctiluca scintillans</i> and Mixotrophic Ciliate <i>Mesodinium rubrum</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
29872	Integration of single-cell transcriptome and chromatin accessibility of early gonads development among goats, pigs, macaques, and humans. <i>Cell Reports</i> , 2022, 41, 111587.	2.9	5
29873	The NESHIE and CP Genetics Resource (NCGR): A database of genes and variants reported in neonatal encephalopathy with suspected hypoxic ischemic encephalopathy (NESHIE) and consequential cerebral palsy (CP). <i>Genomics</i> , 2022, 114, 110508.	1.3	1
29874	Network inference from perturbation time course data. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	1.4	5
29875	Genome and transcriptome-wide study of carbamoyltransferase genes in major fleshy fruits: A multi-omics study of evolution and functional significance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29876	Swine acute diarrhea syndrome coronavirus induces autophagy to promote its replication via the Akt/mTOR pathway. <i>IScience</i> , 2022, 25, 105394.	1.9	2
29877	Rational drug repositioning for coronavirus-associated diseases using directional mapping and side-effect inference. <i>IScience</i> , 2022, 25, 105348.	1.9	3
29878	The impact of <i>Piscirickettsia salmonis</i> infection on genome-wide DNA methylation profile in Atlantic Salmon. <i>Genomics</i> , 2022, 114, 110503.	1.3	5

#	ARTICLE	IF	CITATIONS
29880	Environmental Response to Root Secondary Metabolite Accumulation in <i>Paeonia lactiflora</i> : Insights from Rhizosphere Metabolism and Root-Associated Microbial Communities. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
29881	Insights into symbiotic interactions from metatranscriptome analysis of deep-sea mussel <i>Gigantidas platifrons</i> under long-term laboratory maintenance. <i>Molecular Ecology</i> , 2023, 32, 444-459.	2.0	5
29882	IReNA: Integrated regulatory network analysis of single-cell transcriptomes and chromatin accessibility profiles. <i>IScience</i> , 2022, 25, 105359.	1.9	10
29883	A novel Boolean network inference strategy to model early hematopoiesis aging. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 21-33.	1.9	5
29884	The Rb/E2F axis is a key regulator of the molecular signatures instructing the quiescent and activated adult neural stem cell state. <i>Cell Reports</i> , 2022, 41, 111578.	2.9	7
29885	Genome-wide base editor screen identifies regulators of protein abundance in yeast. <i>ELife</i> , 0, 11, .	2.8	7
29888	Proteomic and metabolomic analysis uncovering Enterovirus A71 reprogramming host cell metabolic pathway. <i>Proteomics</i> , 2023, 23, .	1.3	0
29889	Identification of CKS1B as a prognostic indicator and a predictive marker for immunotherapy in pancreatic cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
29891	Structuring and validating a prognostic model for low-grade gliomas based on the genes for plasma membrane tension. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	3
29892	Transcriptional and functional consequences of alterations to MEF2C and its topological organization in neuronal models. <i>American Journal of Human Genetics</i> , 2022, 109, 2049-2067.	2.6	8
29893	Spatially resolved phosphoproteomics reveals fibroblast growth factor receptor recycling-driven regulation of autophagy and survival. <i>Nature Communications</i> , 2022, 13, .	5.8	9
29894	Identification of Molecular Markers Related to Immune Infiltration in Patients with Severe Asthma: A Comprehensive Bioinformatics Analysis Based on the Human Bronchial Epithelial Transcriptome. <i>Disease Markers</i> , 2022, 2022, 1-20.	0.6	1
29895	Effect of prior drought and heat stress on <i>Camellia sinensis</i> transcriptome changes to <i>Ectropis oblique</i> (Lepidoptera: Geometridae) resistance. <i>Genomics</i> , 2022, 114, 110506.	1.3	3
29896	Pharmacological mechanism and clinical study of Qiming granules in treating diabetic retinopathy based on network pharmacology and literature review. <i>Journal of Ethnopharmacology</i> , 2023, 302, 115861.	2.0	6
29897	Unravelling hub genes as potential therapeutic targets in lung cancer using integrated transcriptomic meta-analysis and in silico approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 9089-9102.	2.0	1
29898	Metabolomic fingerprint of cabbage resistance to <i>Mamestra brassicae</i> L. (Lepidoptera: Tj ETQq1 1 0.784314, 1.75 BT / Overlock 107	1.75	1
29899	Identification and validation of a classifier based on hub aging-related genes and aging subtypes correlation with immune microenvironment for periodontitis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
29900	Nuclear stabilization of p53 requires a functional nucleolar surveillance pathway. <i>Cell Reports</i> , 2022, 41, 111571.	2.9	17

#	ARTICLE	IF	CITATIONS
29901	Identification of key long non-coding RNA-associated competing endogenous RNA axes in Brodmann Area 10 brain region of schizophrenia patients. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	3
29902	Targeted proteomics identifies circulating biomarkers associated with active COVID-19 and post-COVID-19. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	10
29903	Prioritization of microRNA biomarkers for a prospective evaluation in a cohort of myocardial infarction patients based on their mechanistic role using public datasets. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	0
29904	A Systems Biology Approach on the Regulatory Footprint of Human Endogenous Retroviruses (HERVs). <i>Diseases (Basel, Switzerland)</i> , 2022, 10, 98.	1.0	2
29905	The dynamics of lncRNAs transcription in interspecific F1 allotriploid hybrids between Brassica species. <i>Genomics</i> , 2022, 114, 110505.	1.3	3
29906	In silico approaches uncovering the systematic function of N-phosphorylated proteins in human cells. <i>Computers in Biology and Medicine</i> , 2022, 151, 106280.	3.9	1
29907	Exploring the mechanism of andrographolide in the treatment of gastric cancer through network pharmacology and molecular docking. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
29908	Processes in DNA damage response from a whole-cell multi-omics perspective. <i>IScience</i> , 2022, 25, 105341.	1.9	4
29909	G protein controls stress readiness by modulating transcriptional and metabolic homeostasis in <i>Arabidopsis thaliana</i> and <i>Marchantia polymorpha</i> . <i>Molecular Plant</i> , 2022, 15, 1889-1907.	3.9	5
29910	A comparative Proteomics Analysis Identified Differentially Expressed Proteins in Pancreatic Cancer-Associated Stellate Cell Small Extracellular Vesicles. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100438.	2.5	4
29911	Comprehensive in silico prioritization of pathogenic nsSNPs in human $\beta$ -adducin gene towards finding its relation with cancer. , 2022, 34, 201119.		0
29912	Excessive HSP70/TLR2 activation leads to remodeling of the tumor immune microenvironment to resist chemotherapy sensitivity of mFOLFOX in colorectal cancer. <i>Clinical Immunology</i> , 2022, 245, 109157.	1.4	4
29913	Proteomics and histological assessment of an organotypic model of human skin following exposure to <i>Naja nigricollis</i> venom. <i>Toxicon</i> , 2022, 220, 106955.	0.8	5
29914	Metabonomic and transcriptomic analyses of <i>Camellia oleifera</i> flower buds treated with low-temperature stress during the flowering stage. <i>Industrial Crops and Products</i> , 2022, 189, 115874.	2.5	7
29915	Differential gene co-expression network analyses reveal novel molecules associated with transcriptional dysregulation of key biological processes in osteoarthritis knee cartilage. <i>Osteoarthritis and Cartilage Open</i> , 2022, 4, 100316.	0.9	2
29916	Dual RNA and 16S ribosomal DNA sequencing reveal arbuscular mycorrhizal fungi-mediated mitigation of selenate stress in <i>Zea mays</i> L. and reshaping of soil microbiota. <i>Ecotoxicology and Environmental Safety</i> , 2022, 247, 114217.	2.9	5
29917	The LCNetWork: An electronic representation of the mRNA-lncRNA-miRNA regulatory network underlying mechanisms of non-small cell lung cancer in humans, and its explorative analysis. <i>Computational Biology and Chemistry</i> , 2022, 101, 107781.	1.1	1
29918	Network pharmacology-based elucidation of bioactive compounds in propolis and putative underlying mechanisms against type-2 diabetes mellitus. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 5, 100183.	0.5	2

#	ARTICLE	IF	CITATIONS
29919	The regulation role and diagnostic value of fibrinogen-like protein 1 revealed by pan-cancer analysis. <i>Materials Today Bio</i> , 2022, 17, 100470.	2.6	2
29920	The chromosome-level <i>Melaleuca alternifolia</i> genome provides insights into the molecular mechanisms underlying terpenoids biosynthesis. <i>Industrial Crops and Products</i> , 2022, 189, 115819.	2.5	4
29921	Thermal acclimation results in persistent phosphoproteome changes in the freshwater planarian <i>Crenobia alpina</i> (Tricladida: Planariidae). <i>Journal of Thermal Biology</i> , 2022, 110, 103367.	1.1	0
29922	Evolution of the orthopoxvirus core genome. <i>Virus Research</i> , 2023, 323, 198975.	1.1	3
29923	Heterogeneity of sex-biased miRNAs profiling of <i>Cynoglossus semilaevis</i> between exosome and sperm. <i>Aquaculture</i> , 2023, 563, 738898.	1.7	0
29924	Desert plant transcriptomics and adaptation to abiotic stress. , 2023, , 199-256.		0
29925	An integrative analysis of lncRNAs and mRNAs highlights the potential roles of lncRNAs in the process of follicle selection in Taihang chickens. <i>Theriogenology</i> , 2023, 195, 122-130.	0.9	1
29926	Low expression of <i>ESR1</i> correlates with ascending aortic dilation and acute type A aortic dissection. <i>Gene</i> , 2023, 851, 147001.	1.0	2
29927	Metagenomic insight into the distribution of metal resistance genes within cascade reservoir waters: Synergic impacts of geographic variation and anthropogenic pollution. <i>Environmental Research</i> , 2023, 216, 114682.	3.7	4
29928	Å-tubulin contributes to Tongyang Huoxue decoction-induced protection against hypoxia/reoxygenation-induced injury of sinoatrial node cells through SIRT1-mediated regulation of mitochondrial quality surveillance. <i>Phytomedicine</i> , 2023, 108, 154502.	2.3	7
29929	Integrated transcriptomic and metabolomics analysis reveals abscisic acid signal transduction and sugar metabolism pathways as defense responses to cold stress in <i>Argyranthemum frutescens</i> . <i>Environmental and Experimental Botany</i> , 2023, 205, 105115.	2.0	14
29930	Identification of key adipogenic transcription factors for the pork belly parameters via the association weight matrix. <i>Meat Science</i> , 2023, 195, 109015.	2.7	2
29931	Fruit microbiome: A powerful tool to study the epidemiology of dry lenticel rot and white haze “ Emerging postharvest diseases of apple. <i>Postharvest Biology and Technology</i> , 2023, 196, 112163.	2.9	6
29932	Microbial indicators along a metallic contamination gradient in tropical coastal sediments. <i>Journal of Hazardous Materials</i> , 2023, 443, 130244.	6.5	6
29933	Characterization of circular RNA expression profiles in the age-related thymic involution of Magang goose. <i>Developmental and Comparative Immunology</i> , 2023, 139, 104581.	1.0	0
29934	Gephi: An Open Source Software for Exploring and Manipulating Networks. <i>Proceedings of the International AAAI Conference on Weblogs and Social Media</i> , 2009, 3, 361-362.	1.5	4,840
29935	Semantic Breakthrough in Drug Discovery. <i>Synthesis Lectures on Data, Semantics and Knowledge</i> , 2015, , .	3.9	2
29936	Expression Profiles, Prognosis and ceRNA Regulation of SOX Genes in Stomach Adenocarcinoma. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2022, , .	0.6	0

#	ARTICLE	IF	CITATIONS
29937	Analysis of signaling cascades from myeloma cells treated with pristimerin. <i>Advances in Protein Chemistry and Structural Biology</i> , 2023, , 147-174.	1.0	2
29938	Integrated bioinformatics analysis reveals novel key biomarkers in diabetic nephropathy. <i>SAGE Open Medicine</i> , 2022, 10, 205031212211370.	0.7	4
29939	Functional Analysis of Hypothetical Proteins of <i>Vibrio parahaemolyticus</i> Reveals the Presence of Virulence Factors and Growth-Related Enzymes With Therapeutic Potential. <i>Bioinformatics and Biology Insights</i> , 2022, 16, 117793222211360.	1.0	0
29940	Microbial co-occurrence networks as a biomonitoring tool for aquatic environments: a review. <i>Marine and Freshwater Research</i> , 2022, , .	0.7	1
29941	DNA repair-related genes and adipogenesis: Lessons from congenital lipodystrophies. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	1
29942	Simplifying network complexity of soil bacterial community exposed to short-term carbon dioxide and ozone enrichment in a paddy soil. <i>Journal of Environmental Management</i> , 2023, 326, 116656.	3.8	5
29943	Bioaugmentation with a defined bacterial consortium: A key to degrade high molecular weight polylactic acid during traditional composting. <i>Bioresource Technology</i> , 2023, 367, 128237.	4.8	15
29944	Transcriptome sequencing reveals neurotoxicity in embryonic neural stem/progenitor cells under heat stress. <i>Toxicology in Vitro</i> , 2023, 86, 105486.	1.1	0
29945	The common genes involved in the pathogenesis of Alzheimer's disease and type 2 diabetes and their implication for drug repositioning. <i>Neuropharmacology</i> , 2023, 223, 109327.	2.0	8
29946	Metabolic modeling of the International Space Station microbiome reveals key microbial interactions. <i>Microbiome</i> , 2022, 10, .	4.9	19
29947	Prostate cancer resistance leads to a global deregulation of translation factors and unconventional translation. <i>NAR Cancer</i> , 2022, 4, .	1.6	2
29948	Functional and Network Exploration of RNA Seq data of Breast Cancer. <i>Pakistan Biomedical Journal</i> , 0, , 28-33.	0.0	0
29949	Network pharmacology to uncover potential anti-inflammatory and immunomodulatory constituents in <i>Curcuma longa</i> rhizome as complementary treatment in COVID-19. <i>Pharmacia</i> , 2022, 69, 995-1003.	0.4	1
29950	Analysis of Exosomal MicroRNA Dynamics in Response to Rhinovirus Challenge in a Longitudinal Case-Control Study of Asthma. <i>Viruses</i> , 2022, 14, 2444.	1.5	4
29951	APPINetwork: an R package for building and computational analysis of protein-protein interaction networks. <i>PeerJ</i> , 0, 10, e14204.	0.9	0
29952	Resistance Training Modulates Reticulum Endoplasmic Stress, Independent of Oxidative and Inflammatory Responses, in Elderly People. <i>Antioxidants</i> , 2022, 11, 2242.	2.2	0
29953	A 10-year critical review on hydrogen peroxide as a disinfectant: could it be an alternative for household water treatment?. <i>Water Science and Technology: Water Supply</i> , 2022, 22, 8527-8539.	1.0	4
29954	Comparative Genomics of the Genus <i>Pseudomonas</i> Reveals Host- and Environment-Specific Evolution. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11



#	ARTICLE	IF	CITATIONS
29955	DPP9 as a Potential Novel Mediator in Gastrointestinal Virus Infection. <i>Antioxidants</i> , 2022, 11, 2177.	2.2	0
29956	Identification of Differentially Expressed Genes Related to Floral Bud Differentiation and Flowering Time in Three Populations of <i>Lycoris radiata</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 14036.	1.8	5
29957	Genome-wide identification and analysis of bZIP gene family reveal their roles during development and drought stress in Wheel Wingnut ( <i>Cyclocarya paliurus</i> ). <i>BMC Genomics</i> , 2022, 23, .	1.2	5
29958	Characteristics of oral microbiome of healthcare workers in different clinical scenarios: a cross-sectional analysis. <i>BMC Oral Health</i> , 2022, 22, .	0.8	0
29959	Transcriptome analysis of intestine from alk-SMase knockout mice reveals the effect of alk-SMase. <i>Cancer Cell International</i> , 2022, 22, .	1.8	3
29960	Bacterial Magnetosomes Release Iron Ions and Induce Regulation of Iron Homeostasis in Endothelial Cells. <i>Nanomaterials</i> , 2022, 12, 3995.	1.9	2
29961	MicroRNA-217 aggravates breast cancer through activation of NF1-mediated HSF1/ATG7 axis and c-Jun/ATF3/MMP13 axis. <i>Human Cell</i> , 2023, 36, 377-392.	1.2	1
29962	An integrated in silico-in vitro approach for identifying therapeutic targets against osteoarthritis. <i>BMC Biology</i> , 2022, 20, .	1.7	2
29963	Structure-guided product determination of the bacterial type II diterpene synthase Tpn2. <i>Communications Chemistry</i> , 2022, 5, .	2.0	4
29964	Identification of the miR-423-3p/VLDLR Regulatory Network for Glioma Using Transcriptome Analysis. <i>Neurochemical Research</i> , 2022, 47, 3864-3901.	1.6	1
29965	Ten simple rules for developing visualization tools in genomics. <i>PLoS Computational Biology</i> , 2022, 18, e1010622.	1.5	1
29966	Modulation of HERV Expression by Four Different Encephalitic Arboviruses during Infection of Human Primary Astrocytes. <i>Viruses</i> , 2022, 14, 2505.	1.5	3
29967	Identification of the Potential Molecular Mechanism of TGFBI Gene in Persistent Atrial Fibrillation. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-14.	0.7	0
29968	Exploratory Analysis of the Sasang Constitution by Combining Network Analysis and Information Entropy. <i>Healthcare (Switzerland)</i> , 2022, 10, 2248.	1.0	3
29969	The transcription factor IRF2 drives interferon-mediated CD8+ T cell exhaustion to restrict anti-tumor immunity. <i>Immunity</i> , 2022, 55, 2369-2385.e10.	6.6	29
29970	Genetic regulation of serum IgA levels and susceptibility to common immune, infectious, kidney, and cardio-metabolic traits. <i>Nature Communications</i> , 2022, 13, .	5.8	19
29971	Genetic architecture of natural variation of cardiac performance from flies to humans. <i>ELife</i> , 0, 11, .	2.8	5
29972	Systems biology reveals anatabine to be an NRF2 activator. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2

#	ARTICLE	IF	CITATIONS
29976	Computer-Aided Screening and Revealing Action Mechanism of Food-Derived Tripeptides Intervention in Acute Colitis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13471.	1.8	2
29977	Transcriptome Analysis Reveals the Anti-Tumor Mechanism of Eucalyptol Treatment on Neuroblastoma Cell Line SH-SY5Y. <i>Neurochemical Research</i> , 2022, 47, 3854-3862.	1.6	3
29978	Identification of protein profile in metacyclic and amastigote-like stages of <i>Leishmania tropica</i> : a proteomic approach. <i>AMB Express</i> , 2022, 12, .	1.4	2
29979	Multimiomics analysis elucidated molecular mechanism of aromatic amino acid biosynthesis in <i>Akebia trifoliata</i> fruit. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29980	Construction of a potentially functional lncRNA-miRNA-mRNA network in sepsis by bioinformatics analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29981	Distinct immunological and molecular signatures underpinning influenza vaccine responsiveness in the elderly. <i>Nature Communications</i> , 2022, 13, .	5.8	6
29983	Biologically evolved dual-pathway catalytic pattern indicating an efficient bioremediation strategy for phenol removal. <i>Chemical Engineering Journal</i> , 2023, 454, 140195.	6.6	6
29984	Contrasting modes of macro and microsynteny evolution in a eukaryotic subphylum. <i>Current Biology</i> , 2022, 32, 5335-5343.e4.	1.8	8
29985	Comprehensive Genomic Characterization of the NAC Transcription Factors and Their Response to Drought Stress in <i>Dendrobium catenatum</i> . <i>Agronomy</i> , 2022, 12, 2753.	1.3	6
29986	Valorization of Invasive Plant Extracts against the Bispecies Biofilm <i>Staphylococcus aureus</i> – <i>Candida albicans</i> by a Bioguided Molecular Networking Screening. <i>Antibiotics</i> , 2022, 11, 1595.	1.5	2
29988	WDR43 is a potential diagnostic biomarker and therapeutic target for osteoarthritis complicated with Parkinson's disease. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	1.8	3
29989	A Comprehensive Study of De Novo Mutations on the Protein-Protein Interaction Interfaces Provides New Insights into Developmental Delay. <i>Biomolecules</i> , 2022, 12, 1643.	1.8	0
29990	Bioinformatics and systems biology approaches to identify molecular targeting mechanism influenced by COVID-19 on heart failure. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
29991	Towards a knowledge graph for pre-/probiotics and microbiota–gut–brain axis diseases. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
29992	Glial progenitor cells of the adult human white and grey matter are contextually distinct. <i>Glia</i> , 2023, 71, 524-540.	2.5	5
29995	Perturbations in common and distinct inflammatory pathways associated with morning and evening fatigue in outpatients receiving chemotherapy. <i>Cancer Medicine</i> , 2023, 12, 7369-7380.	1.3	5
29996	CHRN2 represses pancreatic cancer migration and invasion via inhibiting $\beta$ -catenin pathway. <i>Cancer Cell International</i> , 2022, 22, .	1.8	3
29997	Microbiome assembly and maintenance across the lifespan of bumble bee workers. <i>Molecular Ecology</i> , 2023, 32, 724-740.	2.0	17

#	ARTICLE	IF	CITATIONS
29999	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	7
30000	Comprehensive Phenotyping in Inflammatory Bowel Disease: Search for Biomarker Algorithms in the Transkingdom Interactions Context. <i>Microorganisms</i> , 2022, 10, 2190.	1.6	1
30001	Integrative cross-species analysis of GABAergic neuron cell types and their functions in Alzheimer's disease. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30003	Evolution patterns of NBS genes in the genus <i>Dendrobium</i> and NBS-LRR gene expression in <i>D. officinale</i> by salicylic acid treatment. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
30004	Pantranscriptome combined with phenotypic quantification reveals germplasm kinship and regulation network of bract color variation in <i>Bougainvillea</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30006	Flexible response and rapid recovery strategies of the plateau forage <i>Poa crymophila</i> to cold and drought. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30008	The evolutionary landscape and expression pattern of plant lincRNAs. <i>RNA Biology</i> , 2022, 19, 1190-1207.	1.5	6
30009	Single-cell RNA-sequencing and microarray analyses to explore the pathological mechanisms of chronic thromboembolic pulmonary hypertension. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
30010	Crosstalk between Thyroid Hormone and Corticosteroid Signaling Targets Cell Proliferation in <i>Xenopus tropicalis</i> Tadpole Liver. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13715.	1.8	1
30011	Trends in extracellular matrix biology. <i>Molecular Biology Reports</i> , 2023, 50, 853-863.	1.0	12
30016	Ferroptosis-related differentially expressed genes serve as new biomarkers in ischemic stroke and identification of therapeutic drugs. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
30018	Identification of six hub genes and two key pathways in two rat renal fibrosis models based on bioinformatics and RNA-seq transcriptome analyses. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
30019	Molecular Insights into the Heterotropic Allosteric Mechanism in Cytochrome P450 3A4-Mediated Midazolam Metabolism. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 5762-5770.	2.5	3
30020	Retinal regions shape human and murine Müller cell proteome profile and functionality. <i>Glia</i> , 2023, 71, 391-414.	2.5	5
30021	Discovery of Levesquamide B through Global Natural Product Social Molecular Networking. <i>Molecules</i> , 2022, 27, 7794.	1.7	2
30022	Transcriptome analysis of differentially expressed circRNAs miRNAs and mRNAs during the challenge of coccidiosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
30024	Multiomic Data Integration in the Analysis of Drought-Responsive Mechanisms in <i>Quercus ilex</i> Seedlings. <i>Plants</i> , 2022, 11, 3067.	1.6	8
30026	Exploration of the shared gene signatures and molecular mechanisms between atherosclerosis and rheumatoid arthritis via multi-microarray data analyses. <i>Annals of Translational Medicine</i> , 2022, 10, 1164-1164.	0.7	0

#	ARTICLE	IF	CITATIONS
30027	Genome-wide profiling reveals pervasive transcriptional alterations in fibroblasts derived from lesional skin in vitiligo including a reduced potential to proliferate. <i>Experimental Dermatology</i> , 0, , .	1.4	2
30029	An RNA granule for translation quality control in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Science</i> , 0, , .	1.2	0
30030	Genistein Modified with 8-Prenyl Group Suppresses Osteoclast Activity Directly via Its Prototype but Not Metabolite by Gut Microbiota. <i>Molecules</i> , 2022, 27, 7811.	1.7	0
30031	A Metabolomics-Based Toolbox to Assess and Compare the Metabolic Potential of Unexplored, Difficult-to-Grow Bacteria. <i>Marine Drugs</i> , 2022, 20, 713.	2.2	0
30032	CORUM: the comprehensive resource of mammalian protein complexesâ€“2022. <i>Nucleic Acids Research</i> , 2023, 51, D539-D545.	6.5	34
30033	Human Gut Metagenomes Encode Diverse GH156 Sialidases. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	5
30034	Transposable elements orchestrate subgenome-convergent and -divergent transcription in common wheat. <i>Nature Communications</i> , 2022, 13, .	5.8	16
30036	Development of a ferroptosis-based model to predict prognosis, tumor microenvironment, and drug response for lung adenocarcinoma with weighted genes co-expression network analysis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
30037	Knockout and Restoration Reveal Differential Functional Roles of PPAR <sup>Î³</sup> 1 and PPAR <sup>Î³</sup> 2 in Chicken Adipogenesis. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 14959-14973.	2.4	4
30038	Multi-omics inference of differential breast cancer-related transcriptional regulatory network gene hubs between young Black and White patients. <i>Cancer Genetics</i> , 2023, 270-271, 1-11.	0.2	4
30039	Deciphering the impact and mechanism of Trikatu, a spices-based formulation on alcoholic liver disease employing network pharmacology analysis and in vivo validation. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	15
30040	<i>Bacteroides fragilis</i> derived metabolites, identified by molecular networking, decrease <i>Salmonella</i> virulence in mice model. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
30042	Discovery of <i>Taxus chinensis</i> fruit wine as potentially functional food against Alzheimer's disease by UHPLC-MS/MS, network pharmacology and molecular docking. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	1
30043	Identification of key biomarkers in neonatal sepsis by integrated bioinformatics analysis and clinical validation. <i>Heliyon</i> , 2022, 8, e11634.	1.4	2
30045	Mapping of the plant SnRK1 kinase signalling network reveals a key regulatory role for the class II T6P synthase-like proteins. <i>Nature Plants</i> , 2022, 8, 1245-1261.	4.7	41
30046	Comparison of the signaling pathways of wing dimorphism regulated by biotic and abiotic stress in the brown planthopper. <i>Insect Science</i> , 2023, 30, 1046-1062.	1.5	2
30047	Noonindoles Aâ€“F: Rare Indole Diterpene Amino Acid Conjugates from a Marine-Derived Fungus, <i>Aspergillus noonimiae</i> CMB-M0339. <i>Marine Drugs</i> , 2022, 20, 698.	2.2	3
30049	The single-cell expression profile of transposable elements and transcription factors in human early biparental and uniparental embryonic development. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	4

#	ARTICLE	IF	CITATIONS
30050	Host Cell Amplification of Nutritional Stress Contributes To Persistence in Chlamydia trachomatis. MBio, 2022, 13, .	1.8	4
30051	Molecular mechanisms underlying hypertensive effect of fructose and the preventive properties of inulin â€“ Global transcriptomic analysis in rat aorta. Nutrition, Metabolism and Cardiovascular Diseases, 2023, 33, 441-456.	1.1	0
30052	Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. F1000Research, 0, 11, 458.	0.8	0
30053	Altered Serum Bile Acid Profile Associated with Chronic Allograft Dysfunction in Kidney Transplant Recipients. Annals of Transplantation, 0, 27, .	0.5	1
30054	Downregulation of miR-671-5p promotes IL-10 mRNA increase in porcine moDCs stimulated with the probiotic BB12. Molecular Biology Reports, 2023, 50, 919-925.	1.0	2
30055	Role of hippocampal circKcnk9 in visceral hypersensitivity and anxiety comorbidity of irritable bowel syndrome. Frontiers in Cellular Neuroscience, 0, 16, .	1.8	2
30056	Genes associated with diagnosis and prognosis of Burkitt lymphoma. IET Systems Biology, 0, , .	0.8	1
30057	Identification of potential key genes related to idiopathic male infertility using RNA-sequencing data: an <i>in-silico</i> approach. Human Fertility, 2023, 26, 1149-1163.	0.7	2
30058	Specific signature biomarkers highlight the potential mechanisms of circulating neutrophils in aneurysmal subarachnoid hemorrhage. Frontiers in Pharmacology, 0, 13, .	1.6	4
30059	Therapeutic effects of Guilu-Erxian-Glue treatment on oligoasthenospermia: Evidence from network pharmacology, molecular docking, and in vivo experimental validation. Pharmacological Research Modern Chinese Medicine, 2022, , 100188.	0.5	0
30061	Microbially driven fate of terrigenous particulate organic matter in oceans. Limnology and Oceanography, 2023, 68, 148-164.	1.6	7
30062	Integrated Genomic and Transcriptomic Elucidation of Flowering in Garlic. International Journal of Molecular Sciences, 2022, 23, 13876.	1.8	1
30063	H2S contributed from CSE during cellular senescence suppresses inflammation and nitrosative stress. Biochimica Et Biophysica Acta - Molecular Cell Research, 2023, 1870, 119388.	1.9	4
30064	Bioinformatics analysis identifies ferroptosisâ€™related genes in the regulatory mechanism of myocardial infarction. Experimental and Therapeutic Medicine, 2022, 24, .	0.8	0
30066	Can machine learning â€™transformâ€™™ peptides/peptidomimetics into small molecules? A case study with ghrelin receptor ligands. Molecular Diversity, 0, , .	2.1	0
30067	NT-proBNP and stem cell factor plasma concentrations are independently associated with cardiovascular outcomes in end-stage renal disease hemodialysis patients. European Heart Journal Open, 2022, 2, .	0.9	1
30068	Buffy Coat Transcriptomic Analysis Reveals Alterations in Host Cell Protein Synthesis and Cell Cycle in Severe COVID-19 Patients. International Journal of Molecular Sciences, 2022, 23, 13588.	1.8	7
30069	Chromosomally Unstable Gastric Cancers Overexpressing Claudin-6 Disclose Cross-Talk between HNF1A and HNF4A, and Upregulated Cholesterol Metabolism. International Journal of Molecular Sciences, 2022, 23, 13977.	1.8	5

#	ARTICLE	IF	CITATIONS
30070	Indirect Immobilised Jagged-1 Enhances Matrisome Proteins Associated with Osteogenic Differentiation of Human Dental Pulp Stem Cells: A Proteomic Study. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13897.	1.8	3
30071	MK-2206 Alleviates Renal Fibrosis by Suppressing the Akt/mTOR Signaling Pathway In Vivo and In Vitro. <i>Cells</i> , 2022, 11, 3505.	1.8	3
30072	Structure and function of prodrug-activating peptidases. <i>Biochimie</i> , 2023, 205, 124-135.	1.3	4
30073	Multiple-Molecule Drug Repositioning for Disrupting Progression of SARS-CoV-2 Infection by Utilizing the Systems Biology Method through Host-Pathogen-Interactive Time Profile Data and DNN-Based DTI Model with Drug Design Specifications. <i>Stresses</i> , 2022, 2, 405-436.	1.8	2
30075	Heterogeneity of neutrophils and inflammatory responses in patients with COVID-19 and healthy controls. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
30076	Architecture of the outbred brown fat proteome defines regulators of metabolic physiology. <i>Cell</i> , 2022, 185, 4654-4673.e28.	13.5	9
30077	Bioinformatic analysis of potential biomarkers and mechanisms of immune infiltration in mitral regurgitation complicated by atrial fibrillation. <i>Annals of Translational Medicine</i> , 2022, 10, 1174-1174.	0.7	0
30078	A Pan-Cancer Atlas of Differentially Interacting Hallmarks of Cancer Proteins. <i>Journal of Personalized Medicine</i> , 2022, 12, 1919.	1.1	4
30079	Comparative Transcriptome Profiling of Two Contrasting Foxtail Millet Cultivars Provides Insights into Molecular Mechanisms Underlying Dehydration Stress Response. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 6425-6443.	2.8	2
30081	Ferroptosis-related biomarkers for Alzheimer's disease: Identification by bioinformatic analysis in hippocampus. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	1.8	7
30082	Mendelian randomization and pathway analysis demonstrate shared genetic associations between lupus and coronary artery disease. <i>Cell Reports Medicine</i> , 2022, 3, 100805.	3.3	11
30083	MiRNA/mRNA network topology in hepatitis virus B-related liver cirrhosis reveals miR-20a-5p/340-5p as hubs initiating fibrosis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	1
30084	Enterococci enhance <i>Clostridioides difficile</i> pathogenesis. <i>Nature</i> , 2022, 611, 780-786.	13.7	48
30085	Rosemary essential oil and its components 1,8-cineole and $\alpha$ -pinene induce ROS-dependent lethality and ROS-independent virulence inhibition in <i>Candida albicans</i> . <i>PLoS ONE</i> , 2022, 17, e0277097.	1.1	10
30086	Drug Repositioning Identifies Six Drug Candidates for Systemic Autoimmune Diseases by Integrative Analyses of Transcriptomes from Scleroderma, Systemic Lupus Erythematosus, and Sjogren's Syndrome. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 683-693.	1.0	1
30087	Traditional Chinese medicine method of tonifying kidney for hypertension: Clinical evidence and molecular mechanisms. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	3
30088	Warmer ambient air temperatures reduce nasal turbinate and brain infection, but increase lung inflammation in the K18-hACE2 mouse model of COVID-19. <i>Science of the Total Environment</i> , 2022, , 160163.	3.9	6
30089	Structural Diversity, LC-MS-MS Analysis and Potential Biological Activities of <i>Brevibacillus laterosporus</i> Extract. <i>Metabolites</i> , 2022, 12, 1102.	1.3	6



#	ARTICLE	IF	CITATIONS
30090	Identification of Key Genes and Pathways Associated with Preeclampsia by a WGCNA and an Evolutionary Approach. <i>Genes</i> , 2022, 13, 2134.	1.0	3
30091	Combination of WFDC2, CHI3L1, and KRT19 in Plasma Defines a Clinically Useful Molecular Phenotype Associated with Prognosis in Critically Ill COVID-19 Patients. <i>Journal of Clinical Immunology</i> , 2023, 43, 286-298.	2.0	7
30092	WINNER: A network biology tool for biomolecular characterization and prioritization. <i>Frontiers in Big Data</i> , 0, 5, .	1.8	2
30093	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. <i>Genomics</i> , 2022, 114, 110518.	1.3	2
30094	Diving into the Molecular Diversity of <i>Aplysina cavernicola</i> ™ Exometabolites: Contribution of Bromo-Spiroisoxazoline Alkaloids. <i>ACS Omega</i> , 0, , .	1.6	1
30095	Deciphering the Role and Signaling Pathways of PKC $\delta$ in Luminal A Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14023.	1.8	1
30096	Cortical Pathology in Vanishing White Matter. <i>Cells</i> , 2022, 11, 3581.	1.8	2
30097	Halogenated boroxine increases propensity to apoptosis in leukemia (UT $\delta$ ) but not non-tumor cells <i>in vitro</i> . <i>FEBS Open Bio</i> , 2023, 13, 143-153.	1.0	1
30098	Construction of a ceRNA network in polycystic ovary syndrome (PCOS) driven by exosomal lncRNA. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
30099	Identifying Prognostic Biomarkers Related to m6A Modification and Immune Infiltration in Renal Cell Carcinoma. <i>Genes</i> , 2022, 13, 2059.	1.0	2
30100	Proteogenomic analysis of lung adenocarcinoma reveals tumor heterogeneity, survival determinants, and therapeutically relevant pathways. <i>Cell Reports Medicine</i> , 2022, 3, 100819.	3.3	15
30101	Integrative transcriptomic and metabolomic analyses reveal the flavonoid biosynthesis of <i>Pyrus hopeiensis</i> flowers under cold stress. <i>Horticultural Plant Journal</i> , 2023, 9, 395-413.	2.3	10
30102	Non-coding transcriptomic profiles in the sheep mammary gland during different lactation periods. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
30103	The bacteriome of the halophyte <i>Atriplex nummularia</i> (old man saltbush) in salt-affected soils - an ecological model. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	2
30104	CEACAM5 inhibits the lymphatic metastasis of head and neck squamous cell carcinoma by regulating epithelial-mesenchymal transition via inhibiting MDM2. <i>Clinical Science</i> , 2022, 136, 1691-1710.	1.8	2
30105	Dynamic analysis of gene signatures in the progression of COPD. <i>ERJ Open Research</i> , 2023, 9, 00343-2022.	1.1	1
30106	A prognostic gene signature for gastric cancer and the immune infiltration-associated mechanism underlying the signature gene, PLG. <i>Clinical and Translational Oncology</i> , 0, , .	1.2	2
30107	Identification of potential microRNAs regulating metabolic plasticity and cellular phenotypes in glioblastoma. <i>Molecular Genetics and Genomics</i> , 0, , .	1.0	0

#	ARTICLE	IF	CITATIONS
30108	In silico analysis of koranimine, a cyclic imine compound from <i>Peribacillus frigoritolerans</i> reveals potential nematocidal activity. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
30109	Single-cell transcriptomic analysis of the tumor ecosystem of adenoid cystic carcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
30110	Bacterial Microbiota and Soil Fertility of <i>Crocus sativus</i> L. Rhizosphere in the Presence and Absence of <i>Fusarium</i> spp.. <i>Land</i> , 2022, 11, 2048.	1.2	2
30111	Integrated Analysis of Long Non-Coding RNA and mRNA to Reveal Putative Candidate Genes Associated with Backfat Quality in Beijing Black Pig. <i>Foods</i> , 2022, 11, 3654.	1.9	0
30112	Alignment and Analysis of a Disparately Acquired Multibatch Metabolomics Study of Maternal Pregnancy Samples. <i>Journal of Proteome Research</i> , 2022, 21, 2936-2946.	1.8	2
30113	Identification and differential analysis of noncoding RNAs in response to drought in <i>Phyllostachys aureosulcata</i> f. <i>spectabilis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30114	Proteomic analysis identifies a signature of disease severity in the plasma of COVID-19 pneumonia patients associated to neutrophil, platelet and complement activation. <i>Clinical Proteomics</i> , 2022, 19, .	1.1	10
30115	DIAMIN: a software library for the distributed analysis of large-scale molecular interaction networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
30116	Systems Biology in ELIXIR: modelling in the spotlight. <i>F1000Research</i> , 0, 11, 1265.	0.8	1
30117	FABP5 controls macrophage alternative activation and allergic asthma by selectively programming long-chain unsaturated fatty acid metabolism. <i>Cell Reports</i> , 2022, 41, 111668.	2.9	19
30121	Comprehensive analysis of the prognostic value and functions of prefoldins in hepatocellular carcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
30122	Protein prediction models support widespread post-transcriptional regulation of protein abundance by interacting partners. <i>PLoS Computational Biology</i> , 2022, 18, e1010702.	1.5	4
30123	Loss of transcription factor TFEB dysregulates the G1/S transition and DNA replication in mammary epithelial cells. <i>Journal of Biological Chemistry</i> , 2022, , 102692.	1.6	0
30124	Sequential gene expression analysis of cervical malignant transformation identifies RFC4 as a novel diagnostic and prognostic biomarker. <i>BMC Medicine</i> , 2022, 20, .	2.3	2
30127	Molecular Networking and On-Tissue Chemical Derivatization for Enhanced Identification and Visualization of Steroid Glycosides by MALDI Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2022, 94, 15971-15979.	3.2	5
30128	NLRscape: an atlas of plant NLR proteins. <i>Nucleic Acids Research</i> , 2023, 51, D1470-D1482.	6.5	9
30129	Overexpression of transmembrane TNF $\pm$ in brain endothelial cells induces schizophrenia-relevant behaviors. <i>Molecular Psychiatry</i> , 2023, 28, 843-855.	4.1	3
30130	Integrative omics indicate FMRP sequesters mRNA from translation and deadenylation in human neuronal cells. <i>Molecular Cell</i> , 2022, 82, 4564-4581.e11.	4.5	6

#	ARTICLE	IF	CITATIONS
30131	Genomic architecture of autism from comprehensive whole-genome sequence annotation. <i>Cell</i> , 2022, 185, 4409-4427.e18.	13.5	66
30132	Identification of the hub genes related to adipose tissue metabolism of bovine. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
30133	Construction of lncRNA TYMSOS/hsa-miR-101-3p/CEP55 and TYMSOS/hsa-miR-195-5p/CHEK1 Axis in Non-small Cell Lung Cancer. <i>Biochemical Genetics</i> , 2023, 61, 995-1014.	0.8	3
30134	Genome-wide identification of GRF gene family and their contribution to abiotic stress response in pitaya ( <i>Hylocereus polyrhizus</i> ). <i>International Journal of Biological Macromolecules</i> , 2022, 223, 618-635.	3.6	10
30135	Identification and validation of core genes as promising diagnostic signature in hepatocellular carcinoma based on integrated bioinformatics approach. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
30136	PARP1 proximity proteomics reveals interaction partners at stressed replication forks. <i>Nucleic Acids Research</i> , 2022, 50, 11600-11618.	6.5	14
30137	A systems biology approach towards oral cancer using computational tools and techniques. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2022, 231, 104709.	1.8	0
30138	Growth, photosynthetic pigment proteins responses and transcriptome analysis provide insights into survival strategies against short-term cold stress in the blue-green algae, <i>Arthrospira</i> . <i>Aquaculture Reports</i> , 2022, 27, 101403.	0.7	1
30139	Mapping the mutual transcriptional responses during <i>Candida albicans</i> and human macrophage interactions by dual RNA-sequencing. <i>Microbial Pathogenesis</i> , 2022, 173, 105864.	1.3	0
30140	Splicing factor SRSF1 controls autoimmune-related molecular pathways in regulatory T cells distinct from FoxP3. <i>Molecular Immunology</i> , 2022, 152, 140-152.	1.0	3
30141	Transcriptomic identification of key genes in Pacific oysters <i>Crassostrea gigas</i> responding to major abiotic and biotic stressors. <i>Fish and Shellfish Immunology</i> , 2022, 131, 1027-1039.	1.6	0
30142	The circ_0002538/miR-138-5p/plasmalipin axis regulates Schwann cell migration and myelination in diabetic peripheral neuropathy. <i>Neural Regeneration Research</i> , 2023, 18, 1591.	1.6	6
30143	Identification of fatty acid metabolism-related molecular subtype biomarkers and their correlation with immune checkpoints in cutaneous melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
30145	MSClustering: A Cytoscape Tool for Multi-Level Clustering of Biological Networks. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14240.	1.8	2
30147	Transcriptome Sequencing Reveals Tgf- $\beta$ -Mediated Noncoding RNA Regulatory Mechanisms Involved in DNA Damage in the 661W Photoreceptor Cell Line. <i>Genes</i> , 2022, 13, 2140.	1.0	2
30148	Integrative metabolic analysis of orbital adipose/connective tissue in patients with thyroid-associated ophthalmopathy. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	4
30149	Integrated analysis of comprehensive metabolomics and network pharmacology to reveal the mechanisms of <i>Abelmoschus manihot</i> (L.) Medik. in the treatment of cisplatin-induced chronic kidney disease. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
30151	Identification of potential targets of cinnamon for treatment against Alzheimer's disease-related GABAergic synaptic dysfunction using network pharmacology. <i>Scientific Reports</i> , 2022, 12, .	1.6	6

#	ARTICLE	IF	CITATIONS
30152	Network pharmacology and molecular docking-based analysis of protective mechanism of MLIF in ischemic stroke. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	0
30153	Investigating the Assemblages of Two Groups of Collembola (Strong Furca and Weak Furca) under Different Agricultural Management Systems, Northeastern China. <i>Diversity</i> , 2022, 14, 994.	0.7	1
30155	Genome-wide dissection of changes in maize root system architecture during modern breeding. <i>Nature Plants</i> , 2022, 8, 1408-1422.	4.7	32
30156	Diverse viruses of marine archaea discovered using metagenomics. <i>Environmental Microbiology</i> , 2023, 25, 367-382.	1.8	12
30157	Transcriptomic study reveals lncRNA-mediated downregulation of innate immune and inflammatory response in the SARS-CoV-2 vaccination breakthrough infections. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
30158	Identification of NRAS Diagnostic Biomarkers and Drug Targets for Endometrial Cancer—An Integrated in Silico Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14285.	1.8	1
30159	Metabolomics study identified bile acids as potential biomarkers for gastric cancer: A case control study. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	6
30160	Ferroptosis related genes participate in the pathogenesis of spinal cord injury via HIF-1 signaling pathway. <i>Brain Research Bulletin</i> , 2023, 192, 192-202.	1.4	8
30162	Gene expression analysis in cervical cancer progression: Towards unveiling alterations from normal to tumoral tissue. , 2022, , 201131.		0
30163	Enteroendocrine peptides, growth, and the microbiome during the porcine weaning transition. <i>Animal Microbiome</i> , 2022, 4, .	1.5	3
30165	Comprehensive bioinformatics analysis and molecular validation of lncRNAs-mediated ceRNAs network in schizophrenia. <i>Life Sciences</i> , 2023, 312, 121205.	2.0	1
30166	A Computationally Constructed lncRNA-Associated Competing Triplet Network in Clear Cell Renal Cell Carcinoma. <i>Disease Markers</i> , 2022, 2022, 1-11.	0.6	0
30168	Atlas of interactions between SARS-CoV-2 macromolecules and host proteins. , 2023, 2, 100068.		6
30172	A Pan-Transcriptome Analysis Indicates Efficient Downregulation of the FIB Genes Plays a Critical Role in the Response of Alfalfa to Cold Stress. <i>Plants</i> , 2022, 11, 3148.	1.6	3
30173	Identification of Competing Endogenous RNAs (ceRNAs) Network Associated with Drought Tolerance in <i>Medicago truncatula</i> with <i>Rhizobium</i> Symbiosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14237.	1.8	2
30175	Spatiotemporal transcriptome analysis reveals critical roles for mechano-sensing genes at the border zone in remodeling after myocardial infarction. , 2022, 1, 1072-1083.		19
30176	Multi-omics to predict changes during cold pressor test. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
30177	Whole-transcriptome sequencing revealed differentially expressed mRNAs and non-coding RNAs played crucial roles in NiONPs-induced liver fibrosis. <i>Ecotoxicology and Environmental Safety</i> , 2022, 248, 114308.	2.9	2

#	ARTICLE	IF	CITATIONS
30178	Single-cell RNA-seq analysis to identify potential biomarkers for diagnosis, and prognosis of non-small cell lung cancer by using comprehensive bioinformatics approaches. <i>Translational Oncology</i> , 2023, 27, 101571.	1.7	9
30180	Time-course transcriptome analysis reveals regulation of Arabidopsis seed dormancy by the transcription factors WOX11/12. <i>Journal of Experimental Botany</i> , 2023, 74, 1090-1106.	2.4	5
30181	Toward building mass spectrometry-based metabolomics and lipidomics atlases for biological and clinical research. <i>TrAC - Trends in Analytical Chemistry</i> , 2023, 158, 116825.	5.8	24
30184	In silico and in vitro approaches allow the identification of the Prosystemin molecular network. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 212-223.	1.9	1
30185	An updated gene regulatory network reconstruction of multidrug-resistant <i>Pseudomonas aeruginosa</i> CCBH4851. <i>Memorias Do Instituto Oswaldo Cruz</i> , 0, 117, .	0.8	1
30186	An Integrative Multi-Omics Analysis of The Molecular Links between Aging and Aggressiveness in Thyroid Cancers. , 2023, 14, 992.		4
30187	Bioinformatic prediction and experimental validation of RiPP recognition elements. <i>Methods in Enzymology</i> , 2023, , 191-233.	0.4	4
30188	Clustering Analysis Indicates Genes Involved in Progesterone-Induced Oxidative Stress in Pancreatic Beta Cells: Insights to Understanding Gestational Diabetes. <i>Lecture Notes in Computer Science</i> , 2022, , 68-78.	1.0	0
30189	Identification of crucial salivary proteins/genes and pathways involved in pathogenesis of temporomandibular disorders. <i>Open Chemistry</i> , 2022, 20, 1378-1401.	1.0	0
30190	Differentially expressed AC077690.1, AL049874.3 and AP001037.1 lncRNAs in prostate cancer. <i>Archives of Biological Sciences</i> , 2022, 74, 359-366.	0.2	0
30191	HPIPred: Host-pathogen interactome prediction with phenotypic scoring. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 6534-6542.	1.9	3
30192	A Network Pharmacological Approach to Explore the Mechanisms of TongXieYaoFang in Inflammatory Bowel Disease. <i>Brazilian Journal of Pharmaceutical Sciences</i> , 0, 58, .	1.2	0
30193	In vitro and in silico assessment of cytotoxicity and chromosome instability induced by saxitoxin in human derived neural cell line. <i>Anais Da Academia Brasileira De Ciencias</i> , 2022, 94, .	0.3	3
30194	Associations of selenoprotein expression and gene methylation with the outcome of clear cell renal carcinoma. <i>Archives of Biochemistry and Biophysics</i> , 2023, 733, 109470.	1.4	0
30195	Effective control of harmful Microcystis blooms by paucibactin A, a novel macrocyclic tambjamine, isolated from <i>Paucibacter aquatile</i> DH15. <i>Journal of Cleaner Production</i> , 2023, 383, 135408.	4.6	1
30196	Combining IP3 affinity chromatography and bioinformatics reveals a novel protein-IP3 binding site on <i>Plasmodium falciparum</i> MDR1 transporter. <i>Current Research in Microbial Sciences</i> , 2023, 4, 100179.	1.4	2
30197	Molecular, biochemical and micromorphological responses of cacao seedlings of the Parinari series, carrying the lethal gene <i>Luteus-Pa</i> , in the presence and absence of cotyledons. <i>Plant Physiology and Biochemistry</i> , 2023, 194, 550-569.	2.8	0
30198	Activation of KLF6 by titanate nanofibers and regulatory roles of KLF6 on ATF3 in the endothelial monolayer and mouse aortas. <i>Molecular Omics</i> , 2023, 19, 150-161.	1.4	4

#	ARTICLE	IF	CITATIONS
30199	Robust identification of common genomic biomarkers from multiple gene expression profiles for the prognosis, diagnosis, and therapies of pancreatic cancer. <i>Computers in Biology and Medicine</i> , 2023, 152, 106411.	3.9	7
30200	Study on the role of calcium channel protein TRPV4 in the inflammatory pathway of type 2 diabetic adipose tissue based on gene databases. <i>Biochemical and Biophysical Research Communications</i> , 2023, 639, 161-168.	1.0	1
30201	Network pharmacology and LC-MS approaches to explore the active compounds and mechanisms of Yuanjiang decoction for treating bradyarrhythmia. <i>Computers in Biology and Medicine</i> , 2023, 152, 106435.	3.9	2
30202	Genome-wide study and functional characterization elucidates the potential association of late embryogenesis abundant (LEA) genes with lotus seed development. <i>International Journal of Biological Macromolecules</i> , 2023, 226, 1-13.	3.6	2
30203	Synbiotics of <i>Bifidobacterium breve</i> MCC1274 and lactulose enhances production of tryptophan metabolites in fermented human fecal communities. <i>Food Research International</i> , 2023, 163, 112308.	2.9	5
30204	Potential shared gene signatures and molecular mechanisms between atherosclerosis and depression: Evidence from transcriptome data. <i>Computers in Biology and Medicine</i> , 2023, 152, 106450.	3.9	3
30205	Targeting Na-H exchanger 1 overcomes nuclear factor kappa B-mediated tumor resistance to radiotherapy. <i>Neoplasia</i> , 2023, 35, 100862.	2.3	0
30206	Dipyridamole interacts with the N-terminal domain of HSP90 and antagonizes the function of the chaperone in multiple cancer cell lines. <i>Biochemical Pharmacology</i> , 2023, 207, 115376.	2.0	2
30207	Identification and analysis of C17orf53 as a prognostic signature for hepatocellular carcinoma. <i>Computers in Biology and Medicine</i> , 2023, 152, 106348.	3.9	1
30208	TFIIS Is Crucial During Early Transcript Elongation for Transcriptional Reprogramming in Response to Heat Stress. <i>Journal of Molecular Biology</i> , 2023, 435, 167917.	2.0	4
30209	T cell-related prognostic risk model and tumor immune environment modulation in lung adenocarcinoma based on single-cell and bulk RNA sequencing. <i>Computers in Biology and Medicine</i> , 2023, 152, 106460.	3.9	4
30210	Hepatitis B virus X protein increases LASP1 SUMOylation to stabilize HER2 and facilitate hepatocarcinogenesis. <i>International Journal of Biological Macromolecules</i> , 2023, 226, 996-1009.	3.6	4
30211	Pan-Cancer analysis of TERT and Validation in Osteosarcoma Cell Lines. <i>Biochemical and Biophysical Research Communications</i> , 2023, 639, 106-116.	1.0	2
30212	Osteopontin associates with brain TRM-cell transcriptome and compartmentalization in donors with and without multiple sclerosis. <i>IScience</i> , 2023, 26, 105785.	1.9	10
30213	Ancient origin and conserved gene function in terpene pheromone and defense evolution of stink bugs and hemipteran insects. <i>Insect Biochemistry and Molecular Biology</i> , 2023, 152, 103879.	1.2	9
30214	Solving the bottlenecks of sugarcane vinasse biodigestion: Impacts of temperature and substrate exchange on sulfate removal during dark fermentation. <i>Chemical Engineering Journal</i> , 2023, 455, 140965.	6.6	7
30215	Aggregated alpha-synuclein transcriptionally activates pro-inflammatory canonical and non-canonical NF- $\kappa$ B signaling pathways in peripheral monocytic cells. <i>Molecular Immunology</i> , 2023, 154, 1-10.	1.0	2
30216	Mechanical stimulation reprograms the sorghum internode transcriptome and broadly alters hormone homeostasis. <i>Plant Science</i> , 2023, 327, 111555.	1.7	2



#	ARTICLE	IF	CITATIONS
30217	Polystyrene nanoplastics enhance the toxicological effects of DDE in zebrafish ( <i>Danio rerio</i> ) larvae. <i>Science of the Total Environment</i> , 2023, 859, 160457.	3.9	9
30218	Proteomics analysis indicates the involvement of immunity and inflammation in the onset stage of SOD1-G93A mouse model of ALS. <i>Journal of Proteomics</i> , 2023, 272, 104776.	1.2	4
30219	Integrated analysis of transcriptomic and protein-protein interaction data reveals cadmium stress response in <i>Geobacter sulfurreducens</i> . <i>Environmental Research</i> , 2023, 218, 115063.	3.7	1
30220	Unique guanidine-conjugated catechins from the leaves of <i>Alchornea rugosa</i> and their autophagy modulating activity. <i>Phytochemistry</i> , 2023, 206, 113521.	1.4	1
30221	Gene regulators associating the T2DM and periodontitis contributing disease prognostic markers and therapeutic target. <i>Journal of King Saud University - Science</i> , 2023, 35, 102469.	1.6	0
30222	Composition and function of viruses in sauce-flavor baijiu fermentation. <i>International Journal of Food Microbiology</i> , 2023, 387, 110055.	2.1	4
30223	Transcriptomic dissection underlying physiological and anatomical characteristics of poplar wood in response to changes in light intensity and nitrogen availability. <i>Environmental and Experimental Botany</i> , 2023, 206, 105186.	2.0	1
30224	A peptide-centric approach to analyse quantitative proteomics data- an application to prostate cancer biomarker discovery. <i>Journal of Proteomics</i> , 2023, 272, 104774.	1.2	1
30225	Proteomic alterations in the cerebellum and hippocampus in an Alzheimer's disease mouse model: Alleviating effect of palmatine. <i>Biomedicine and Pharmacotherapy</i> , 2023, 158, 114111.	2.5	9
30226	Serum metabolomic profiling revealed potential diagnostic biomarkers in patients with panic disorder. <i>Journal of Affective Disorders</i> , 2023, 323, 461-471.	2.0	2
30227	Spatio-temporal succession of microbial communities in platisphere and their potentials for plastic degradation in freshwater ecosystems. <i>Water Research</i> , 2023, 229, 119406.	5.3	26
30228	Integrated omics profiling and network pharmacology uncovers the prognostic genes and multi-targeted therapeutic bioactives to combat lung cancer. <i>European Journal of Pharmacology</i> , 2023, 940, 175479.	1.7	4
30229	Targeted isolation of sesquiterpene lactone dimers from <i>Aucklandia lappa</i> guided by LC-HRMS/MS-based molecular networking. <i>Phytochemistry</i> , 2023, 206, 113557.	1.4	3
30230	Apoptosis promoting activity of selected plant steroid in MRMT-1 breast cancer cell line by modulating mitochondrial permeation pathway. <i>Steroids</i> , 2023, 190, 109151.	0.8	1
30231	Co-variance between free-living bacteria and <i>Cochlodinium polykrikoides</i> (Dinophyta) harmful algal blooms, South Korea. <i>Harmful Algae</i> , 2023, 122, 102371.	2.2	3
30232	In silico investigation of acyclovir derivatives potency against herpes simplex virus. <i>Scientific African</i> , 2023, 19, e01461.	0.7	0
30233	Structural patterns of SARS-CoV-2 variants of concern (alpha, beta, gamma, delta) spike protein are influenced by variant-specific amino acid mutations: A computational study with implications on viral evolution. <i>Journal of Theoretical Biology</i> , 2023, 558, 111376.	0.8	2
30234	TMT-based proteomics analysis of growth advantage of triploid <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101043.	0.4	1

#	ARTICLE	IF	CITATIONS
30235	How to dissect viral infections and their interplay with the host-proteome by immunoaffinity and mass spectrometry: A tutorial. <i>Microchemical Journal</i> , 2023, 186, 108323.	2.3	0
30236	Transcriptomic insight into the hybridization mechanism of the Tambacu, a hybrid from <i>Colossoma macropomum</i> (Tambaqui) and <i>Piaractus mesopotamicus</i> (Pacu). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101041.	0.4	2
30237	Microbial community dynamics responding to nutrient allocation associated with soybean cultivar "Jake" ozone adaptation. <i>Science of the Total Environment</i> , 2023, 864, 161008.	3.9	3
30238	Cross-stress memory: Salt priming at vegetative growth stages improves tolerance to drought stress during grain-filling in rice plants. <i>Environmental and Experimental Botany</i> , 2023, 206, 105187.	2.0	6
30239	Protective effect of <i>Hovenia dulcis</i> Thunb. leaf extracts against ethanol-induced DNA damage in SH-SY5Y cells. <i>Journal of Ethnopharmacology</i> , 2023, 304, 116042.	2.0	2
30240	Predatory protists play predominant roles in suppressing soil-borne fungal pathogens under organic fertilization regimes. <i>Science of the Total Environment</i> , 2023, 863, 160986.	3.9	12
30241	Rhizosphere effect and water constraint jointly determined the roles of microorganism in soil phosphorus cycling in arid desert regions. <i>Catena</i> , 2023, 222, 106809.	2.2	6
30242	Network analysis of the autophagy biochemical network in relation to various autophagy-targeted proteins found among SARS-CoV-2 variants of concern. <i>Journal of Molecular Graphics and Modelling</i> , 2023, 119, 108396.	1.3	0
30243	Comparative proteomic analysis reveals the different hepatotoxic mechanisms of human hepatocytes exposed to silver nanoparticles. <i>Journal of Hazardous Materials</i> , 2023, 445, 130599.	6.5	4
30244	Potential target identification for osteosarcoma treatment: Gene expression re-analysis and drug repurposing. <i>Gene</i> , 2023, 856, 147106.	1.0	0
30245	Isoliquiritigenin from licorice flavonoids attenuates NLRP3-mediated pyroptosis by SIRT6 in vascular endothelial cells. <i>Journal of Ethnopharmacology</i> , 2023, 303, 115952.	2.0	9
30246	Shen-Qi-Jiang-Tang granule ameliorates diabetic nephropathy via modulating tumor necrosis factor signaling pathway. <i>Journal of Ethnopharmacology</i> , 2023, 303, 116031.	2.0	3
30247	Controlling factors for soil bacterial and fungal diversity and composition vary with vegetation types in alpine grasslands. <i>Applied Soil Ecology</i> , 2023, 184, 104777.	2.1	6
30248	Comparative study of the rhizosphere microbiome of <i>Coffea arabica</i> grown in different countries reveals a small set of prevalent and keystone taxa. <i>Rhizosphere</i> , 2023, 25, 100652.	1.4	2
30249	A multiomics integrative analysis of color de-synchronization with softening of "Hass" avocado fruit: A first insight into a complex physiological disorder. <i>Food Chemistry</i> , 2023, 408, 135215.	4.2	5
30250	Effects of short-term exposure to volatile pesticide dichlorvos on the olfactory systems in <i>Spodoptera litura</i> : Calcium homeostasis, synaptic plasticity and apoptosis. <i>Science of the Total Environment</i> , 2023, 864, 161050.	3.9	2
30251	Expression profiling of miR-146a-3p and miR-1343 with their target genes after classical swine fever vaccination. <i>Indian Journal of Animal Sciences</i> , 2022, 90, 191-194.	0.1	0
30252	Phosphorylation of T897 in the dimerization domain of Gemin5 modulates protein interactions and translation regulation. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 6182-6191.	1.9	2

#	ARTICLE	IF	CITATIONS
30253	Scientific Workflow Interactions: An Application to Cancer Gene Identification. Lecture Notes in Computer Science, 2022, , 14-19.	1.0	0
30254	Identifying key transcription factors and miRNAs coregulatory networks associated with immune infiltrations and drug interactions in idiopathic pulmonary arterial hypertension. Mathematical Biosciences and Engineering, 2022, 20, 4153-4177.	1.0	1
30255	Expression profiling of host long non-coding RNAs under ORF virus infection. Indian Journal of Animal Sciences, 2022, 90, 336-340.	0.1	0
30259	Multi-Omics Immune Interaction Networks in Lung Cancer Tumorigenesis, Proliferation, and Survival. International Journal of Molecular Sciences, 2022, 23, 14978.	1.8	7
30260	Identification of the Inner Cell Mass and the Trophectoderm Responses after an In Vitro Exposure to Glucose and Insulin during the Preimplantation Period in the Rabbit Embryo. Cells, 2022, 11, 3766.	1.8	1
30261	Genome-wide detection of genotype environment interactions for flowering time in Brassica napus. Frontiers in Plant Science, 0, 13, .	1.7	7
30262	Gene expression profile of placentomes and clinical parameters in the cows with retained placenta. BMC Genomics, 2022, 23, .	1.2	1
30263	Targeting Class I Histone Deacetylases in Human Uterine Leiomyosarcoma. Cells, 2022, 11, 3801.	1.8	6
30264	Depth wide distribution and metabolic potential of chemolithoautotrophic microorganisms reactivated from deep continental granitic crust underneath the Deccan Traps at Koyna, India. Frontiers in Microbiology, 0, 13, .	1.5	1
30266	Chitin amendments eliminate the negative impacts of continuous cropping obstacles on soil properties and microbial assemblage. Frontiers in Plant Science, 0, 13, .	1.7	6
30267	Identification of Liver Fibrosis-Related MicroRNAs in Human Primary Hepatic Stellate Cells Using High-Throughput Sequencing. Genes, 2022, 13, 2201.	1.0	4
30268	Optimal construction of a functional interaction network from pooled library CRISPR fitness screens. BMC Bioinformatics, 2022, 23, .	1.2	3
30269	Comprehensive bioinformatics analysis for MEF2 family genes in gastric cancer. Translational Cancer Research, 2022, 11, 4057-4069.	0.4	0
30270	Transcription Factors and ncRNAs Associated with CYP3A Expression in Human Liver and Small Intestine Assessed with Weighted Gene Co-Expression Network Analysis. Biomedicines, 2022, 10, 3061.	1.4	1
30271	Molecular, Circuit, and Stress Response Characterization of Ventral Pallidum Npas1-Neurons. Journal of Neuroscience, 2023, 43, 405-418.	1.7	15
30272	The mechanical regulation of RNA binding protein hnRNPC in the failing heart. Science Translational Medicine, 2022, 14, .	5.8	6
30273	Transcriptomic Study of Spermatogenesis in the Testis of Hu Sheep and Tibetan Sheep. Genes, 2022, 13, 2212.	1.0	2
30274	Genes Associated with Biological Nitrogen Fixation Efficiency Identified Using RNA Sequencing in Red Clover ( <i>Trifolium pratense</i> L.). Life, 2022, 12, 1975.	1.1	5

#	ARTICLE	IF	CITATIONS
30275	A risk model developed based on necroptosis to assess progression for ischemic cardiomyopathy and identify possible therapeutic drugs. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
30276	Effect of Cepharanthine on the Stemness of Lung Squamous Cell Carcinoma Based on Network Pharmacology and Bioinformatics. <i>BioMed Research International</i> , 2022, 2022, 1-13.	0.9	0
30277	The Transcriptome and Proteome Networks of Malignant Tumours Reveal Atavistic Attractors of Polyploidy-Related Asexual Reproduction. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14930.	1.8	6
30278	The combination of molecular docking and network pharmacology reveals the molecular mechanism of Danggui Niantong decoction in treating gout. <i>Medicine (United States)</i> , 2022, 101, e31535.	0.4	5
30279	A Bibliometrics-Enhanced, PAGER-Compliant Scoping Review of the Literature on Paralympic Powerlifting: Insights for Practices and Future Research. <i>Healthcare (Switzerland)</i> , 2022, 10, 2319.	1.0	5
30280	Ependyma: a new target for autoantibodies in neuromyelitis optica?. <i>Brain Communications</i> , 2022, 4, .	1.5	2
30281	N6-methyladenosine regulators-related immune genes enable predict graft loss and discriminate T-cell mediate rejection in kidney transplantation biopsies for cause. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
30282	Tyroviruses are a new group of temperate phages that infect <i>Bacillus</i> species in soil environments worldwide. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
30283	Network Pharmacology and Experimental Validation to Investigate the Antidepressant Potential of <i>Atractylodes lancea</i> (Thunb.) DC.. <i>Life</i> , 2022, 12, 1925.	1.1	3
30284	Prognostic Role of Long-Chain Acyl-Coenzyme A Synthetase Family Genes in Patients with Clear Cell Renal Cell Carcinoma: A Comprehensive Bioinformatics Analysis Confirmed with External Validation Cohorts. <i>Clinical Genitourinary Cancer</i> , 2023, 21, 91-104.	0.9	1
30285	Genome-wide screening for genetic variants in polyadenylation signal (PAS) sites in mouse selection lines for fatness and leanness. <i>Mammalian Genome</i> , 2023, 34, 12-31.	1.0	1
30288	Genome-Scale Metabolic Modeling Reveals Sequential Dysregulation of Glutathione Metabolism in Livers from Patients with Alcoholic Hepatitis. <i>Metabolites</i> , 2022, 12, 1157.	1.3	2
30289	BDE-47, -99, -209 and Their Ternary Mixture Disrupt Glucose and Lipid Metabolism of Hepg2 Cells at Dietary Relevant Concentrations: Mechanistic Insight through Integrated Transcriptomics and Proteomics Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14465.	1.8	3
30290	Analysis of the Clinical Efficacy and Molecular Mechanism of Xuefu Zhuyu Decoction in the Treatment of COPD Based on Meta-Analysis and Network Pharmacology. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-24.	0.7	3
30291	Distinct conformational and energetic features define the specific recognition of (di)aromatic peptide motifs by PEX14. <i>Biological Chemistry</i> , 2023, 404, 179-194.	1.2	3
30292	Rapid identification of stigmasterane-type steroid saponins from <i>Vernonia amygdalina</i> leaf based on $\beta$ -glucosidase inhibiting activity and molecular networking. <i>Chinese Journal of Natural Medicines</i> , 2022, 20, 846-853.	0.7	0
30293	Exploration of potential targets and mechanisms of Naringenin in treating autism spectrum disorder via network pharmacology and molecular docking. <i>Medicine (United States)</i> , 2022, 101, e31787.	0.4	4
30294	Comparative Genomics Reveal the Utilization Ability of Variable Carbohydrates as Key Genetic Features of <i>Listeria</i> Pathogens in Their Pathogenic Lifestyles. <i>Pathogens</i> , 2022, 11, 1430.	1.2	1

#	ARTICLE	IF	CITATIONS
30295	Integrative Analysis of Potential Biomarkers Involved in the Progression of Papillary Thyroid Cancer. <i>Applied Biochemistry and Biotechnology</i> , 2023, 195, 2917-2932.	1.4	1
30296	Identification of Novel mRNA Isoforms Associated with Acute Heat Stress Response Using RNA Sequencing Data in Sprague Dawley Rats. <i>Biology</i> , 2022, 11, 1740.	1.3	0
30297	Brain Region-Dependent Alternative Splicing of Alzheimer Disease (AD)-Risk Genes Is Associated With Neuropathological Features in AD. <i>International Neurology Journal</i> , 2022, 26, S126-136.	0.5	6
30298	Developing a Diagnostic Model to Predict the Risk of Asthma Based on Ten Macrophage-Related Gene Signatures. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	5
30299	Lactiplantibacillus plantarum ST-III-fermented milk improves autistic-like behaviors in valproic acid-induced autism spectrum disorder mice by altering gut microbiota. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	4
30300	A Transversal Approach Combining In Silico, In Vitro and In Vivo Models to Describe the Metabolism of the Receptor Interacting Protein 1 Kinase Inhibitor Sibiriline. <i>Pharmaceutics</i> , 2022, 14, 2665.	2.0	3
30301	LncRNA/miRNA/mRNA Network Introduces Novel Biomarkers in Prostate Cancer. <i>Cells</i> , 2022, 11, 3776.	1.8	4
30302	Protein painting reveals pervasive remodeling of conserved proteostasis machinery in response to pharmacological stimuli. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	1.4	1
30304	Structural variation and eQTL analysis in two experimental populations of chickens divergently selected for feather-pecking behavior. <i>Neurogenetics</i> , 0, , .	0.7	1
30305	Validation of a high-confidence regulatory network for gene-to-NUE phenotype in field-grown rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30306	A novel defined cuproptosis-related gene signature for predicting the prognosis of colon adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
30307	Genomic Analysis of the Proteasome Subunit Gene Family and Their Response to High Density and Saline-Alkali Stresses in Grass Carp. <i>Fishes</i> , 2022, 7, 350.	0.7	1
30308	Exploring the mechanism of Epimedii folium and notoginseng radix against vascular dementia based on network pharmacology and molecular docking analysis: pharmacological mechanisms of EH-PN for VD. <i>Medicine (United States)</i> , 2022, 101, e31969.	0.4	0
30309	A Label-Free Quantitative Analysis for the Search of Proteomic Differences between Goat Breeds. <i>Animals</i> , 2022, 12, 3336.	1.0	4
30310	Transcriptome Analysis and Identification of Chemosensory Genes in Baryscapus dioryctriae (Hymenoptera: Eulophidae). <i>Insects</i> , 2022, 13, 1098.	1.0	2
30311	Screening of high-risk deleterious missense variations in the <i>CYP1B1</i> gene implicated in the pathogenesis of primary congenital glaucoma: A comprehensive <i>in silico</i> approach. <i>PeerJ</i> , 0, 10, e14132.	0.9	3
30312	A phase I/II trial and biological correlate analysis of neoadjuvant SBRT with single-dose durvalumab in HPV-unrelated locally advanced HNSCC. <i>Nature Cancer</i> , 2022, 3, 1300-1317.	5.7	21
30313	Reconstructing horizontal gene flow network to understand prokaryotic evolution. <i>Open Biology</i> , 2022, 12, .	1.5	2

#	ARTICLE	IF	CITATIONS
30314	Identification of potential microRNA diagnostic panels and uncovering regulatory mechanisms in breast cancer pathogenesis. <i>Scientific Reports</i> , 2022, 12, .	1.6	11
30315	Carbon nanoparticles induce DNA repair and PARP inhibitor resistance associated with nanozyme activity in cancer cells. <i>Cancer Nanotechnology</i> , 2022, 13, .	1.9	7
30316	Nature-Derived Compounds as Potential Bioactive Leads against CDK9-Induced Cancer: Computational and Network Pharmacology Approaches. <i>Processes</i> , 2022, 10, 2512.	1.3	1
30317	Investigation of reversible histone acetylation and dynamics in gene expression regulation using 3D liver spheroid model. <i>Epigenetics and Chromatin</i> , 2022, 15, .	1.8	4
30318	MYB44-ENAP1/2 restricts HDT4 to regulate drought tolerance in Arabidopsis. <i>PLoS Genetics</i> , 2022, 18, e1010473.	1.5	15
30319	In silico characterization of bla <sub>NDM</sub> -harboring plasmids in <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
30320	Combination of esomeprazole and pirfenidone enhances antifibrotic efficacy in vitro and in a mouse model of TGF $\beta$ <sup>2</sup> -induced lung fibrosis. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
30321	Integrated Transcriptome Analysis Reveals mRNA-miRNA Pathway Crosstalk in Roman Laying Hens <sup>TM</sup> Immune Organs Induced by AFB1. <i>Toxins</i> , 2022, 14, 808.	1.5	2
30322	Data-driven analysis to identify prognostic immune-related biomarkers in BRAF mutated cutaneous melanoma microenvironment. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30323	Taxonomic and functional profiling of Indian smokeless tobacco bacteriome uncovers several bacterial-derived risks to human health. <i>World Journal of Microbiology and Biotechnology</i> , 2023, 39, .	1.7	4
30324	Anticholinesterase Activity of Budmunchiamine Alkaloids Revealed by Comparative Chemical Profiling of Two <i>Albizia</i> spp., Molecular Docking and Dynamic Studies. <i>Plants</i> , 2022, 11, 3286.	1.6	7
30325	Identification of hub genes, signaling pathways and immune infiltration of recurrent spontaneous abortion based on bioinformatics analysis with clinical verification. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2022, 61, 1027-1036.	0.5	0
30326	Caerin 1.1/1.9 Enhances Antitumour Immunity by Activating the IFN- $\gamma$ Response Signalling Pathway of Tumour Macrophages. <i>Cancers</i> , 2022, 14, 5785.	1.7	1
30327	A longitudinal census of the bacterial community in raw milk correlated with <i>Staphylococcus aureus</i> clinical mastitis infections in dairy cattle. <i>Animal Microbiome</i> , 2022, 4, .	1.5	3
30329	Comprehensive bioinformatics analysis reveals biomarkers of DNA methylation-related genes in varicose veins. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30330	Neuron-specific protein network mapping of autism risk genes identifies shared biological mechanisms and disease-relevant pathologies. <i>Cell Reports</i> , 2022, 41, 111678.	2.9	17
30332	Effects of Circadian Rhythm and Feeding Modes on Rumen Fermentation and Microorganisms in Hu Sheep. <i>Microorganisms</i> , 2022, 10, 2308.	1.6	3
30333	Computation and molecular pharmacology to trace the anti-rheumatoid activity of <i>Angelicae Pubescentis Radix</i> . <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	4



#	ARTICLE	IF	CITATIONS
30334	Multi-omics signatures of the human early life exposome. <i>Nature Communications</i> , 2022, 13, .	5.8	31
30337	The preliminary study of exosomes derived from thymosin beta 4-treated adipose-derived stem cells in fat grafting. <i>Genes and Genomics</i> , 2023, 45, 413-427.	0.5	2
30339	Genome-Scale Investigation of GARP Family Genes Reveals Their Pivotal Roles in Nutrient Stress Resistance in Allotetraploid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14484.	1.8	3
30340	Global miRNA expression reveals novel nuclear and mitochondrial interactions in Type 1 diabetes mellitus. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
30341	Identification and expression profiles of xylogen-like arabinogalactan protein (XYLP) gene family in <i>Phyllostachys edulis</i> in different developmental tissues and under various abiotic stresses. <i>International Journal of Biological Macromolecules</i> , 2023, 227, 1098-1118.	3.6	1
30344	Glucocorticoid receptor hypersensitivity enhances inflammatory signaling and inhibits cell cycle progression in porcine PBMCs. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
30345	Quantitative proteomic analysis of exosomes from umbilical cord mesenchymal stem cells and rat bone marrow stem cells. <i>Proteomics</i> , 2023, 23, .	1.3	2
30346	New insights into candidate genes for autism spectrum disorder in 8p23.1 duplication syndrome. <i>Brazilian Journal of Case Reports</i> , 2022, 3, 16-23.	0.0	0
30347	Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdaoid phages. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
30348	Detecting potential mechanism of vitamin D in treating rheumatoid arthritis based on network pharmacology and molecular docking. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
30349	iDMET: network-based approach for integrating differential analysis of cancer metabolomics. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
30350	Identifying key m6A-methylated lncRNAs and genes associated with neural tube defects via integrative MeRIP and RNA sequencing analyses. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
30351	Molecular and metabolic insights into floral scent biosynthesis during flowering in <i>Dendrobium chrysotoxum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30353	Co-Prevalence of Virulence and Pathogenic Potential in Multiple Antibiotic Resistant <i>Aeromonas</i> spp. from Diseased Fishes with In Silico Insight on the Virulent Protein Network. <i>Life</i> , 2022, 12, 1979.	1.1	0
30355	Alternative polyadenylation events in epithelial cells sense endometritis progression in dairy cows. <i>Journal of Integrative Agriculture</i> , 2023, 22, 1820-1832.	1.7	1
30356	Bioinformatic Analysis of Plus Gene Expression Related to Progression from Leukoplakia to Oral Squamous Cell Carcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2022, 23, 3833-3842.	0.5	0
30357	Coexpression Network Construction and Visualization from Transcriptomes Underlying ER Stress Responses. <i>Methods in Molecular Biology</i> , 2023, , 385-401.	0.4	2
30358	Evolutionary Divergence of Phosphorylation to Regulate Interactive Protein Networks in Lower and Higher Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14429.	1.8	4

#	ARTICLE	IF	CITATIONS
30359	Transcriptional Profiling Provides New Insights into Organ Culture-Induced Changes in Human Donor Corneas. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14507.	1.8	2
30360	Rumen microbiota-host transcriptome interaction mediates the protective effects of trans-10, cis-12 CLA on facilitating weaning transition of lambs. <i>Animal Nutrition</i> , 2023, 12, 345-359.	2.1	4
30361	Microbiota Community Structure and Interaction Networks within <i>Dermacentor silvarum</i> , <i>Ixodes persulcatus</i> , and <i>Haemaphysalis concinna</i> . <i>Animals</i> , 2022, 12, 3237.	1.0	0
30362	Longitudinal single-cell analysis of SARS-CoV-2-reactive B cells uncovers persistence of early-formed, antigen-specific clones. <i>JCI Insight</i> , 2023, 8, .	2.3	6
30364	N6-Methyladenosine Regulator-Mediated RNA Methylation Is Involved in Primary Sjögren's Syndrome Immunoinfiltration. <i>Disease Markers</i> , 2022, 2022, 1-12.	0.6	3
30365	A Comprehensive Sequencing Analysis of Testis-Born miRNAs in Immature and Mature Indigenous Wandong Cattle ( <i>Bos taurus</i> ). <i>Genes</i> , 2022, 13, 2185.	1.0	4
30366	Comprehensive proteomic and metabolomic analysis uncover the response of okra to drought stress. <i>PeerJ</i> , 0, 10, e14312.	0.9	0
30367	Differential Expression, Functional and Machine Learning Analysis of High-Throughput Omics Data Using Open-Source Tools. <i>Methods in Molecular Biology</i> , 2023, , 317-351.	0.4	0
30368	Transcriptomic meta-analysis reveals unannotated long non-coding RNAs related to the immune response in sheep. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30369	Mining Small Molecules from <i>Teredinibacter turnerae</i> Strains Isolated from Philippine Teredinidae. <i>Metabolites</i> , 2022, 12, 1152.	1.3	0
30370	Susceptibility of Rice Crop to Salt Threat: Proteomic, Metabolomic, and Physiological Inspections. <i>Journal of Proteome Research</i> , 2023, 22, 152-169.	1.8	1
30372	Transcriptome analysis reveals potential marker genes for diagnosis of Alzheimer's disease and vascular dementia. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30373	Proteotranscriptomics Analysis Reveals Signature Pathways Associated with Colorectal Cancer Progression: a Pilot Study. , 2022, , .		0
30374	Single-cell multiomics reveals the complexity of TGF $\beta$ signalling to chromatin in iPSC-derived kidney organoids. <i>Communications Biology</i> , 2022, 5, .	2.0	3
30375	IFI44L and C1QTNF5 as promising biomarkers of proliferative diabetic retinopathy. <i>Medicine (United States)</i> , 2024, 103(10), e34782.	0.24	2
30376	Tsukushi proteoglycan maintains RNA splicing and developmental signaling network in GFAP-expressing subventricular zone neural stem/progenitor cells. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
30377	Comparative transcriptomic analysis reveals candidate genes for seasonal breeding in the male Lion-Head goose. <i>British Poultry Science</i> , 2023, 64, 157-163.	0.8	1
30378	Respirasome Proteins Are Regulated by Sex-Hormone Interactions in the Brain. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14754.	1.8	3

#	ARTICLE	IF	CITATIONS
30379	Surviving the host: Microbial metabolic genes required for growth of <i>Pseudomonas aeruginosa</i> in physiologically-relevant conditions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
30380	Impact of antibiotic perturbation on fecal viral communities in mice. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	1
30381	Transcriptomic Mapping of Neurotoxicity Pathways in the Rat Brain in Response to Intraventricular Polymyxin B. <i>Molecular Neurobiology</i> , 2023, 60, 1317-1330.	1.9	1
30382	Meta-Analysis of RNA-Seq Datasets Identifies Novel Players in Glioblastoma. <i>Cancers</i> , 2022, 14, 5788.	1.7	0
30383	Identification and Functional Analysis of Long Non-Coding RNA (lncRNA) in Response to Seed Aging in Rice. <i>Plants</i> , 2022, 11, 3223.	1.6	7
30384	High-throughput functional annotation of natural products by integrated activity profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	2
30385	Exploring the Antiovarian Cancer Mechanisms of <i>Salvia Miltiorrhiza Bunge</i> by Network Pharmacological Analysis and Molecular Docking. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-12.	0.7	1
30386	Complete Genome Sequence Resource of <i>Pectobacterium colocasium</i> strain F1-1 that Causes Soft Rot Disease of Taro. <i>Plant Disease</i> , 0, , .	0.7	0
30388	ChiMera: an easy to use pipeline for bacterial genome based metabolic network reconstruction, evaluation and visualization. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	6
30390	Identifying the Effect of COVID-19 Infection in Multiple Myeloma and Diffuse Large B-Cell Lymphoma Patients Using Bioinformatics and System Biology. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-12.	0.7	3
30391	Weighted Gene Coexpression Network Analysis of Candidate Pathways and Genes in Soft Rot Resistance of <i>Amorphophallus</i> . <i>Journal of the American Society for Horticultural Science</i> , 2022, 147, 322-333.	0.5	1
30392	Expression patterns of platinum resistance-related genes in lung adenocarcinoma and related clinical value models. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30394	A Genome-Wide Association Study Reveals a BDNF-Centered Molecular Network Associated with Alcohol Dependence and Related Clinical Measures. <i>Biomedicines</i> , 2022, 10, 3007.	1.4	1
30395	Comparative transcriptomic provides novel insights into the soybean response to <i>Colletotrichum truncatum</i> infection. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30396	Genomic profiling and network-level understanding uncover the potential genes and the pathways in hepatocellular carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
30397	Novel Bisamide Alkaloids Enantiomers from Pepper Roots ( <i>Piper nigrum L.</i> ) with Acetylcholinesterase Inhibitory and Anti-Neuroinflammatory Effects. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 15487-15498.	2.4	4
30398	Postnatal expansion of mesenteric lymph node stromal cells towards reticular and CD34+ stromal cell subsets. <i>Nature Communications</i> , 2022, 13, .	5.8	2
30399	Ethnological validation of Ashwagandha ( <i>Withania somnifera L. Dunal</i> ) ghrita as <i>Vajikarana Rasayana</i> <sup>™</sup> : In-silico, in-vitro and in-vivo approach. <i>Journal of Ethnopharmacology</i> , 2023, 304, 116064.	2.0	5

#	ARTICLE	IF	CITATIONS
30400	Whole transcriptome expression profiles in kidney samples from rats with hyperuricaemic nephropathy. <i>PLoS ONE</i> , 2022, 17, e0276591.	1.1	0
30401	Neuronal-epithelial cross-talk drives acinar specification via NRG1-ERBB3-mTORC2 signaling. <i>Developmental Cell</i> , 2022, 57, 2550-2565.e5.	3.1	6
30402	Proteogenomic insights into the biology and treatment of pancreatic ductal adenocarcinoma. <i>Journal of Hematology and Oncology</i> , 2022, 15, .	6.9	9
30403	Network Pharmacology and Molecular Docking Study on the Multi-Target Mechanisms of Aloe vera for Non-Alcoholic Steatohepatitis Treatment. <i>Plants</i> , 2022, 11, 3585.	1.6	1
30404	Heightened cocaine-seeking in male rats associates with a distinct transcriptomic profile in the medial prefrontal cortex. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
30405	Characterization and genetic dissection of maize ear leaf midrib acquired by 3D digital technology. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30406	Host genetic susceptibility underlying SARS-CoV-2-associated Multisystem Inflammatory Syndrome in Brazilian Children. <i>Molecular Medicine</i> , 2022, 28, .	1.9	8
30408	Organoids. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	130
30409	Identification of key programmed cell death-related genes and immune infiltration in extracorporeal membrane oxygenation treatment for acute myocardial infarction based on bioinformatics analysis. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	0
30410	Integrated transcriptome-proteome analyses of human stem cells reveal source-dependent differences in their regenerative signature. <i>Stem Cell Reports</i> , 2022, , .	2.3	4
30412	Identification of QTN-by-environment interactions and their candidate genes for soybean seed oil-related traits using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
30413	Expression analysis of hsa_circ_0020397, hsa_circ_0005986, hsa_circ_0003028, and hsa_circ_0006990 in renal cell carcinoma. <i>Experimental and Molecular Pathology</i> , 2023, 129, 104848.	0.9	1
30414	Gilthead Seabream Liver Integrative Proteomics and Metabolomics Analysis Reveals Regulation by Different Prosurvival Pathways in the Metabolic Adaptation to Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15395.	1.8	6
30415	PPDP: A Data Portal of Paris polyphylla for Polyphyllin Biosynthesis and Germplasm Resource Exploration. <i>Diversity</i> , 2022, 14, 1057.	0.7	1
30416	Comprehensive analysis of pre-mRNA alternative splicing regulated by m6A methylation in pig oxidative and glycolytic skeletal muscles. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
30417	An Approach for Systems-Level Understanding of Prostate Cancer from High-Throughput Data Integration to Pathway Modeling and Simulation. <i>Cells</i> , 2022, 11, 4121.	1.8	7
30418	Bioinformatic Analysis Revealed the Essential Regulatory Genes and Pathways of Early and Advanced Atherosclerotic Plaque in Humans. <i>Cells</i> , 2022, 11, 3976.	1.8	2
30419	Transcriptional Specificity Analysis of Testis and Epididymis Tissues in Donkey. <i>Genes</i> , 2022, 13, 2339.	1.0	2

#	ARTICLE	IF	CITATIONS
30420	amica: an interactive and user-friendly web-platform for the analysis of proteomics data. BMC Genomics, 2022, 23, .	1.2	8
30421	Pathogen-driven gene expression patterns lead to a novel approach to the identification of common therapeutic targets. Scientific Reports, 2022, 12, .	1.6	1
30422	Integrated Analysis of Bulk RNA-Seq and Single-Cell RNA-Seq Unravels the Influences of SARS-CoV-2 Infections to Cancer Patients. International Journal of Molecular Sciences, 2022, 23, 15698.	1.8	1
30423	Identification of biological pathways and processes regulated by NEK5 in breast epithelial cells via an integrated proteomic approach. Cell Communication and Signaling, 2022, 20, .	2.7	2
30425	Conservation and Divergence of the Trihelix Genes in Brassica and Expression Profiles of BnaTH Genes in Brassica napus under Abiotic Stresses. International Journal of Molecular Sciences, 2022, 23, 15766.	1.8	7
30426	Gestation and lactation triphenyl phosphate exposure disturbs offspring gut microbiota in a sex-dependent pathway. Food and Chemical Toxicology, 2022, , 113579.	1.8	2
30427	Bariatric Surgery Associates with Nonalcoholic Steatohepatitis/Hepatocellular Carcinoma Amelioration via SPP1 Suppression. Metabolites, 2023, 13, 11.	1.3	0
30428	Endometrial small extracellular vesicles regulate human trophoctodermal cell invasion by reprogramming the phosphoproteome landscape. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	7
30430	Sleep and circadian rhythm disruption alters the lung transcriptome to predispose to viral infection. IScience, 2023, 26, 105877.	1.9	5
30432	Cellular features of localized microenvironments in human meniscal degeneration: a single-cell transcriptomic study. ELife, 0, 11, .	2.8	9
30433	Label-Free Quantification from Direct Infusion Shotgun Proteome Analysis (DISPA-LFQ) with CsoDIAq Software. Analytical Chemistry, 0, , .	3.2	3
30434	A protein signature associated with active tuberculosis identified by plasma profiling and network-based analysis. IScience, 2022, 25, 105652.	1.9	5
30436	Bifunctional Epimerase/Reductase Enzymes Facilitate the Modulation of 6-Deoxy-Heptoses Found in the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . Biochemistry, 2023, 62, 134-144.	1.2	5
30437	Identification of potential target genes of honokiol in overcoming breast cancer resistance to tamoxifen. Frontiers in Oncology, 0, 12, .	1.3	2
30438	Banxia baizhu tianma decoction, a Chinese herbal formula, for hypertension: Integrating meta-analysis and network pharmacology. Frontiers in Pharmacology, 0, 13, .	1.6	5
30439	Insight into Glyproline Peptides™ Activity through the Modulation of the Inflammatory and Neurosignaling Genetic Response Following Cerebral Ischemia“Reperfusion. Genes, 2022, 13, 2380.	1.0	3
30440	Genome-wide identification of the VOZ transcription factors in tomato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (lyco of Horticultural Science and Biotechnology, 2023, 98, 468-482.	0.9	1
30441	Identification of Critical Molecular Factors and Side Effects Underlying the Response to Thalictuberine in Prostate Cancer: A Systems Biology Approach. Avicenna Journal of Medical Biotechnology, 0, , .	0.2	0

#	ARTICLE	IF	CITATIONS
30442	Evolutionarily conserved gene expression patterns for affective disorders revealed using cross-species brain transcriptomic analyses in humans, rats and zebrafish. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
30443	Transcriptome and Gene Regulatory Network Analyses Reveal New Transcription Factors in Mature Fruit Associated with Harvest Date in <i>Prunus persica</i> . <i>Plants</i> , 2022, 11, 3473.	1.6	0
30444	Combinatorial library design for improving isobutanol production in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	1
30445	Vertical and temporal distribution of chytrids infecting diatoms in the Gulf of Naples (Italy.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	0.4	5
30446	Ear mite infection restructures otic microbial networks in conservation-reliant Santa Catalina Island foxes ( <i>Urocyon littoralis catalinae</i> ). <i>Molecular Ecology</i> , 2023, 32, 892-903.	2.0	4
30447	Two vacuolar invertase inhibitors PpINHa and PpINH3 display opposite effects on fruit sugar accumulation in peach. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30448	The potential mechanism of Neu5Gc inducing colorectal cancer based on network pharmacology and experimental validation. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2023, 396, 705-718.	1.4	1
30449	Autophagic reprogramming of bone marrow-derived macrophages. <i>Immunologic Research</i> , 2023, 71, 229-246.	1.3	3
30450	Prediction of Diagnostic Gene Biomarkers Associated with Immune Infiltration for Basal Cell Carcinoma. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 0, Volume 15, 2657-2673.	0.8	2
30451	The dynamic dysregulated network identifies stage-specific markers during lung adenocarcinoma malignant progression and metastasis. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 30, 633-647.	2.3	2
30452	Genome-wide identification and comprehensive analysis reveal potential roles of long non-coding RNAs in fruit development of southern highbush blueberry ( <i>Vaccinium corymbosum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
30453	Identifying novel regulators of placental development using time-series transcriptome data. <i>Life Science Alliance</i> , 2023, 6, e202201788.	1.3	1
30455	<i>Jasminum sambac</i> Cell Extract as Antioxidant Booster against Skin Aging. <i>Antioxidants</i> , 2022, 11, 2409.	2.2	0
30456	Developing a Novel Immune-Related Seven-Gene Signature and Immune Infiltration Pattern in Patients with COVID-19 and Cardiovascular Disease. <i>Journal of Cardiovascular Development and Disease</i> , 2022, 9, 450.	0.8	1
30457	Transcriptomic profiling of canine decidualization and effects of antigestagens on decidualized dog uterine stromal cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
30460	Micronome Revealed miR-205-5p as Key Regulator of VEGFA During Cancer Related Angiogenesis in Hepatocellular Carcinoma. <i>Molecular Biotechnology</i> , 2023, 65, 1178-1186.	1.3	8
30461	Co-alteration Network Architecture of Major Depressive Disorder: A Multi-modal Neuroimaging Assessment of Large-scale Disease Effects. <i>Neuroinformatics</i> , 2023, 21, 443-455.	1.5	1
30462	Compensatory Transcriptional Response of <i>Fischerella thermalis</i> to Thermal Damage of the Photosynthetic Electron Transfer Chain. <i>Molecules</i> , 2022, 27, 8515.	1.7	0



#	ARTICLE	IF	CITATIONS
30463	Genome-Wide Identification and Expression Pattern of the GRAS Gene Family in Pitaya ( <i>Selenicereus</i> ) Tj ETQq0 0 0 198 /Overlock 10 Tf	3.3	6
30464	A population-based study of precision health assessments using multi-omics network-derived biological functional modules. <i>Cell Reports Medicine</i> , 2022, 3, 100847.	3.3	1
30465	Genome-wide identification and characterization of PIN-FORMED (PIN) and PIN-LIKES (PILS) gene family reveals their role in adventitious root development in tea nodal cutting ( <i>Camellia Sinensis</i> ). <i>International Journal of Biological Macromolecules</i> , 2023, 229, 791-802.	3.6	6
30466	In silico Analysis of OsNRT2.3 Reveals OsAMT1.3, OsZIFL9, OsbZIP27, and OsIRT1 as Potential Drought-related Genes During Nitrogen Use Efficiency in <i>Oryza sativa</i> L.. <i>Pertanika Journal of Science and Technology</i> , 2022, 46, .	0.1	0
30467	Small RNA sequencing and profiling of serum-derived exosomes from African swine fever virus-infected pigs. <i>Journal of Animal Science</i> , 0, , .	0.2	0
30468	Dickkopf1 fuels inflammatory cytokine responses. <i>Communications Biology</i> , 2022, 5, .	2.0	2
30469	TransFlow: a Snakemake workflow for transmission analysis of <i>Mycobacterium tuberculosis</i> whole-genome sequencing data. <i>Bioinformatics</i> , 0, , .	1.8	0
30471	Pharmacological Mechanism of NRICM101 for COVID-19 Treatments by Combined Network Pharmacology and Pharmacodynamics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15385.	1.8	3
30472	Differentially expressed gene profiles and associated ceRNA network in ATG7-Deficient lens epithelial cells under oxidative stress. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30474	Systems Biology in Chronic Heart Failureâ€”Identification of Potential miRNA Regulators. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15226.	1.8	7
30475	Genome-Wide Transcriptome Analysis Revealing the Genes Related to Sugar Metabolism in Kernels of Sweet Corn. <i>Metabolites</i> , 2022, 12, 1254.	1.3	1
30477	Upregulation of leucine-rich alpha-2 glycoprotein: A key regulator of inflammation and joint fibrosis in patients with severe knee osteoarthritis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
30478	Identification of the Genetic Association Between Type-2-Diabetes and Pancreatic Cancer. <i>Biochemical Genetics</i> , 2023, 61, 1143-1162.	0.8	0
30479	Pleiotropic architectures of porcine immune and growth trait pairs revealed by a selfâ€”productâ€”based transcriptome method. <i>Animal Genetics</i> , 0, , .	0.6	0
30480	Transcriptomic and functional analyses reveal a tumour-promoting role for the IL-36 receptor in colon cancer and crosstalk between IL-36 signalling and the IL-17/IL-23 axis. <i>British Journal of Cancer</i> , 2023, 128, 735-747.	2.9	7
30481	Exploring the Potential Mechanism of Danshen in the Treatment of Concurrent Ischemic Heart Disease and Depression Using Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulation. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211436.	0.2	0
30482	Recognition of Core-Fucosylated Glycopeptides Based on the Y1+Fuc/Y1 Ratio in Low-Energy HCD Spectra. <i>Analytical Chemistry</i> , 2022, 94, 17349-17353.	3.2	3
30483	Proteogenomic landscape of human pancreatic ductal adenocarcinoma in an Asian population reveals tumor cell-enriched and immune-rich subtypes. <i>Nature Cancer</i> , 2023, 4, 290-307.	5.7	11

#	ARTICLE	IF	CITATIONS
30484	Identification of an immune-related gene prognostic index for predicting prognosis, immunotherapeutic efficacy, and candidate drugs in amyotrophic lateral sclerosis. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	1.8	0
30486	Expression Profile of Housekeeping Genes and Tissue-Specific Genes in Multiple Tissues of Pigs. <i>Animals</i> , 2022, 12, 3539.	1.0	2
30487	Proteomics as a tool to decipher plant responses in arbuscular mycorrhizal interactions: A meta-analysis. <i>Proteomics</i> , 0, , 2200108.	1.3	2
30488	Senescence atlas reveals an aged-like inflamed niche that blunts muscle regeneration. <i>Nature</i> , 2023, 613, 169-178.	13.7	90
30489	Resolvin D1 attenuated liver injury caused by chronic ethanol and acute LPS challenge in mice. <i>FASEB Journal</i> , 2023, 37, .	0.2	5
30490	A wheat integrative regulatory network from large-scale complementary functional datasets enables trait-associated gene discovery for crop improvement. <i>Molecular Plant</i> , 2023, 16, 393-414.	3.9	12
30491	<i>Agave REVEILLE1</i> regulates the onset and release of seasonal dormancy in <i>Populus</i> . <i>Plant Physiology</i> , 0, , .	2.3	2
30492	Integrated analysis of necroptosis-related genes for evaluating immune infiltration and colon cancer prognosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
30493	Diverse monogenic subforms of human spermatogenic failure. <i>Nature Communications</i> , 2022, 13, .	5.8	17
30496	<i>SCUBE2</i> as a Marker of Resistance to Taxane-based Neoadjuvant Chemotherapy and a Potential Therapeutic Target in Breast Cancer. <i>The Journal of Breast Health</i> , 2022, 19, 45-54.	0.4	1
30497	Genome-wide analysis of hyperosmolality-gated calcium-permeable channel (OSCA) family members and their involvement in various osmotic stresses in <i>Brassica napus</i> . <i>Gene</i> , 2023, 856, 147137.	1.0	2
30498	Identifying crosstalk genetic biomarkers linking a neurodegenerative disease, Parkinson's disease, and periodontitis using integrated bioinformatics analyses. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	10
30499	A comparative transcriptome analysis of the head of 1 and 9 days old worker honeybees ( <i>Apis</i> ) Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50	0.5	1
30500	Transcriptomic analysis reveals the dynamic changes of transcription factors during early development of chicken embryo. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
30501	Phosphoproteomic Analysis of Dopamine D2 Receptor Signaling Reveals Interplay of G Protein- and $\beta$ -Arrestin-Mediated Effects. <i>Journal of Proteome Research</i> , 2023, 22, 259-271.	1.8	1
30502	Genome-Wide Identification of WRKY Family Genes and the Expression Profiles in Response to Nitrogen Deficiency in Poplar. <i>Genes</i> , 2022, 13, 2324.	1.0	2
30503	Development of dynamical network biomarkers for regulation in Epstein-Barr virus positive peripheral T cell lymphoma unspecified type. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30504	High Throughput Sequencing Reveals Distinct Bacterial Communities and Functional Diversity in Two Typical Coastal Bays. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1878.	1.2	1

#	ARTICLE	IF	CITATIONS
30505	Mechanism of Action of a Chinese Herbal Compound Containing Quercetin, Luteolin, and Kaempferol in the Treatment of Vitiligo Based on Network Pharmacology and Experimental Verification. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	1
30507	CD163 as a Potential Biomarker in Colorectal Cancer for Tumor Microenvironment and Cancer Prognosis: A Swedish Study from Tissue Microarrays to Big Data Analyses. Cancers, 2022, 14, 6166.	1.7	4
30508	Identification of familial networks reveals sex-specific density dependence in the dispersal and reproductive success of an endangered ungulate. Frontiers in Ecology and Evolution, 0, 10, .	1.1	1
30509	Genome-wide identification of cystathionine beta synthase genes in wheat and its relationship with anther male sterility under heat stress. Frontiers in Plant Science, 0, 13, .	1.7	0
30510	Progress in kidney transplantation: The role for systems immunology. Frontiers in Medicine, 0, 9, .	1.2	1
30511	The identification and verification of hub genes associated with pulmonary arterial hypertension using weighted gene co-expression network analysis. BMC Pulmonary Medicine, 2022, 22, .	0.8	3
30512	Target Identification of 22-(4-Pyridinecarbonyl) Jorunnamycin A, a Tetrahydroisoquinoline Derivative from the Sponge Xestospongia sp., in Mediating Non-Small-Cell Lung Cancer Cell Apoptosis. Molecules, 2022, 27, 8948.	1.7	6
30513	Guiding the choice of informatics software and tools for lipidomics research applications. Nature Methods, 2023, 20, 193-204.	9.0	18
30514	Proteomic profile of in situ acquired pellicle on tooth and restorative material surfaces. Journal of Dentistry, 2023, 129, 104389.	1.7	1
30516	iPSC-Derived Macrophages: The Differentiation Protocol Affects Cell Immune Characteristics and Differentiation Trajectories. International Journal of Molecular Sciences, 2022, 23, 16087.	1.8	4
30517	The proteomic landscape shows oncologic relevance in cystitis glandularis. Journal of Pathology and Translational Medicine, 0, , .	0.4	0
30518	Comparative RNA-Sequencing Analysis Reveals High Complexity and Heterogeneity of Transcriptomic and Immune Profiles in Hepatocellular Carcinoma Tumors of Viral (HBV, HCV) and Non-Viral Etiology. Medicina (Lithuania), 2022, 58, 1803.	0.8	0
30519	Sourcing thermotolerant poly(ethylene terephthalate) hydrolase scaffolds from natural diversity. Nature Communications, 2022, 13, .	5.8	51
30521	NEB mutations disrupt the super-relaxed state of myosin and remodel the muscle metabolic proteome in nemaline myopathy. Acta Neuropathologica Communications, 2022, 10, .	2.4	13
30522	Silico analysis of the target and possible mechanism of lomustine in the treatment of primary glioblastoma. Journal of Molecular Modeling, 2023, 29, .	0.8	2
30523	Phellinus baumii Polyphenol: A Potential Therapeutic Candidate against Lung Cancer Cells. International Journal of Molecular Sciences, 2022, 23, 16141.	1.8	3
30524	Gene expression profile analysis to discover molecular signatures for early diagnosis and therapies of triple-negative breast cancer. Frontiers in Molecular Biosciences, 0, 9, .	1.6	4
30525	Identification of Key Genes and Biological Pathways Associated with Skeletal Muscle Maturation and Hypertrophy in Bos taurus, Ovis aries, and Sus scrofa. Animals, 2022, 12, 3471.	1.0	7

#	ARTICLE	IF	CITATIONS
30526	Detection of SARS-CoV-2 infection clusters: The useful combination of spatiotemporal clustering and genomic analyses. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	1
30527	Potential bioactive compounds and mechanisms of <i>Fibraurea recisa</i> Pierre for the treatment of Alzheimer's disease analyzed by network pharmacology and molecular docking prediction. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	4
30528	Impact of Asp/Glu-ADP-ribosylation on protein-protein interaction and protein function. <i>Proteomics</i> , 2023, 23, .	1.3	3
30529	Transcriptomes of Testes at Different Developmental Stages in the <i>Opsariichthys bidens</i> Predict Key Genes for Testis Development and Spermatogenesis. <i>Marine Biotechnology</i> , 2023, 25, 123-139.	1.1	2
30530	A Pan-Cancer Landscape of ABCG2 across Human Cancers: Friend or Foe?. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15955.	1.8	2
30531	p53 regulates expression of nuclear envelope components in cancer cells. <i>Biology Direct</i> , 2022, 17, .	1.9	19
30532	MUTYH is a potential prognostic biomarker and correlates with immune infiltrates in hepatocellular carcinoma. <i>Liver Research</i> , 2022, , .	0.5	1
30533	Co-expression pan-network reveals genes involved in complex traits within maize pan-genome. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
30534	Disrupting the ArcA Regulatory Network Amplifies the Fitness Cost of Tetracycline Resistance in <i>Escherichia coli</i> . <i>MSystems</i> , 2023, 8, .	1.7	5
30535	The new ceRNA crosstalk between mRNAs and miRNAs in intervertebral disc degeneration. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
30536	Knockdown of hsa_circ_0008922 inhibits the progression of glioma. <i>PeerJ</i> , 0, 10, e14552.	0.9	0
30537	Bioactive Insulin-Loaded Electrospun Wound Dressings for Localized Drug Delivery and Stimulation of Protein Expression Associated with Wound Healing. <i>Molecular Pharmaceutics</i> , 2023, 20, 241-254.	2.3	7
30538	Therapeutic Targeting of LIF Overcomes Macrophage-mediated Immunosuppression of the Local Tumor Microenvironment. <i>Clinical Cancer Research</i> , 2023, 29, 791-804.	3.2	8
30539	Asperosaponin VI induces osteogenic differentiation of human umbilical cord mesenchymal stem cells via the estrogen signaling pathway. <i>Medicine (United States)</i> , 2022, 101, e32344.	0.4	1
30540	Novel correlative analysis identifies multiple genomic variations impacting ASD with macrocephaly. <i>Human Molecular Genetics</i> , 2023, 32, 1589-1606.	1.4	1
30541	<i>HLH57</i> confers chilling tolerance and grain yield improvement in rice. <i>Plant, Cell and Environment</i> , 2023, 46, 1402-1418.	2.8	5
30542	Genome-Wide Characterization of Trehalose-6-Phosphate Synthase Gene Family of <i>Brassica napus</i> and Potential Links with Agronomic Traits. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15714.	1.8	2
30543	Autophagy modulates growth and development in the moss <i>Physcomitrium patens</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1

#	ARTICLE	IF	CITATIONS
30545	In Silico Prediction of Hub Genes Involved in Diabetic Kidney and COVID-19 Related Disease by Differential Gene Expression and Interactome Analysis. <i>Genes</i> , 2022, 13, 2412.	1.0	0
30546	A molecular classification of gastric cancer associated with distinct clinical outcomes and validated by an XGBoost-based prediction model. <i>Molecular Therapy - Nucleic Acids</i> , 2023, 31, 224-240.	2.3	6
30547	Muscle Regeneration in Holothurians without the Upregulation of Muscle Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16037.	1.8	3
30548	An atlas of late prenatal human neurodevelopment resolved by single-nucleus transcriptomics. <i>Nature Communications</i> , 2022, 13, .	5.8	11
30549	Bioinformatic Analysis of Genetic Factors from Human Blood Samples and Postmortem Brains in Parkinson's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-18.	1.9	5
30550	Comparative Transcriptome Profiling of Cassava Tuberos Roots in Response to Postharvest Physiological Deterioration. <i>International Journal of Molecular Sciences</i> , 2023, 24, 246.	1.8	4
30551	Multispecies comparison of host responses to <i>Fusarium circinatum</i> challenge in tropical pines show consistency in resistance mechanisms. <i>Plant, Cell and Environment</i> , 2023, 46, 1705-1725.	2.8	1
30552	N6-methyladenosine modulation classes and immune microenvironment regulation in ischemic stroke. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	5
30553	Kinetic modulation of bacterial hydrolases by microbial community structure in coastal waters. <i>Environmental Microbiology</i> , 0, , .	1.8	0
30554	In-depth analysis of the Sirtuin 5-regulated mouse brain malonylome and succinylome using library-free data-independent acquisitions. <i>Proteomics</i> , 2023, 23, .	1.3	3
30555	Identification of hub genes associated with prognosis of lung cancer via integrated bioinformatics and <i>in vitro</i> approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 11204-11218.	2.0	5
30556	Novel circRNA-miRNA-mRNA networks regulated by maternal exercise in fetal hearts of pregestational diabetes. <i>Life Sciences</i> , 2023, 314, 121308.	2.0	0
30557	Comparative transcriptomes of nine tissues for the Heilongjiang brown frog ( <i>Rana amurensis</i> ). <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30558	Bioinformatics analysis of genes related to ferroptosis in hepatic ischemia-reperfusion injury. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30559	The blackgrass genome reveals patterns of non-parallel evolution of polygenic herbicide resistance. <i>New Phytologist</i> , 2023, 237, 1891-1907.	3.5	14
30560	Volatile Compound Abundance Correlations Provide a New Insight into Odor Balances in Sauce-Aroma Baijiu. <i>Foods</i> , 2022, 11, 3916.	1.9	5
30561	A comprehensive review on rhubarb astringent/ laxative actions and the role of aquaporins as hub genes. <i>Phytochemistry Reviews</i> , 2023, 22, 565-586.	3.1	2
30562	Exploring the mechanism of MP gel against skin photoaging based on network pharmacology, molecular docking, and experimental validation. <i>Journal of Cosmetic Dermatology</i> , 2023, 22, 1108-1123.	0.8	2

#	ARTICLE	IF	CITATIONS
30563	Identification and Expression Analysis of MPK and MKK Gene Families in Pecan ( <i>Carya illinoensis</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 15190.	1.8	0
30564	SARS-CoV-2 induces "cytokine storm" hyperinflammatory responses in RA patients through pyroptosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
30565	Transcriptome reveals insights into biosynthesis of ginseng polysaccharides. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
30566	Electrostatic anti-CD33-antibody" protamine nanocarriers as platform for a targeted treatment of acute myeloid leukemia. <i>Journal of Hematology and Oncology</i> , 2022, 15, .	6.9	1
30567	Grape Berry Responses to Sequential Flooding and Heatwave Events: A Physiological, Transcriptional, and Metabolic Overview. <i>Plants</i> , 2022, 11, 3574.	1.6	0
30569	Genome-wide identification and expression analysis of peach multiple organellar RNA editing factors reveals the roles of RNA editing in plant immunity. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
30570	Prognostic value, immune signature and molecular mechanisms of the SUMO family in pancreatic adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	0
30571	An integrative approach for exploring the nature of fibroepithelial neoplasms. <i>British Journal of Cancer</i> , 0, , .	2.9	0
30572	Molecular cartooning with knowledge graphs. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
30574	High Expression of E2F4 Is an Adverse Prognostic Factor and Related to Immune Infiltration in Oral Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2022, 2022, 1-13.	0.9	1
30576	Single-Cell RNA Sequencing of the Testis of <i>Ciona intestinalis</i> Reveals the Dynamic Transcriptional Profile of Spermatogenesis in Protochordates. <i>Cells</i> , 2022, 11, 3978.	1.8	0
30578	Impacts of maize hybrids with different nitrogen use efficiency on root-associated microbiota based on distinct rhizosphere soil metabolites. <i>Environmental Microbiology</i> , 2023, 25, 473-492.	1.8	1
30579	Whole-genome RNA sequencing identifies distinct transcriptomic profiles in impingement cartilage between patients with femoroacetabular impingement and hip osteoarthritis. <i>Journal of Orthopaedic Research</i> , 2023, 41, 1517-1530.	1.2	0
30580	Arginine-rich C9ORF72 ALS proteins stall ribosomes in a manner distinct from a canonical ribosome-associated quality control substrate. <i>Journal of Biological Chemistry</i> , 2023, 299, 102774.	1.6	7
30581	Development of a peripheral blood transcriptomic gene signature to predict bronchopulmonary dysplasia. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2023, 324, L76-L87.	1.3	5
30583	Machine learning multi-omics analysis reveals cancer driver dysregulation in pan-cancer cell lines compared to primary tumors. <i>Communications Biology</i> , 2022, 5, .	2.0	4
30584	Rhizosphere <i>Priestia</i> species altered cowpea root transcriptome and enhanced growth under drought and nutrient deficiency. <i>Planta</i> , 2023, 257, .	1.6	4
30585	Elucidating type 2 diabetes mellitus risk factor by promoting lipid metabolism with gymnemagenin: An in vitro and in silico approach. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4



#	ARTICLE	IF	CITATIONS
30586	Genomic, transcriptomic and RNA editing analysis of human MM1 and VV2 sporadic Creutzfeldt-Jakob disease. <i>Acta Neuropathologica Communications</i> , 2022, 10, .	2.4	0
30587	The variation of intestinal autochthonous bacteria in cultured tiger pufferfish <i>Takifugu rubripes</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
30588	Temporal Analysis Reveals the Transient Differential Expression of Transcription Factors That Underlie the Trans-Differentiation of Human Monocytes to Macrophages. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15830.	1.8	0
30589	Exploring breast cancer exosomes for novel biomarkers of potential diagnostic and prognostic importance. <i>3 Biotech</i> , 2023, 13, .	1.1	3
30590	Revisiting fecal metatranscriptomics analyses of macaques with idiopathic chronic diarrhoea with a focus on trichomonad parasites. <i>Parasitology</i> , 2023, 150, 248-261.	0.7	0
30593	Gou Qi Zi inhibits proliferation and induces apoptosis through the PI3K/AKT1 signaling pathway in non-small cell lung cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
30594	Exploring Molecular Signatures in Spondyloarthritis: A Step Towards Early Diagnosis. , 2023, , 142-155.		0
30595	Hsa_circ_0015278 Regulates FLT3-ITD AML Progression via Ferroptosis-Related Genes. <i>Cancers</i> , 2023, 15, 71.	1.7	4
30596	Achiasmatic meiosis in the unisexual Amazon molly, <i>Poecilia formosa</i> . <i>Chromosome Research</i> , 2022, 30, 443-457.	1.0	10
30597	Downregulated miR-367-3p, miR-548aq-5p, and miR-4710 in Human Whole Blood: Potential Biomarkers for Breast Cancer With Axillary Lymph Node Metastasis. <i>Clinical Breast Cancer</i> , 2023, 23, 189-198.	1.1	3
30598	Integrative Multiomics and Regulatory Network Analyses Uncovers the Role of OAS3, TRAFD1, miR-222-3p, and miR-125b-5p in Hepatitis E Virus Infection. <i>Genes</i> , 2023, 14, 42.	1.0	6
30599	Low Sulfur Amino Acid, High Polyunsaturated Fatty Acid Diet Inhibits Breast Cancer Growth. <i>International Journal of Molecular Sciences</i> , 2023, 24, 249.	1.8	2
30600	Comprehensive Genome Analysis of <i>Neisseria meningitidis</i> from South America Reveals a Distinctive Pathogenicity-Related Prophage Repertoire. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15731.	1.8	0
30601	<sc>FUBP3</sc> regulates chronic myeloid leukaemia progression through <sc>PRC2</sc> complex regulated <sc>PAK1</sc> signalling. <i>Journal of Cellular and Molecular Medicine</i> , 2023, 27, 15-29.	1.6	4
30602	The transcriptomic landscape of neurons carrying PSEN1 mutations reveals changes in extracellular matrix components and non-coding gene expression. <i>Neurobiology of Disease</i> , 2023, 178, 105980.	2.1	6
30603	Binimetinib ameliorates the severity of septic cardiomyopathy by downregulating inflammatory factors. <i>International Immunopharmacology</i> , 2022, 113, 109454.	1.7	1
30604	Changes in the membrane lipid composition of a <i>Sulfurimonas</i> species depend on the electron acceptor used for sulfur oxidation. <i>ISME Communications</i> , 2022, 2, .	1.7	5
30605	Analysis of miRNA rare variants in amyotrophic lateral sclerosis and in silico prediction of their biological effects. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1

#	ARTICLE	IF	CITATIONS
30606	Efficacy and Mechanism of Quercetin in the Treatment of Experimental Colitis Using Network Pharmacology Analysis. <i>Molecules</i> , 2023, 28, 146.	1.7	2
30607	The landscape of therapeutic vulnerabilities in EGFR inhibitor osimertinib drug tolerant persister cells. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	5
30608	Deciphering Transcriptional Networks during Human Cardiac Development. <i>Cells</i> , 2022, 11, 3915.	1.8	2
30609	ONE-seq: epitranscriptome and gene-specific profiling of NAD-capped RNA. <i>Nucleic Acids Research</i> , 2023, 51, e12-e12.	6.5	9
30612	RNA-Interference-Mediated miR-122-Based Gene Regulation in Colon Cancer, a Structural In Silico Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15257.	1.8	1
30613	MS/MS Molecular Networking Unveils the Chemical Diversity of Biscembranoid Derivatives, Neutrophilic Inflammatory Mediators from the Cultured Soft Coral <i>Sarcophyton trocheliophorum</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 15464.	1.8	4
30614	Metastatic phenotype and immunosuppressive tumour microenvironment in pancreatic ductal adenocarcinoma: Key role of the urokinase plasminogen activator (PLAU). <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
30616	New developments in non-exosomal and exosomal ncRNAs in coronary artery disease. <i>Epigenomics</i> , 2022, 14, 1355-1372.	1.0	4
30617	Comprehensive analysis of prognostic value, relationship to cell cycle, immune infiltration and m6A modification of ZSCAN20 in hepatocellular carcinoma. <i>Aging</i> , 0, , .	1.4	0
30618	Global phylogenomic novelty of the Cas1 gene from hot spring microbial communities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
30619	Common targetable inflammatory pathways in brain transcriptome of autism spectrum disorders and Tourette syndrome. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	2
30620	Investigation of the underlying mechanism of Zhibai Dihuang Pill in treating osteoporosis by using network pharmacology and molecular dynamics simulation. <i>Endocrine, Metabolic and Immune Disorders - Drug Targets</i> , 2022, 23, .	0.6	1
30621	Chemical and Biological Insights on <i>Phaulopsis falcisepala</i> : A Source of Bioactive Compounds with Multifunctional Anticancer Potentials. <i>Chemistry Africa</i> , 0, , .	1.2	0
30622	Systems biology network reveals the correlation between COX-2 expression and Ch 7q copy number alterations in Ch 11q-deleted pediatric neuroblastoma tumors. <i>Genes and Cancer</i> , 2022, 13, 60-71.	0.6	0
30623	Proteomic and Transcriptomic Landscapes of Alström and Bardet-Biedl Syndromes. <i>Genes</i> , 2022, 13, 2370.	1.0	2
30624	NF- $\kappa$ B drives epithelial-mesenchymal mechanisms of lung fibrosis in a translational lung cell model. <i>JCI Insight</i> , 2023, 8, .	2.3	9
30625	Characterization and genomic analysis of a novel halovirus infecting <i>Chromohalobacter beijerinckii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
30626	Developing and validating a survival prediction model based on blood exosomal ceRNA network in patients with PAAD. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	0

#	ARTICLE	IF	CITATIONS
30627	Exploring High-Throughput Immunoassays for Biomarker Validation in Rheumatic Diseases in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2023, 22, 1105-1115.	1.8	4
30628	Heat and drought induced transcriptomic changes in barley varieties with contrasting stress response phenotypes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10
30629	Identifying susceptibility genes for essential hypertension by transcriptome-wide association study. <i>Biochemistry and Biophysics Reports</i> , 2022, 32, 101387.	0.7	1
30630	Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. <i>Molecular Cell</i> , 2022, 82, 4627-4646.e14.	4.5	11
30631	Linking single nucleotide polymorphisms to signaling blueprints in abdominal aortic aneurysms. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30632	SNARE protein USE1 is involved in the glycosylation and the expression of mumps virus fusion protein and important for viral propagation. <i>PLoS Pathogens</i> , 2022, 18, e1010949.	2.1	1
30633	Identification and validation of a novel four-gene diagnostic model for neonatal early-onset sepsis with bacterial infection. <i>European Journal of Pediatrics</i> , 2023, 182, 977-985.	1.3	3
30634	Study on the Mechanism of Radix Astragali against Renal Aging Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	2
30635	<scp>RMI2</scp> is a novel prognostic and predictive biomarker for breast cancer. <i>Cancer Medicine</i> , 2023, 12, 8331-8350.	1.3	3
30636	Epigenetics of type 2 diabetes and diabetes-related outcomes in the Strong Heart Study. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	4
30637	Cytoscape stringApp 2.0: Analysis and Visualization of Heterogeneous Biological Networks. <i>Journal of Proteome Research</i> , 2023, 22, 637-646.	1.8	29
30639	Systematic Pharmacology-Based Strategy to Explore the Mechanism of Bufe Huoxue Capsule in the Treatment of Chronic Obstructive Pulmonary Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	1
30640	Comparative Transcriptome and Co-Expression Network Analyses Reveal the Molecular Mechanism of Calcium-Deficiency-Triggered Tipburn in Chinese Cabbage ( <i>Brassica rapa</i> L. ssp. <i>Pekinensis</i> ). <i>Plants</i> , 2022, 11, 3555.	1.6	0
30641	Uncovering the gene regulatory network of type 2 diabetes through multi-omic data integration. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	10
30642	Natural Variation in Diauxic Shift between Patagonian <i>Saccharomyces eubayanus</i> Strains. <i>MSystems</i> , 2022, 7, .	1.7	2
30644	Metabolomics combined with transcriptomics analyses of mechanism regulating testa pigmentation in peanut. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
30645	Molecular Network Analysis Discloses the Limited Contribution to HIV Transmission for Patients with Late HIV Diagnosis in Northeast China. <i>Archives of Sexual Behavior</i> , 0, , .	1.2	1
30646	Molecular signatures in the progression of COVID-19 severity. <i>Scientific Reports</i> , 2022, 12, .	1.6	4

#	ARTICLE	IF	CITATIONS
30647	Transcriptomic profiling reveals sex-specific molecular signatures of adipose endothelial cells under obesogenic conditions. <i>IScience</i> , 2023, 26, 105811.	1.9	7
30648	Sex-stratified RNA-seq analysis reveals traumatic brain injury-induced transcriptional changes in the female hippocampus conducive to dementia. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	0
30649	Transcriptional responses of human intestinal epithelial HT-29 cells to spore-displayed p40 derived from <i>Lactisacibacillus rhamnosus</i> GG. <i>BMC Microbiology</i> , 2022, 22, .	1.3	0
30651	Untargeted Fecal Metabolomic Analyses across an Industrialization Gradient Reveal Shared Metabolites and Impact of Industrialization on Fecal Microbiome-Metabolome Interactions. <i>MSystems</i> , 2022, 7, .	1.7	2
30652	In-depth analysis of alternative splicing landscape in multiple myeloma and potential role of dysregulated splicing factors. <i>Blood Cancer Journal</i> , 2022, 12, .	2.8	4
30653	Identification and differential expression of long non-coding RNAs and their association with XIST gene during early embryonic developmental stages of <i>Bos taurus</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 229, 896-908.	3.6	1
30655	Cancer immunotherapies transition endothelial cells into HEVs that generate TCF1+ T lymphocyte niches through a feed-forward loop. <i>Cancer Cell</i> , 2022, 40, 1600-1618.e10.	7.7	40
30657	Social networks and tolerance differences associated to grouping patterns in <i>Ateles geoffroyi</i> . <i>Folia Primatologica</i> , 2022, 94, 51-72.	0.3	0
30658	Identification of Key Genes from the Visceral Adipose Tissues of Overweight/Obese Adults with Hypertension through Transcriptome Sequencing. <i>Cytogenetic and Genome Research</i> , 2022, 162, 541-559.	0.6	1
30659	Metabolite profiling of leaves of three <i>Epilobium</i> species. <i>Ecological Genetics</i> , 2022, 20, 279-293.	0.1	3
30660	Bile proteome analysis by high-precision mass spectrometry to examine novel biomarkers of primary sclerosing cholangitis. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2023, 30, 914-923.	1.4	2
30663	Identification of novel immune-related targets mediating disease progression in acute pancreatitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3
30664	The impact of modifier genes on cone-rod dystrophy heterogeneity: An explorative familial pilot study and a hypothesis on neurotransmission impairment. <i>PLoS ONE</i> , 2022, 17, e0278857.	1.1	27
30668	Understanding the Potential Gene Regulatory Network of Starch Biosynthesis in Tartary Buckwheat by RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15774.	1.8	1
30669	Transcriptomic analysis of secretory endometrium reveals essential immune factors associated with pregnancy after single euploid blastocyst transfer. <i>American Journal of Reproductive Immunology</i> , 0, , .	1.2	0
30670	Targeting myeloid cell coagulation signaling blocks MAP kinase/TGF- $\beta$ 1-driven fibrotic remodeling in ischemic heart failure. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	11
30671	Genome-wide identification of sucrose non-fermenting-1-related protein kinase genes in maize and their responses to abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30673	Mitochondria and Endoplasmic Reticulum Stress in Retinal Organoids from Patients with Vision Loss. <i>American Journal of Pathology</i> , 2023, 193, 1721-1739.	1.9	6

#	ARTICLE	IF	CITATIONS
30674	A Novel Immune Gene-Related Prognostic Score Predicts Survival and Immunotherapy Response in Glioma. <i>Medicina (Lithuania)</i> , 2023, 59, 23.	0.8	1
30675	Targeting Nup358/RanBP2 by a viral protein disrupts stress granule formation. <i>PLoS Pathogens</i> , 2022, 18, e1010598.	2.1	2
30676	Phosphoproteomic analysis identifies differentially expressed phosphorylation sites that affect muscle fiber type in pigs. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
30677	Identifying diagnostic markers and constructing a prognostic model for small-cell lung cancer based on blood exosome-related genes and machine-learning methods. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
30678	Methylome-wide association study of different responses to risperidone in schizophrenia. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
30679	Bioinformatics Analysis of miRNAs Targeting TRAF5 in DLBCL Involving in NF- $\kappa$ B Signaling Pathway and Affecting the Apoptosis and Signal Transduction. <i>Genetical Research</i> , 2022, 2022, 1-14.	0.3	0
30680	DNA Methylation Alterations in Fractionally Irradiated Rats and Breast Cancer Patients Receiving Radiotherapy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16214.	1.8	4
30681	Evolutionary analysis of endogenous intronic retroviruses in primates reveals an enrichment in transcription binding sites associated with key regulatory processes. <i>PeerJ</i> , 0, 10, e14431.	0.9	0
30682	Metabolomics and Proteomics Characterizing Hepatic Reactions to Dietary Linseed Oil in Duck. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15690.	1.8	2
30683	miRNA-mediated regulation of SK locus in rice under induced submergence. <i>Journal of Crop Science and Biotechnology</i> , 0, , .	0.7	0
30684	The novel subclusters based on cancer-associated fibroblast for pancreatic adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
30685	5mC modification patterns provide novel direction for early acute myocardial infarction detection and personalized therapy. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	1
30686	Comprehensive analysis of the significance of METTL7A gene in the prognosis of lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	5
30688	Human functional genomics reveals toxicological mechanism underlying genotoxicants-induced inflammatory responses under low doses exposure. <i>Chemosphere</i> , 2022, , 137658.	4.2	0
30691	Identification of prognostic values of the transcription factor-CpG-gene triplets in lung adenocarcinoma: A narrative review. <i>Medicine (United States)</i> , 2022, 101, e32045.	0.4	1
30693	Integrative stemness characteristics associated with prognosis and the immune microenvironment in lung adenocarcinoma. <i>BMC Pulmonary Medicine</i> , 2022, 22, .	0.8	1
30694	Anti-Psoriatic Effect of <i>Rheum palmatum</i> L. and Its Underlying Molecular Mechanisms. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16000.	1.8	6
30695	Proteomics Profiling Reveals Regulation of Immune Response to <i>Salmonella enterica</i> Serovar Typhimurium Infection in Mice. <i>Infection and Immunity</i> , 2023, 91, .	1.0	2

#	ARTICLE	IF	CITATIONS
30696	SNCA genetic lowering reveals differential cognitive function of alpha-synuclein dependent on sex. <i>Acta Neuropathologica Communications</i> , 2022, 10, .	2.4	1
30698	Network-based approach for targeting human kinases commonly associated with amyotrophic lateral sclerosis and cancer. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
30699	CHOglycoNET: Comprehensive glycosylation reaction network for CHO cells. <i>Metabolic Engineering</i> , 2023, 76, 87-96.	3.6	3
30700	Dietary Fish Meal Level and a Package of Choline, Î²-Glucan, and Nucleotides Modulate Gut Function, Microbiota, and Health in Atlantic Salmon ( <i>Salmo salar</i> , L.). <i>Aquaculture Nutrition</i> , 2023, 2023, 1-29.	1.1	2
30701	Comprehensive identification and analysis of circRNAs during hickory ( <i>Carya cathayensis</i> Sarg.) flower bud differentiation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
30702	Integration of LC-MS, NMR and molecular docking for profiling of bioactive diterpenes from <i>Euphorbia mauritanica</i> L. with in vitro anti-SARS-CoV-2 activity. <i>Chemistry and Biodiversity</i> , 0, , .	1.0	0
30703	m6A eraser FTO modulates autophagy by targeting SQSTM1/P62 in the prevention of canagliflozin against renal fibrosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
30704	Transcription analyses of differentially expressed mRNAs, lncRNAs, circRNAs, and miRNAs in the growth plate of rats with glucocorticoid-induced growth retardation. <i>PeerJ</i> , 0, 11, e14603.	0.9	0
30706	Transcriptome Analysis Revealed Osmoregulation Related Regulatory Networks and Hub Genes in the Gills of Hilsa shad, <i>Tenulosa ilisha</i> , during the Migratory Osmotic Stress. <i>Marine Biotechnology</i> , 2023, 25, 161-173.	1.1	3
30707	A Novel and Functionally Diverse Class of Acetylcholine-Gated Ion Channels. <i>Journal of Neuroscience</i> , 2023, 43, 1111-1124.	1.7	4
30708	A Cocktail of Polyherbal Bioactive Compounds and Regular Mobility Training as Senolytic Approaches in Age-dependent Alzheimer's: the In Silico Analysis, Lifestyle Intervention in Old Age. <i>Journal of Molecular Neuroscience</i> , 2023, 73, 171-184.	1.1	10
30709	SGLT2 inhibitors mitigate kidney tubular metabolic and mTORC1 perturbations in youth-onset type 2 diabetes. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	23
30710	Network pharmacology-based analysis of heat clearing and detoxifying drug JC724 on the treatment of colorectal cancer. <i>World Journal of Gastrointestinal Oncology</i> , 0, 15, 90-101.	0.8	2
30713	Comparative Genetic Association Analysis of Human Genetic Susceptibility to Pulmonary and Lymph Node Tuberculosis. <i>Genes</i> , 2023, 14, 207.	1.0	1
30714	Cannabinoid Biosynthesis Using Noncanonical Cannabinoid Synthases. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1259.	1.8	4
30716	Enhanced Glutaminolysis Drives Hypoxia-Induced Chemoresistance in Pancreatic Cancer. <i>Cancer Research</i> , 2023, 83, 735-752.	0.4	11
30717	Comprehensive Analysis of the lncRNA-miRNA-mRNA Regulatory Network for Intramuscular Fat in Pigs. <i>Genes</i> , 2023, 14, 168.	1.0	4
30718	TSPAN4 is a prognostic and immune target in Glioblastoma multiforme. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4



#	ARTICLE	IF	CITATIONS
30719	Competing endogenous <sc>RNA</sc> network construction based on long non-coding <sc>RNAs</sc> , <sc>microRNAs</sc> , and <sc>mRNAs</sc> related to fat deposition in Songliao black swine. <i>Animal Genetics</i> , 0, , .	0.6	0
30720	Identification of a CircRNA-miRNA-mRNA Network and Integrated Analysis of Immune Infiltration in Oral Squamous Cell Carcinoma. <i>Journal of Cancer</i> , 2023, 14, 250-261.	1.2	0
30722	N6-Methyladenosine RNA Modifications Regulate the Response to Platinum Through Nicotinamide N-methyltransferase. <i>Molecular Cancer Therapeutics</i> , 2023, 22, 393-405.	1.9	3
30723	Network Analysis of Anti-inflammatory Phytochemicals and Omics Data for Rheumatoid Arthritis. <i>Current Computer-Aided Drug Design</i> , 2023, 19, 356-366.	0.8	0
30724	Suppression of exosomal hsa_circ_0001005 eliminates the Vemurafenib resistance of melanoma. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 5921-5936.	1.2	2
30725	Signaling landscape of mitochondrial non-coding RNAs. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-10.	2.0	0
30726	Systems biology of asphalt pollutants and their human molecular targets. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	2
30727	Protein kinase B (AKT) upregulation and Thy-1- $\beta$ integrin-induced phosphorylation of Connexin43 by activated AKT in astroglia. <i>Journal of Neuroinflammation</i> , 2023, 20, .	3.1	5
30728	A proteome-wide atlas of drug mechanism of action. <i>Nature Biotechnology</i> , 2023, 41, 845-857.	9.4	28
30729	Lactylome analysis suggests lactylation-dependent mechanisms of metabolic adaptation in hepatocellular carcinoma. <i>Nature Metabolism</i> , 2023, 5, 61-79.	5.1	77
30731	Alpha-B-Crystallin overexpression is sufficient to promote tumorigenesis and metastasis in mice. <i>Experimental Hematology and Oncology</i> , 2023, 12, .	2.0	2
30732	Proteomic profiling of urinary small extracellular vesicles in children with pneumonia: a pilot study. <i>Pediatric Research</i> , 0, , .	1.1	0
30734	Thioparib inhibits homologous recombination repair, activates the <sc>type I IFN</sc> response, and overcomes olaparib resistance. <i>EMBO Molecular Medicine</i> , 2023, 15, .	3.3	6
30735	A PREVENTIVE TOOL FOR PREDICTING BLOODSTREAM INFECTIONS IN CHILDREN WITH BURNS. <i>Shock</i> , 2023, 59, 393-399.	1.0	1
30736	Transcriptomic comparison of seeds and silique walls from two rapeseed genotypes with contrasting seed oil content. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
30738	Integration of mRNA and protein expression data for the identification of potential biomarkers associated with pancreatic ductal adenocarcinoma. <i>Computers in Biology and Medicine</i> , 2023, 157, 106529.	3.9	3
30739	Studying the Association between Antibiotic Resistance Genes and Insertion Sequences in Metagenomes: Challenges and Pitfalls. <i>Antibiotics</i> , 2023, 12, 175.	1.5	2
30740	Identification and Characterization of CCD Gene Family in Rose ( <i>Rosa chinensis</i> Jacq. "Old Blush"™) and Gene Co-Expression Network in Biosynthesis of Flower Scent. <i>Horticulturae</i> , 2023, 9, 115.	1.2	2

#	ARTICLE	IF	CITATIONS
30742	Miracle fruit seed as a potential supplement for the treatment of learning and memory disorders in Alzheimer's disease. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
30743	Spatially Resolved Top-Down Proteomics of Tissue Sections Based on a Microfluidic Nanodroplet Sample Preparation Platform. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100491.	2.5	6
30744	Fibril treatment changes protein interactions of tau and $\beta$ -synuclein in human neurons. <i>Journal of Biological Chemistry</i> , 2023, 299, 102888.	1.6	2
30745	Genome-wide characterization, chromosome localization, and expression profile analysis of poplar nonspecific lipid transfer proteins. <i>International Journal of Biological Macromolecules</i> , 2023, , 123226.	3.6	2
30746	Cellular mechanism of action of forsythiaside for the treatment of diabetic kidney disease. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
30747	Identifying M1-like macrophage related genes for prognosis prediction in lung adenocarcinoma based on a gene co-expression network. <i>Heliyon</i> , 2023, 9, e12798.	1.4	1
30748	Annexin A1 is a polarity cue that directs mitotic spindle orientation during mammalian epithelial morphogenesis. <i>Nature Communications</i> , 2023, 14, .	5.8	4
30749	Pathogenesis of Human Immunodeficiency Virus and <i>Mycobacterium tuberculosis</i> Infection as Revealed by Transcriptome and Interactome Data. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 15-23.	1.0	0
30750	Insights into the Effects and Mechanism of Andrographolide-Mediated Recovery of Susceptibility of Methicillin-Resistant <i>Staphylococcus aureus</i> to $\beta$ -Lactam Antibiotics. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
30752	Blood proteome of acute intracranial hemorrhage in infant victims of abusive head trauma. <i>Proteomics</i> , 0, , 2200078.	1.3	2
30753	Integrative analysis of small non-coding RNAs predicts a piRNA/miRNA-CCND1/BRAF/HRH1/ATXN3 regulatory circuit that drives oncogenesis in glioblastoma. <i>Molecular Omics</i> , 2023, 19, 252-261.	1.4	3
30754	A network pharmacology study on mechanism of resveratrol in treating preeclampsia via regulation of AGE-RAGE and HIF-1 signalling pathways. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
30756	Alternative splicing event associated with immunological features in bladder cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
30757	CCDC66 regulates primary cilium length and signaling via interactions with transition zone and axonemal proteins. <i>Journal of Cell Science</i> , 2023, 136, .	1.2	6
30758	Proteomic Assessment of the Murine Mammary Gland Extracellular Matrix. <i>Methods in Molecular Biology</i> , 2023, , 261-271.	0.4	1
30759	Type 2 Diabetes in Obesity: A Systems Biology Study on Serum and Adipose Tissue Proteomic Profiles. <i>International Journal of Molecular Sciences</i> , 2023, 24, 827.	1.8	6
30760	Prognostic value of NOX2 as a potential biomarker for lung adenocarcinoma using TCGA and clinical validation. <i>Molecular Medicine Reports</i> , 2023, 27, .	1.1	0
30761	Comparative Transcriptome Analysis Reveals the Interaction of Sugar and Hormone Metabolism Involved in the Root Hair Morphogenesis of the Endangered Fir <i>Abies beshanzuensis</i> . <i>Plants</i> , 2023, 12, 276.	1.6	1

#	ARTICLE	IF	CITATIONS
30762	Transcriptome analysis reveals synergistic modulation of E-cadherin/N-cadherin in hMSC aggregates chondrogenesis. <i>Genes and Genomics</i> , 0, , .	0.5	0
30763	From Omics to Multi-omics Technologies: the Discovery of Novel Causal Mediators. <i>Current Atherosclerosis Reports</i> , 2023, 25, 55-65.	2.0	6
30764	GBCdb: RNA expression landscapes and ncRNA-mRNA interactions in gallbladder carcinoma. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
30765	NucEnvDB: A Database of Nuclear Envelope Proteins and Their Interactions. <i>Membranes</i> , 2023, 13, 62.	1.4	0
30766	Comprehensive Analysis of PPMs in Pancreatic Adenocarcinoma Indicates the Value of PPM1K in the Tumor Microenvironment. <i>Cancers</i> , 2023, 15, 474.	1.7	1
30767	Mechanism of Enhancing Pyrazines in Daqu via Inoculating <i>Bacillus licheniformis</i> with Strains Specificity. <i>Foods</i> , 2023, 12, 304.	1.9	7
30768	An NmrA-like enzyme-catalysed redox-mediated Diels-Alder cycloaddition with anti-selectivity. <i>Nature Chemistry</i> , 2023, 15, 526-534.	6.6	9
30769	What determines plant species diversity along the Modern Silk Road in the east?. , 2023, 2, .		2
30770	Identification of diagnostic biomarkers for idiopathic pulmonary hypertension with metabolic syndrome by bioinformatics and machine learning. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
30771	Transcriptome changes induced by Arbuscular mycorrhizal Symbiosis in leaves of durum wheat ( <i>Triticum durum</i> Desf.) promote higher salt tolerance. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
30773	Exploring the mechanism of regulating the microbial community and metabolizing trait in Chinese Baijiu fermentation via Huizao. <i>LWT - Food Science and Technology</i> , 2023, 174, 114445.	2.5	2
30774	Integrated analysis of transcription factor-mRNA-miRNA regulatory network related to immune characteristics in medullary thyroid carcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
30775	Study on the muscle transcriptome of two diverse Indian backyard poultry breeds acclimatized to different agro-ecological conditions. <i>Molecular Biology Reports</i> , 2023, 50, 2453-2461.	1.0	2
30776	Biological Functions of Selenoprotein Glutathione Peroxidases (GPXs) and their Expression in Osteoarthritis. <i>Journal of Inflammation Research</i> , 0, Volume 16, 183-196.	1.6	2
30777	Deciphering basic and key traits of antibiotic resistome in influent and effluent of hospital wastewater treatment systems. <i>Water Research</i> , 2023, 231, 119614.	5.3	23
30779	Investigating host-gut microbial relationship in <i>Penaeus monodon</i> upon exposure to <i>Vibrio harveyi</i> . <i>Aquaculture</i> , 2023, 567, 739252.	1.7	5
30780	Environmental chemicals and endogenous metabolites in bile of USA and Norway patients with primary sclerosing cholangitis. <i>Exposome</i> , 2023, 3, .	1.2	1
30781	High-fiber-diet-related metabolites improve neurodegenerative symptoms in patients with obesity with diabetes mellitus by modulating the hippocampal hypothalamic endocrine axis. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	0

#	ARTICLE	IF	CITATIONS
30782	Comparative transcriptomic analyzes of human lung epithelial cells infected with wild-type SARS-CoV-2 and its variant with a 12-bp missing in the E gene. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
30783	Identification of a CD4+ conventional T cells-related lncRNAs signature associated with hepatocellular carcinoma prognosis, therapy, and tumor microenvironment. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
30784	Gene gain facilitated endosymbiotic evolution of Chlamydiae. <i>Nature Microbiology</i> , 2023, 8, 40-54.	5.9	19
30785	Functional impact of multi-omic interactions in breast cancer subtypes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30786	Investigating regulatory patterns of NLRP3 Inflammasome features and association with immune microenvironment in Crohn's disease. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
30787	Cytoscape.js 2023 update: a graph theory library for visualization and analysis. <i>Bioinformatics</i> , 2023, 39, .	1.8	15
30788	Cross-species high-resolution transcriptome profiling suggests biomarkers and therapeutic targets for ulcerative colitis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	0
30789	A Live Cell Protein Complementation Assay for ORFeome-Wide Probing of Human HOX Interactomes. <i>Cells</i> , 2023, 12, 200.	1.8	3
30790	Cuproptosis-associated CDKN2A is targeted by plicamycin to regulate the microenvironment in patients with head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30792	Covariance of Marine Nucleocytoplasmic Large DNA Viruses with Eukaryotic Plankton Communities in the Sub-Arctic Kongsfjorden Ecosystem: A Metagenomic Analysis of Marine Microbial Ecosystems. <i>Microorganisms</i> , 2023, 11, 169.	1.6	5
30793	Activated SOX9+ renal epithelial cells promote kidney repair through secreting factors. <i>Cell Proliferation</i> , 2023, 56, .	2.4	4
30794	Maize resistance to witchweed through changes in strigolactone biosynthesis. <i>Science</i> , 2023, 379, 94-99.	6.0	22
30795	Genome-wide landscape of RNA-binding protein (RBP) networks as potential molecular regulators of psychiatric co-morbidities: a computational analysis. <i>Egyptian Journal of Medical Human Genetics</i> , 2023, 24, .	0.5	2
30797	Signaling through the Dystrophin Glycoprotein Complex affects the stress-dependent transcriptome in <i>Drosophila</i> . <i>DMM Disease Models and Mechanisms</i> , 0, , .	1.2	2
30798	Proteome profiling of ductal carcinoma in situ. <i>Breast Disease</i> , 2023, 41, 513-520.	0.4	1
30799	Identification and analysis of lncRNA, miRNA and mRNA related to subcutaneous and intramuscular fat in Laiwu pigs. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	0
30800	Longitudinal proteomic profiling of the inflammatory response in dengue patients. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011041.	1.3	2
30801	Identification of the bZIP Gene Family and Investigation of Their Response to Drought Stress in <i>Dendrobium catenatum</i> . <i>Agronomy</i> , 2023, 13, 236.	1.3	2

#	ARTICLE	IF	CITATIONS
30802	Wumei Wan attenuates angiogenesis and inflammation by modulating RAGE signaling pathway in IBD: Network pharmacology analysis and experimental evidence. <i>Phytomedicine</i> , 2023, 111, 154658.	2.3	17
30803	The involvement of collagen family genes in tumor enlargement of gastric cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
30804	Efficient Bioinspired Feature Selection and Machine Learning Based Framework Using Omics Data and Biological Knowledge Data Bases in Cancer Clinical Endpoint Prediction. <i>IEEE Access</i> , 2023, 11, 2674-2699.	2.6	2
30805	Single-cell RNA sequencing reveals changes in glioma-associated macrophage polarization and cellular states of malignant gliomas with high AQP4 expression. <i>Cancer Gene Therapy</i> , 2023, 30, 716-726.	2.2	3
30806	Transcriptomic Signature of the Simulated Microgravity Response in <i>Caenorhabditis elegans</i> and Comparison to Spaceflight Experiments. <i>Cells</i> , 2023, 12, 270.	1.8	2
30807	Evolutionary Landscape of Tea Circular RNAs and Its Contribution to Chilling Tolerance of Tea Plant. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1478.	1.8	6
30808	Three Novel Adenylate Cyclase Genes Show Significant Biological Functions in Plant. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 1149-1161.	2.4	8
30809	MAGNET: A web-based application for gene set enrichment analysis using macrophage data sets. <i>PLoS ONE</i> , 2023, 18, e0272166.	1.1	0
30810	IDENTIFICATION AND IN SILICO ANALYSIS OF INHIBITOR ON THE WNT/ $\beta$ -CATENIN SIGNALING PATHWAY AS POTENTIAL DRUG FOR COLON CANCER. <i>International Journal of Applied Pharmaceutics</i> , 0, , 111-120.	0.3	0
30811	Cardiovascular diseases display etiological and seasonal trend in human population: Evidence from seasonal cardiovascular comorbid diseases (SCCD) index. <i>American Journal of Human Biology</i> , 2023, 35, .	0.8	3
30812	Gelsemium Intoxication in a child detected using targeted and untargeted urinary toxicological screening. <i>Toxicologie Analytique Et Clinique</i> , 2023, , .	0.1	0
30813	Comparative network analysis reveals the dynamics of organic acid diversity during fruit ripening in peach ( <i>Prunus persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2023, 23, .	1.6	4
30814	The Potential of Ameliorating COVID-19 and Sequelae From <i>Andrographis paniculata</i> via Bioinformatics. <i>Bioinformatics and Biology Insights</i> , 2023, 17, 117793222211496.	1.0	1
30816	Investigation of early molecular alterations in tauopathy with generative adversarial networks. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
30817	Comprehensive bulk and single-cell transcriptome profiling give useful insights into the characteristics of osteoarthritis associated synovial macrophages. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
30818	Cognitive network reconstruction in individuals who use opioids compared to those who do not: Topological analysis of cognitive function through graph model and centrality measures. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	1
30819	Cell type-specific histone acetylation profiling of Alzheimer's disease subjects and integration with genetics. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	6
30820	Identification and Functional Analysis of Serum Specific miRNAs in Recurrent Aphthous Stomatitis Patients with Excess-heat or Yin-deficiency. <i>Clinical Complementary Medicine and Pharmacology</i> , 2023, , 100079.	0.9	0

#	ARTICLE	IF	CITATIONS
30821	Vasculitis, CA19-9, and PNI differentially predict response and surgical outcome in pancreatic ductal adenocarcinoma. <i>International Journal of Radiation Oncology Biology Physics</i> , 2023, , .	0.4	1
30822	Stem transcriptome screen for selection in wild and cultivated pitahaya (<i>Selenicereus</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	1
30823	Analysis of co-expression and gene regulatory networks associated with sterile lemma development in rice. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
30824	Whole transcriptomic analysis of mesenchymal stem cells cultured in Nichoid micro-scaffolds. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	2
30826	A chromosome-level genome assembly reveals that a bipartite gene cluster formed via an inverted duplication controls monoterpene biosynthesis in <i>Schizonepeta tenuifolia</i> . <i>Molecular Plant</i> , 2023, 16, 533-548.	3.9	7
30827	PPNet: Identifying Functional Association Networks by Phylogenetic Profiling of Prokaryotic Genomes. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
30828	The relevance of arsenic speciation analysis in health & medicine. <i>Chemosphere</i> , 2023, 316, 137735.	4.2	5
30829	The meningeal transcriptional response to traumatic brain injury and aging. <i>ELife</i> , 0, 12, .	2.8	17
30830	The gene regulatory network of <i>Staphylococcus aureus</i> ST239-SCCmecIII strain Bmb9393 and assessment of genes associated with the biofilm in diverse backgrounds. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
30831	Transcriptomic Analysis of Glycosylation and Neuroregulatory Pathways in Rodent Models in Response to Psychedelic Molecules. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1200.	1.8	2
30832	Data-Driven Approaches Used for Compound Library Design for the Treatment of Parkinsonâ€™s Disease. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1134.	1.8	1
30834	RNA sequencing of blood from sex- and age-matched discordant siblings supports immune and transcriptional dysregulation in autism spectrum disorder. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
30835	Comparative analysis of genome-scale, base-resolution DNA methylation profiles across 580 animal species. <i>Nature Communications</i> , 2023, 14, .	5.8	23
30836	Cell death-related biomarker SLC2A1 has a significant role in prognosis prediction and immunotherapy efficacy evaluation in pan-cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
30837	Lung Cancer Gene Regulatory Network of Transcription Factors Related to the Hallmarks of Cancer. <i>Current Issues in Molecular Biology</i> , 2023, 45, 434-464.	1.0	6
30838	Network Pharmacology and Mechanism Studies of the Protective Effect of Ginseng against Alzheimer's Disease Based on A $\beta$ Pathogenesis. <i>Planta Medica</i> , 2023, 89, 990-1000.	0.7	1
30839	Flt3- and Tie2-Cre tracing identifies regeneration in sepsis from multipotent progenitors but not hematopoietic stem cells. <i>Cell Stem Cell</i> , 2023, 30, 207-218.e7.	5.2	13
30840	Differential gene expression in the contralateral hemisphere of the rat brain after focal ischemia. <i>Scientific Reports</i> , 2023, 13, .	1.6	6



#	ARTICLE	IF	CITATIONS
30843	Integrating Analysis to Identify Differential circRNAs Involved in Goat Endometrial Receptivity. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1531.	1.8	0
30844	Using a Network-Based Analysis Approach to Investigate the Involvement of <i>S. aureus</i> in the Pathogenesis of Granulomatosis with Polyangiitis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1822.	1.8	1
30845	WGCNA Reveals Genes Associated with Lignification in the Secondary Stages of Wood Formation. <i>Forests</i> , 2023, 14, 99.	0.9	2
30846	From metabarcoding time series to plankton food webs: The hidden role of trophic hierarchy in providing ecological resilience. <i>Marine Ecology</i> , 2023, 44, .	0.4	2
30847	Identification of oxidative stress-related genes and potential mechanisms in atherosclerosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
30848	Network pharmacology and bioinformatics approach reveals the therapeutic mechanism of action of curcumin in Alzheimer disease. <i>Metabolic Brain Disease</i> , 2023, 38, 1205-1220.	1.4	5
30850	Enrichment of keystone fungal taxa after flue gas desulphurization gypsum application drives reclamation of the saline-sodic soil. <i>Land Degradation and Development</i> , 2023, 34, 2276-2287.	1.8	3
30851	The Fibrotic Effects of LINC00663 in Human Hepatic Stellate LX-2 Cells and in Bile Duct-Ligated Cholestasis Mice Are Mediated through the Splicing Factor 2-Fibronectin. <i>Cells</i> , 2023, 12, 215.	1.8	1
30852	Mapping the common gene networks that underlie related diseases. <i>Nature Protocols</i> , 2023, 18, 1745-1759.	5.5	3
30853	A Genome-Wide Functional Screen Identifies Enhancer and Protective Genes for Amyloid Beta-Peptide Toxicity. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1278.	1.8	1
30854	Bioinformatics and Connectivity Map Analysis Suggest Viral Infection as a Critical Causative Factor of Hashimoto's Thyroiditis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1157.	1.8	4
30855	Global analysis of the association between pig muscle fatty acid composition and gene expression using RNA-Seq. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
30856	Identification of Artemisia Argyi (AA) Therapy in Alzheimer's Disease (AD) Using Network Pharmacology and Molecular Docking. <i>Advanced Biology</i> , 2023, 7, .	1.4	1
30857	Systems and in vitro pharmacology profiling of diosgenin against breast cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	14
30859	Molecular subtypes of ALS are associated with differences in patient prognosis. <i>Nature Communications</i> , 2023, 14, .	5.8	17
30860	Peripheral blood transcriptome analysis of patients with ovarian hyperstimulation syndrome through high-throughput sequencing. <i>Reproductive and Developmental Medicine</i> , 2023, 7, 115-121.	0.2	1
30861	Increased expression of TBC1D10B as a potential prognostic and immunotherapy relevant biomarker in liver hepatocellular carcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
30863	Untangling the complex interactions between turtle ants and their microbial partners. <i>Animal Microbiome</i> , 2023, 5, .	1.5	3

#	ARTICLE	IF	CITATIONS
30864	Discovery and Functional Analysis of Secondary Hair Follicle miRNAs during Annual Cashmere Growth. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1063.	1.8	2
30865	Identifying and validating molecular subtypes of biliary atresia using multiple high-throughput data integration analysis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
30866	Research trends and hotspots of neurodegenerative diseases employing network pharmacology: A bibliometric analysis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
30867	Transcriptome dynamics provides insights into divergences of photosynthesis pathway between <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . <i>Plant Journal</i> , 0, , .	2.8	0
30868	Exploring the mechanism of Cassiae semen in regulating lipid metabolism through network pharmacology and experimental validation. <i>Bioscience Reports</i> , 0, , .	1.1	0
30870	The Role of Superoxide Dismutase 1 in Amyotrophic Lateral Sclerosis: Identification of Signaling Pathways, Regulators, Molecular Interaction Networks, and Biological Functions through Bioinformatics. <i>Brain Sciences</i> , 2023, 13, 151.	1.1	3
30871	Discovery and Characterization of Polymyxin-Resistance Genes <i>pmrE</i> and <i>pmrF</i> from Sediment and Seawater Microbiome. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
30872	Genome-Wide Analysis and Expression of the GRAS Transcription Factor Family in <i>Avena sativa</i> . <i>Genes</i> , 2023, 14, 164.	1.0	1
30873	Capture, Release, and Identification of Newly Synthesized Proteins for Improved Profiling of Functional Translatomes. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100497.	2.5	1
30874	Levofloxacin prophylaxis and parenteral nutrition have a detrimental effect on intestinal microbial networks in pediatric patients undergoing HSCT. <i>Communications Biology</i> , 2023, 6, .	2.0	4
30875	Integrative analysis of microRNAs and mRNAs reveals the regulatory networks of triterpenoid saponin metabolism in Soapberry ( <i>Sapindus mukorossi</i> Gaertn.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30876	Cuproptosis regulatory genes greatly contribute to clinical assessments of hepatocellular carcinoma. <i>BMC Cancer</i> , 2023, 23, .	1.1	5
30877	Uncovering the molecular mechanisms between heart failure and end-stage renal disease via a bioinformatics study. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30878	Identification of Lipocalin 2 as a Ferroptosis-Related Key Gene Associated with Hypoxic-Ischemic Brain Damage via STAT3/NF- $\kappa$ B Signaling Pathway. <i>Antioxidants</i> , 2023, 12, 186.	2.2	6
30879	Identification of dysregulated canonical pathways associated with pathogenesis and progression of Amyotrophic Lateral Sclerosis—An integrated bioinformatics approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2023, , 21-52.	1.0	1
30880	Salivary protein kinase C alpha and novel microRNAs as diagnostic and therapeutic resistance markers for oral squamous cell carcinoma in Indian cohorts. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
30881	Comparison of Antioxidant Capacity and Network Pharmacology of Phloretin and Phlorizin against Neuroinflammation in Traumatic Brain Injury. <i>Molecules</i> , 2023, 28, 919.	1.7	3
30882	A binary interaction map between turnip mosaic virus and <i>Arabidopsis thaliana</i> proteomes. <i>Communications Biology</i> , 2023, 6, .	2.0	8

#	ARTICLE	IF	CITATIONS
30884	A multiplexed in vivo approach to identify driver genes in small cell lung cancer. <i>Cell Reports</i> , 2023, 42, 111990.	2.9	8
30885	Identification of Comorbidities, Genomic Associations, and Molecular Mechanisms for COVID-19 Using Bioinformatics Approaches. <i>BioMed Research International</i> , 2023, 2023, 1-24.	0.9	4
30886	Investigation of the Active Compounds and Important Pathways of Huaqihuang Granule for the Treatment of Immune Thrombocytopenia Using Network Pharmacology and Molecular Docking. <i>BioMed Research International</i> , 2023, 2023, 1-13.	0.9	2
30887	Z-Guggulsterone Induces Cell Cycle Arrest and Apoptosis by Targeting the p53/CCNB1/PLK1 Pathway in Triple-Negative Breast Cancer. <i>ACS Omega</i> , 2023, 8, 2780-2792.	1.6	3
30888	Cell type characterization of spatiotemporal gene co-expression modules in Down syndrome brain. <i>IScience</i> , 2023, 26, 105884.	1.9	3
30889	Investigating the effects of chronic low-dose radiation exposure in the liver of a hypothermic zebrafish model. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
30890	Characterization of the Gut Microbiota in Urban Thai Individuals Reveals Enterotype-Specific Signature. <i>Microorganisms</i> , 2023, 11, 136.	1.6	2
30891	Differential expression analysis in epithelial ovarian cancer using functional genomics and integrated bioinformatics approaches. <i>Informatics in Medicine Unlocked</i> , 2023, 37, 101172.	1.9	0
30892	Mass Spectrometry-Based Proteomics Workflows in Cancer Research: The Relevance of Choosing the Right Steps. <i>Cancers</i> , 2023, 15, 555.	1.7	8
30893	Integrated whole transcriptome analysis for the crucial regulators and functional pathways related to cardiac fibrosis in rats. <i>Mathematical Biosciences and Engineering</i> , 2023, 20, 5413-5429.	1.0	0
30894	LGALS1 was related to the prognosis of clear cell renal cell carcinoma identified by weighted correlation gene network analysis combined with differential gene expression analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30895	Comprehensive analysis of transcriptomics and metabolomics to understand tail-suspension-induced myocardial injury in rat. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	1
30896	Compound Danshen Dripping Pills moderate intestinal flora and the TLR4/MyD88/NF- $\kappa$ B signaling pathway in alleviating cognitive dysfunction in type 2 diabetic KK-Ay mice. <i>Phytomedicine</i> , 2023, 111, 154656.	2.3	1
30897	Identification of a survival associated gene trio in chemical induced breast cancer. <i>Biochimie</i> , 2023, , .	1.3	0
30898	Integrated comparative transcriptome and weighted gene co-expression network analysis provide valuable insights into the response mechanisms of crayfish ( <i>Procambarus clarkii</i> ) to copper stress. <i>Journal of Hazardous Materials</i> , 2023, 448, 130820.	6.5	8
30899	Identification and validation of immune cells and hub genes alterations in recurrent implantation failure: A GEO data mining study. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30900	Combination of size exclusion chromatography and ion exchange adsorption for improving the proteomic analysis of plasma-derived extracellular vesicles. <i>Proteomics</i> , 0, , 2200364.	1.3	3
30901	Network and pathway-based analysis of genes associated with esophageal squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2023, 11, 102-102.	0.7	1

#	ARTICLE	IF	CITATIONS
30902	Employing non-targeted interactomics approach and subcellular fractionation to increase our understanding of the ghost proteome. <i>IScience</i> , 2023, 26, 105943.	1.9	3
30903	Identification of Hub Genes Correlated with the Initiation and Development in Chronic Kidney Disease via Bioinformatics Analysis. <i>Kidney and Blood Pressure Research</i> , 2023, 48, 79-91.	0.9	0
30904	Understanding the evolution of miRNA biogenesis machinery in plants with special focus on rice. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
30905	Soil depth as a driver of microbial and carbon dynamics in a planted forest ( <i>Pinus radiata</i> ) pumice soil. <i>Soil</i> , 2023, 9, 55-70.	2.2	2
30906	Identification of immune signatures in Parkinson's disease based on co-expression networks. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
30907	Duplicate mutations of GhCYP450 lead to the production of ms5m6 male sterile line in cotton. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	4
30908	A Genome of Temperate Enterococcus Bacteriophage Placed in a Space of Pooled Viral Dark Matter Sequences. <i>Viruses</i> , 2023, 15, 216.	1.5	0
30909	Screening and identification of potential hub genes and immune cell infiltration in the synovial tissue of rheumatoid arthritis by bioinformatic approach. <i>Heliyon</i> , 2023, 9, e12799.	1.4	3
30911	Blood leukocyte transcriptional modules and differentially expressed genes associated with disease severity and age in COVID-19 patients. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
30913	Gut bacterial species in late trimester of pregnant sows influence the occurrence of stillborn piglet through pro-inflammation response. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
30915	Development and Application of EST-SSR Markers Related to Lead Stress Responses in Kenaf Based on Transcriptome Sequencing Data. <i>Sustainability</i> , 2023, 15, 1514.	1.6	1
30916	Identification of Molecular Mechanisms Involved in Viral Infection Progression Based on Text Mining: Case Study for HIV Infection. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1465.	1.8	3
30917	High-expression of the innate-immune related gene UNC93B1 predicts inferior outcomes in acute myeloid leukemia. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
30918	Multiscale analysis of human tissue engineered matrices for next generation heart valve applications. <i>Acta Biomaterialia</i> , 2023, 158, 101-114.	4.1	3
30919	Grape-associated fungal community patterns persist from berry to wine on a fine geographical scale. <i>FEMS Yeast Research</i> , 2023, 23, .	1.1	4
30920	Genetic, DNA methylation, and immune profile discrepancies between early-stage single primary lung cancer and synchronous multiple primary lung cancer. <i>Clinical Epigenetics</i> , 2023, 15, .	1.8	1
30921	Identification of key regulatory genes and their working mechanisms in type 1 diabetes. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	0
30922	Integrated network pharmacology and experimental validation to explore the mechanisms underlying naringenin treatment of chronic wounds. <i>Scientific Reports</i> , 2023, 13, .	1.6	5

#	ARTICLE	IF	CITATIONS
30923	Analysis of long noncoding RNAs and messenger RNAs expression profiles in the hearts of mice with acute viral myocarditis. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	0
30925	Crystal Structure of the SH3 Domain of ASAP1 in Complex with the Proline Rich Motif (PRM) of MICAL1 Reveals a Unique SH3/PRM Interaction Mode. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1414.	1.8	2
30926	The mitigative effect of lotus root ( <i>Nelumbo nucifera</i> Gaertn) extract on acute alcoholism through activation of alcohol catabolic enzyme, reduction of oxidative stress, and protection of liver function. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
30927	Proteomic analysis of protein lysine 2-hydroxyisobutyrylation (Khib) in soybean leaves. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
30928	Limited Metabolomic Overlap between Commensal Bacteria and Marine Sponge Holobionts Revealed by Large Scale Culturing and Mass Spectrometry-Based Metabolomics: An Undergraduate Laboratory Pedagogical Effort at Georgia Tech. <i>Marine Drugs</i> , 2023, 21, 53.	2.2	2
30929	Metabolic Sensing of Extracytoplasmic Copper Availability via Translational Control by a Nascent Exported Protein. <i>MBio</i> , 2023, 14, .	1.8	2
30930	Phenome-wide association study of genetically predicted B vitamins and homocysteine biomarkers with multiple health and disease outcomes: analysis of the UK Biobank. <i>American Journal of Clinical Nutrition</i> , 2023, 117, 564-575.	2.2	3
30931	Construction and analysis of a survival-associated competing endogenous RNA network in breast cancer. <i>Frontiers in Surgery</i> , 0, 9, .	0.6	0
30932	Immune environment and antigen specificity of the T cell receptor repertoire of malignant ascites in ovarian cancer. <i>PLoS ONE</i> , 2023, 18, e0279590.	1.1	1
30933	Proteotranscriptomic analysis of advanced colorectal cancer patient derived organoids for drug sensitivity prediction. <i>Journal of Experimental and Clinical Cancer Research</i> , 2023, 42, .	3.5	14
30934	Identification of prognostic genes signature and construction of ceRNA network in pirarubicin treatment of triple-negative breast cancer. <i>Breast Cancer</i> , 2023, 30, 379-392.	1.3	2
30935	Cerebrospinal fluid proteomics indicates immune dysregulation and neuronal dysfunction in antibody associated autoimmune encephalitis. <i>Journal of Autoimmunity</i> , 2023, 135, 102985.	3.0	2
30936	High-frequency electrical stimulation reduced hyperalgesia and the activation of the Myd88 and NF- $\kappa$ B pathways in chronic constriction injury of sciatic nerve-induced neuropathic pain mice. <i>Neuroscience Letters</i> , 2023, 796, 137064.	1.0	1
30937	The role of unfolded protein response-associated miRNAs in immunogenic cell death amplification: A literature review and bioinformatics analysis. <i>Life Sciences</i> , 2023, 314, 121341.	2.0	2
30938	Study on subacute inhalation toxicity and offspring teratogenicity of C4F7N: An environmentally friendly insulating gas to replace SF6. <i>Journal of Cleaner Production</i> , 2023, 387, 135799.	4.6	5
30939	The gut microbiota and metabolome are associated with diminished COVID-19 vaccine-induced antibody responses in immunosuppressed inflammatory bowel disease patients. <i>EBioMedicine</i> , 2023, 88, 104430.	2.7	19
30940	Unravelling structural, functional, evolutionary and genetic basis of SWEET transporters regulating abiotic stress tolerance in maize. <i>International Journal of Biological Macromolecules</i> , 2023, 229, 539-560.	3.6	4
30941	Peptidomics analysis of Jiang-Flavor Daqu from high-temperature fermentation to mature and in different preparation season. <i>Journal of Proteomics</i> , 2023, 273, 104804.	1.2	1

#	ARTICLE	IF	CITATIONS
30942	DNA methylation-mediated phenylpropane and starch metabolism causes male poplars to be more tolerant to nitrogen deficiency than females. <i>Plant Physiology and Biochemistry</i> , 2023, 195, 144-154.	2.8	0
30943	Bioactive triterpenes of jujube in the prevention of colorectal cancer and their molecular mechanism research. <i>Phytomedicine</i> , 2023, 110, 154639.	2.3	5
30944	Identification of new telomere- and telomerase-associated autoantigens in systemic sclerosis. <i>Journal of Autoimmunity</i> , 2023, 135, 102988.	3.0	7
30945	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort ( <i>Oenanthe sinensis</i> ). <i>Industrial Crops and Products</i> , 2023, 193, 116203.	2.5	7
30946	Genetic mapping and regional association analysis revealed a CYTOKININ RESPONSE FACTOR 10 gene controlling flowering time in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2023, 193, 116239.	2.5	3
30947	A genome-wide computational approach to define microRNA-Polycomb/trithorax gene regulatory circuits in <i>Drosophila</i> . <i>Developmental Biology</i> , 2023, 495, 63-75.	0.9	0
30948	Fu Fang Gang Liu aqueous extract inhibits the proliferation of HeLa cells by causing deoxyribonucleic acid damage. <i>Journal of Ethnopharmacology</i> , 2023, 304, 116083.	2.0	0
30949	CHRNA1 and its correlated-myogenesis/cell cycle genes are prognosis-related markers of metastatic melanoma. <i>Biochemistry and Biophysics Reports</i> , 2023, 33, 101425.	0.7	1
30950	Identification of novel nutrient-sensitive gene regulatory networks in amniocytes from fetuses with spina bifida. <i>Reproductive Toxicology</i> , 2023, 116, 108333.	1.3	2
30951	Recent advances in kinase signaling network profiling by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2023, 73, 102260.	2.8	7
30952	Integrated analysis of mRNA and extrachromosomal circular DNA profiles to identify the potential mRNA biomarkers in breast cancer. <i>Gene</i> , 2023, 857, 147174.	1.0	4
30953	On the dependency heaviness of CRAN/Bioconductor ecosystem. <i>Journal of Systems and Software</i> , 2023, 198, 111610.	3.3	0
30954	Comparative proteomics analyses of whey proteins from breastmilk collected from two ethnic groups in northeast China. <i>Food Chemistry: X</i> , 2023, 17, 100568.	1.8	0
30955	Multi-omics and network pharmacology study reveals the effects of Dengzhan Shengmai capsule against neuroinflammatory injury and thrombosis induced by ischemic stroke. <i>Journal of Ethnopharmacology</i> , 2023, 305, 116092.	2.0	1
30956	Bioinformatic Analysis of lncRNA Mediated CeRNA Network in Intestinal Ischemia/Reperfusion Injury. <i>Journal of Surgical Research</i> , 2023, 284, 280-289.	0.8	1
30957	Identification of Key Genes as Potential Drug Targets for Gastric Cancer. <i>Tsinghua Science and Technology</i> , 2023, 28, 649-664.	4.1	2
30958	Divergent responses of phoD- and pqqC-harboring bacterial communities across soil aggregates to long fertilization practices. <i>Soil and Tillage Research</i> , 2023, 228, 105634.	2.6	9
30959	Building a QoS Testing Framework for Simulating Real-World Network Topologies in a Software-defined Networking Environment. , 2022, , .		1



#	ARTICLE	IF	CITATIONS
30960	The Fate of Duplicated Enzymes in Prokaryotes: The Case of Isomerases. <i>Journal of Molecular Evolution</i> , 2023, 91, 76-92.	0.8	1
30961	Transcriptomic Network Analysis Using Exfoliative Cervical Cells Could Discriminate a Potential Risk of Progression to Cancer in HPV-related Cervical Lesions: A Pilot Study. <i>Cancer Genomics and Proteomics</i> , 2023, 20, 75-87.	1.0	2
30962	Comprehensive Analysis of Necroptosis-Related Genes as Prognostic Factors and Immunological Biomarkers in Breast Cancer. <i>Journal of Personalized Medicine</i> , 2023, 13, 44.	1.1	2
30963	Circulating miR-320a-3p and miR-483-5p level associated with pharmacokinetic and pharmacodynamic profiles of rivaroxaban. <i>Human Genomics</i> , 2022, 16, .	1.4	2
30964	Helopeltis theivora-Responsive Transcriptomic Reprogramming Uncovers Long Non-coding RNAs as Possible Regulators of Primary and Secondary Metabolism in Tea Plant. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	1
30965	Multiomics Approach Captures Hepatic Metabolic Network Altered by Chronic Ethanol Administration. <i>Biology</i> , 2023, 12, 28.	1.3	2
30966	Ferroptosis-related genes with post-transcriptional regulation mechanisms in hepatocellular carcinoma determined by bioinformatics and experimental validation. <i>Annals of Translational Medicine</i> , 2022, 10, 1390-1390.	0.7	5
30968	Upregulation of MTHFD2 is associated with PD-L1 activation in bladder cancer via the PI3K/AKT pathway. <i>International Journal of Molecular Medicine</i> , 2022, 51, .	1.8	4
30969	Protein composition of axonal dopamine release sites in the striatum. <i>ELife</i> , 0, 11, .	2.8	7
30970	Genomic diversification of the specialized parasite of the fungus-growing ant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
30972	Anatomically resolved transcriptome and proteome landscapes reveal disease-relevant molecular signatures and systematic changes in heart function of end-stage dilated cardiomyopathy. <i>View</i> , 2023, 4, .	2.7	0
30973	Mechanism of Datura metel on sinus bradycardia based on network pharmacology and molecular docking. <i>Medicine (United States)</i> , 2022, 101, e32190.	0.4	0
30975	Hippocampal Changes Elicited by Metabolic and Inflammatory Stressors following Prenatal Maternal Infection. <i>Genes</i> , 2023, 14, 77.	1.0	4
30976	Pharmacology Mechanism of Polygonum Bistorta in Treating Ulcerative Colitis Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	5
30977	Network Neuroscience Untethered: Brain-Wide Immediate Early Gene Expression for the Analysis of Functional Connectivity in Freely Behaving Animals. <i>Biology</i> , 2023, 12, 34.	1.3	5
30978	Comparative Transcriptomics Reveals the microRNA-Mediated Immune Response of Large Yellow Croaker ( <i>Larimichthys crocea</i> ) to <i>Pseudomonas plecoglossicida</i> Infection. <i>Fishes</i> , 2023, 8, 10.	0.7	1
30979	Genome-Wide Comprehensive Analysis of the Nitrogen Metabolism Toolbox Reveals Its Evolution and Abiotic Stress Responsiveness in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2023, 24, 288.	1.8	6
30980	The Regulation Networks of Chinese Medicines Against Rheumatoid Arthritis with Syndrome of Deficiency of Liver and Kidney. , 2022, , .		1

#	ARTICLE	IF	CITATIONS
30981	The Potential Regulation Networks of A Core Formula of Chinese Medicine Against Insomnia. , 2022, , .		0
30982	Diversity of Bacterial Secondary Metabolite Biosynthetic Gene Clusters in Three Vietnamese Sponges. Marine Drugs, 2023, 21, 29.	2.2	2
30983	Analyzing the multi-target pharmacological mechanism of folium Artemisia argyi acting on breast cancer: a network pharmacology approach. Annals of Translational Medicine, 2022, 10, 1368-1368.	0.7	3
30985	Integrative analysis of metabolome and transcriptome reveals a dynamic regulatory network of potato tuber pigmentation. IScience, 2023, 26, 105903.	1.9	3
30986	Connecting Ships: Using Dendrochronological Network Analysis to Determine the Wood Provenance of Roman-Period River Barges Found in the Lower Rhine Region and Visualise Wood Use Patterns. International Journal of Wood Culture, 2022, 3, 123-151.	0.1	2
30987	Exploring the role of plant lysin motif receptor-like kinases in regulating plant-microbe interactions in the bioenergy crop Populus. Computational and Structural Biotechnology Journal, 2023, 21, 1122-1139.	1.9	1
30988	Total saponins of panax ginseng via the <sc>CX3CL1</sc>/<sc>CX3CR1</sc> axis attenuates neuroinflammation and exerted antidepressant-like effects in chronic unpredictable mild stress in rats. Phytotherapy Research, 2023, 37, 1823-1838.	2.8	4
30989	MS/MS-Based Molecular Networking: An Efficient Approach for Natural Products Dereplication. Molecules, 2023, 28, 157.	1.7	11
30990	bulkAnalyseR: an accessible, interactive pipeline for analysing and sharing bulk multi-modal sequencing data. Briefings in Bioinformatics, 2023, 24, .	3.2	4
30991	Uncovering the molecular mechanism of Gynostemma pentaphyllum (Thunb.) Makino against breast cancer using network pharmacology and molecular docking. Medicine (United States), 2022, 101, e32165.	0.4	0
30993	Multi Omics Analysis Revealed a Resistance Mechanism of Tibetan Barley (Hordeum vulgare L., Qingke) Infected by Ustilago hordei. Plants, 2023, 12, 157.	1.6	1
30994	DNAH7 mutations benefit colorectal cancer patients receiving immune checkpoint inhibitors. Annals of Translational Medicine, 2022, 10, 1335-1335.	0.7	1
30996	Network Pharmacology: An Emphasis on Traditional Chinese Medicines and Its Adaptability for Ayurveda Medicines in India. International Journal of Medical Science and Clinical Research Studies, 2022, 02, .	0.0	1
30997	Single-nucleus <sc>RNA</sc> and <sc>ATAC</sc> sequencing uncovers the molecular and cellular characteristics in the musk gland of Chinese forest musk deer ( <i>Moschus berezovskii</i> ). FASEB Journal, 2023, 37, .	0.2	0
30999	The Single Distinct Leader Protease Encoded by Alpinia oxyphylla Mosaic Virus (Genus Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (<i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td</i>)) Synthesis. Phytopathology, 2023, 113, 1103-1114.	1.1	2
31000	Analysis of differentially expressed long non-coding RNAs in LPS-induced human HMC3 microglial cells. BMC Genomics, 2022, 23, .	1.2	1
31001	Transcriptional expression and prognostic roles of MCM7 in human bladder, breast, and lung cancers: a multi-omics analysis. Network Modeling Analysis in Health Informatics and Bioinformatics, 2023, 12, .	1.2	0
31002	Comparative genomics with evolutionary lineage in Streptomyces bacteria reveals high biosynthetic potentials. World Journal of Microbiology and Biotechnology, 2023, 39, .	1.7	2

#	ARTICLE	IF	CITATIONS
31003	Analysis and identification of potential key genes in hepatic ischemia-reperfusion injury. <i>Annals of Translational Medicine</i> , 2022, 10, 1375-1375.	0.7	1
31004	Advances in pharmacology, biosynthesis, and metabolic engineering of <i>Scutellaria</i> -specialized metabolites. <i>Critical Reviews in Biotechnology</i> , 2024, 44, 302-318.	5.1	7
31006	The multilayered hierarchical gene regulatory network reveals interaction of transcription factors in response to cadmium in <i>Tamarix hispida</i> roots. <i>Tree Physiology</i> , 2023, 43, 630-642.	1.4	3
31007	Biased gene expression reveals the contribution of subgenome to altitude adaptation in allopolyploid <i>Isoetes sinensis</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
31009	TCMSID: a simplified integrated database for drug discovery from traditional chinese medicine. <i>Journal of Cheminformatics</i> , 2022, 14, .	2.8	7
31010	Acute stress response on Atlantic salmon: a time-course study of the effects on plasma metabolites, mucus cortisol levels, and head kidney transcriptome profile. <i>Fish Physiology and Biochemistry</i> , 2023, 49, 97-116.	0.9	4
31011	Unveiling chronic spontaneous urticaria pathophysiology through systems biology. <i>Journal of Allergy and Clinical Immunology</i> , 2023, 151, 1005-1014.	1.5	5
31012	Bioprosthetic heart valve structural degeneration associated with metabolic syndrome: Mitigation with polyoxazoline modification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	0
31013	FABP5 Deficiency Impaired Macrophage Inflammation by Regulating AMPK/NF- $\kappa$ B Signaling Pathway. <i>Journal of Immunology</i> , 2022, 209, 2181-2191.	0.4	14
31015	LPS-Induced Liver Injury of Magang Geese through Toll-like Receptor and MAPK Signaling Pathway. <i>Animals</i> , 2023, 13, 127.	1.0	1
31016	Genome-Wide Characterization and Analysis of R2R3-MYB Genes Related to Fruit Ripening and Stress Response in Banana ( <i>Musa acuminata</i> L. AAA Group, cv. "Cavendish"). <i>Plants</i> , 2023, 12, 152.	1.6	1
31017	The Chinese Medicines Reduce Osteoporosis Caused by Therapy of Glucocorticoids and Tafacitinib Against Rheumatoid Arthritis. , 2022, , .		0
31018	Identification of miRNA-mediated gene regulatory networks in L-methionine exposure counteracts cocaine-conditioned place preference in mice. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
31019	Network Analysis for the Discovery of Common Oncogenic Biomarkers in Liver Cancer Experimental Models. <i>Biomedicines</i> , 2023, 11, 342.	1.4	1
31020	Distinct response patterns of plants and soil microorganisms to agronomic practices and seasonal variation in a floodplain ecosystem. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
31021	Selection of target-binding proteins from the information of weakly enriched phage display libraries by deep sequencing and machine learning. <i>MABs</i> , 2023, 15, .	2.6	2
31022	Genome-wide identification of germin-like proteins in peanut ( <i>Arachis hypogea</i> L.) and expression analysis under different abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
31023	Dauer fate in a <i>Caenorhabditis elegans</i> Boolean network model. <i>PeerJ</i> , 0, 11, e14713.	0.9	0

#	ARTICLE	IF	CITATIONS
31024	Catechol-O-methyl transferase suppresses cell invasion and interplays with MET signaling in estrogen dependent breast cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
31025	Identification of biomarkers related to copper metabolism in patients with pulmonary arterial hypertension. <i>BMC Pulmonary Medicine</i> , 2023, 23, .	0.8	3
31026	A structure-function analysis of chlorophyllase reveals a mechanism for activity regulation dependent on disulfide bonds. <i>Journal of Biological Chemistry</i> , 2023, 299, 102958.	1.6	3
31027	Computational Gene Expression and Network Analysis of Myc Reveal Insights into Its Diagnostic and Prognostic Role in Subtypes of Renal Cancer. <i>Applied Biochemistry and Biotechnology</i> , 2023, 195, 4251-4276.	1.4	5
31028	Low expression of the dynamic network markers FOS/JUN in pre-deteriorated epithelial cells is associated with the progression of colorectal adenoma to carcinoma. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	2
31029	Microbial biofilms: A persisting public health challenge. , 2023, , 291-314.		1
31030	Exploring the mechanism by which aqueous <i>Gynura divaricata</i> inhibits diabetic foot based on network pharmacology, molecular docking and experimental verification. <i>Molecular Medicine</i> , 2023, 29, .	1.9	1
31031	Network pharmacology- and molecular simulation-based exploration of therapeutic targets and mechanisms of heparin for the treatment of sepsis/COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 12586-12598.	2.0	5
31032	A temporal classifier predicts histopathology state and parses acute-chronic phasing in inflammatory bowel disease patients. <i>Communications Biology</i> , 2023, 6, .	2.0	1
31033	Integration of transcriptomics and metabolomics to reveal the effect of ginsenoside Rg3 on allergic rhinitis in mice. <i>Food and Function</i> , 2023, 14, 2416-2431.	2.1	0
31036	The Influence of the FFAR4 Agonist TUG-891 on Liver Steatosis in ApoE-Knockout Mice. <i>Cardiovascular Drugs and Therapy</i> , 0, , .	1.3	1
31037	Influence of sex, age and diabetes on brain transcriptome and proteome modifications following cerebral ischemia. <i>BMC Neuroscience</i> , 2023, 24, .	0.8	1
31038	Variable impact of geochemical gradients on the functional potential of bacteria, archaea, and phages from the permanently stratified Lac Pavin. <i>Microbiome</i> , 2023, 11, .	4.9	4
31039	Twelve-hour rhythms in transcript expression within the human dorsolateral prefrontal cortex are altered in schizophrenia. <i>PLoS Biology</i> , 2023, 21, e3001688.	2.6	5
31040	Global transcriptome profiling reveals differential regulatory, metabolic and hormonal networks during somatic embryogenesis in <i>Coffea arabica</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	6
31041	Systematically Investigating the Pharmacological Mechanism of <i>Momordica grosvenori</i> in the Treatment of Spinal Cord Injury by Network Pharmacology and Experimental Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-13.	0.5	1
31042	Oncogenic PKA signaling increases c-MYC protein expression through multiple targetable mechanisms. <i>ELife</i> , 0, 12, .	2.8	12
31043	Metabolic modelling of the human gut microbiome in type 2 diabetes patients in response to metformin treatment. <i>Npj Systems Biology and Applications</i> , 2023, 9, .	1.4	8

#	ARTICLE	IF	CITATIONS
31044	Chromosome-scale genomics, metabolomics, and transcriptomics provide insight into the synthesis and regulation of phenols in <i>Vitis adenocladia</i> grapes. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31045	Single-cell sequencing combined with machine learning reveals the mechanism of interaction between epilepsy and stress cardiomyopathy. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
31046	Distinguish the Characteristic Mechanism of 3 Drug Pairs of <i>Corydalis</i> Rhizome in Ameliorating Angina Pectoris: Network Pharmacology and Meta-Analysis. <i>Natural Product Communications</i> , 2023, 18, 1934578X2311523.	0.2	0
31047	Exploiting Multi-Omics Profiling and Systems Biology to Investigate Functions of TOMM34. <i>Biology</i> , 2023, 12, 198.	1.3	3
31048	Candidate Genes and Pathways in Cervical Cancer: A Systematic Review and Integrated Bioinformatic Analysis. <i>Cancers</i> , 2023, 15, 853.	1.7	1
31049	Identifying Potential Molecules Downregulating APOBEC3B Mutation for Controlling Breast Cancer. <i>Procedia Computer Science</i> , 2023, 218, 1209-1219.	1.2	0
31050	Linking processes to community functions—insights into litter decomposition combining fungal metatranscriptomics and environmental NMR profiling. <i>Mycological Progress</i> , 2023, 22, .	0.5	4
31051	Structural Insights into the Substrate Range of a Bacterial Monoamine Oxidase. <i>Biochemistry</i> , 2023, 62, 851-862.	1.2	2
31053	Comparative Protein Structural Network Analysis Reveals C-Terminal Tail Phosphorylation Structural Communication Fingerprint in <i>PTEN</i> -Associated Mutations in Autism and Cancer. <i>Journal of Physical Chemistry B</i> , 2023, 127, 634-647.	1.2	1
31054	Multiplatform molecular analysis of vestibular schwannoma reveals two robust subgroups with distinct microenvironment. <i>Journal of Neuro-Oncology</i> , 0, , .	1.4	2
31055	Genome-wide characterization of the PP2C gene family in peanut ( <i>Arachis hypogaea</i> L.) and the identification of candidate genes involved in salinity-stress response. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	8
31056	Identification of potential biomarkers and immune infiltration characteristics in recurrent implantation failure using bioinformatics analysis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
31057	Human alveolar macrophage metabolism is compromised during <i>Mycobacterium tuberculosis</i> infection. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
31058	Immune infiltration and diagnostic value of immune-related genes in periodontitis using bioinformatics analysis. <i>Journal of Periodontal Research</i> , 0, , .	1.4	0
31059	RSL24D1 sustains steady-state ribosome biogenesis and pluripotency translational programs in embryonic stem cells. <i>Nature Communications</i> , 2023, 14, .	5.8	4
31060	Early peripheral blood gene expression associated with good and poor 90-day ischemic stroke outcomes. <i>Journal of Neuroinflammation</i> , 2023, 20, .	3.1	7
31061	<i>DELLA</i> proteins regulate spore germination and reproductive development in <i>Physcomitrium patens</i> . <i>New Phytologist</i> , 2023, 238, 654-672.	3.5	3
31062	Angiopoietin-like protein 3 promotes colorectal cancer progression and liver metastasis partly via the mitogen-activated protein kinase 14 pathway. <i>Molecular Carcinogenesis</i> , 2023, 62, 546-560.	1.3	3

#	ARTICLE	IF	CITATIONS
31063	The Interplay between RNA Editing Regulator ADAR1 and Immune Environment in Colorectal Cancer. <i>Journal of Oncology</i> , 2023, 2023, 1-13.	0.6	4
31065	Mapping the signaling network of BIN2 kinase using TurboID-mediated biotin labeling and phosphoproteomics. <i>Plant Cell</i> , 2023, 35, 975-993.	3.1	28
31066	Genome-wide liver transcriptomic profiling of a malaria mouse model reveals disturbed immune and metabolic responses. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	3
31067	Dual viscosity mixture vehicle for intratympanic steroid treatment modifies the ROS and inflammation related proteomes. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	1
31068	A Novel Prognostic Pyroptosis-Related Gene Signature Correlates to Oxidative Stress and Immune-Related Features in Gliomas. <i>Oxidative Medicine and Cellular Longevity</i> , 2023, 2023, 1-28.	1.9	3
31069	Building, Visualizing, and Analyzing Glycosaminoglycan-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2023, , 211-224.	0.4	1
31071	Identification of key genes and biological regulatory mechanisms in diabetic nephropathy: Meta-analysis of gene expression datasets. <i>Nefrologia</i> , 2023, 43, 575-586.	0.2	1
31073	Unraveling the genetics underlying micronutrient signatures of diversity panel present in brown rice through genome-ionome linkages. <i>Plant Journal</i> , 2023, 113, 749-771.	2.8	5
31074	Identifying potential ligand molecules EGFR mediated TNBC targeting the kinase domain-identification of customized drugs through in silico methods. <i>Research in Pharmaceutical Sciences</i> , 2023, 18, 121.	0.6	0
31075	In silico investigation of uncoupling protein function in avian genomes. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
31078	A Data-Driven Approach to Construct a Molecular Map of <i>Trypanosoma cruzi</i> to Identify Drugs and Vaccine Targets. <i>Vaccines</i> , 2023, 11, 267.	2.1	2
31079	Selenium stress response of the fruit origin strain <i>Fructobacillus tropaeoli</i> CRL 2034. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 1329-1339.	1.7	0
31081	The Potential Mechanism of Zishen Yutai Pills against Threatened Abortion: An Approach Involving Network Pharmacology and Experimental Evidence. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-16.	0.5	0
31082	Crude Extracts of <i>Talaromyces</i> Strains (Ascomycota) Affect Honey Bee ( <i>Apis mellifera</i> ) Resistance to Chronic Bee Paralysis Virus. <i>Viruses</i> , 2023, 15, 343.	1.5	1
31083	Phthalates impact on the epigenetic factors contributed specifically by the father at fertilization. <i>Epigenetics and Chromatin</i> , 2023, 16, .	1.8	0
31086	Application of feature-based molecular networking in the field of algal research with special focus on mycosporine-like amino acids. <i>Journal of Applied Phycology</i> , 2023, 35, 1377-1392.	1.5	2
31087	Effect of Xuefu Zhuyu Capsule on Myocardial Infarction: Network Pharmacology and Experimental Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-11.	0.5	1
31088	A novel prognostic model of methylation-associated genes in acute myeloid leukemia. <i>Clinical and Translational Oncology</i> , 0, , .	1.2	0



#	ARTICLE	IF	CITATIONS
31090	Biomarker prediction in autism spectrum disorder using a network-based approach. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	2
31091	Grass-microbial inter-domain ecological networks associated with alpine grassland productivity. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
31092	Characterization of proteome-size scaling by integrative omics reveals mechanisms of proliferation control in cancer. <i>Science Advances</i> , 2023, 9, .	4.7	6
31094	Data mining combines bioinformatics discover immunoinfiltration-related gene SERPINE1 as a biomarker for diagnosis and prognosis of stomach adenocarcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
31095	In Silico Analysis of Cellular Interactors of PQBP1 for Potential Drug Repurposing. , 2023, , 47-51.		0
31097	Cell Cycle-Related Gene SPC24: A Novel Potential Diagnostic and Prognostic Biomarker for Laryngeal Squamous Cell Cancer. <i>BioMed Research International</i> , 2023, 2023, 1-14.	0.9	1
31098	Bioinformatic analysis of the obesity paradox and possible associated factors in colorectal cancer using TCGA cohorts. <i>Journal of Cancer</i> , 2023, 14, 379-392.	1.2	2
31099	Novel diagnostic biomarkers related to immune infiltration in Parkinson's disease by bioinformatics analysis. <i>Frontiers in Neuroscience</i> , 0, 17, .	1.4	2
31100	Proteogenomics of diffuse gliomas reveal molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. <i>Nature Communications</i> , 2023, 14, .	5.8	7
31101	Transcriptome analysis indicates the involvement of herbicide-responsive and plant-pathogen interaction pathways in the development of resistance to ACCase inhibitors in <i>Apera spica-venti</i> . <i>Pest Management Science</i> , 2023, 79, 1944-1962.	1.7	6
31102	Differential proteomics of Zika virus (ZIKV) infection reveals molecular changes potentially involved in immune system evasion by a Brazilian strain of ZIKV. <i>Archives of Virology</i> , 2023, 168, .	0.9	1
31103	Trends in modern drug discovery and development: A glance in the present millennium. , 2023, , 27-38.		1
31104	Annotation of natural product compound families using molecular networking topology and structural similarity fingerprinting. <i>Nature Communications</i> , 2023, 14, .	5.8	14
31106	DNA Double-Strand Break-Related Competitive Endogenous RNA Network of Noncoding RNA in Bovine Cumulus Cells. <i>Genes</i> , 2023, 14, 290.	1.0	2
31109	Contrasting Mechanisms Determine the Microeukaryotic and Syndiniales Community Assembly in a Eutrophic bay. <i>Microbial Ecology</i> , 2023, 86, 1575-1588.	1.4	2
31110	Anti-inflammatory Therapy Protects Spiral Ganglion Neurons After Aminoglycoside Antibiotic-Induced Hair Cell Loss. <i>Neurotherapeutics</i> , 2023, 20, 578-601.	2.1	5
31111	Hierarchical architecture of dopaminergic circuits enables second-order conditioning in <i>Drosophila</i> . <i>ELife</i> , 0, 12, .	2.8	13
31112	Comprehending the impact of #Breastcancer, #Breastsurgery and related hashtags on Twitter: A content and social network cross-sectional analysis #Breastcancer#Breastsurgery. <i>European Journal of Surgical Oncology</i> , 2023, 49, 716-723.	0.5	3

#	ARTICLE	IF	CITATIONS
31113	AFM negatively regulates the infiltration of monocytes to mediate sepsis-associated acute kidney injury. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
31114	Tissue-specific metabolic profile drives iNKT cell function during obesity and liver injury. <i>Cell Reports</i> , 2023, 42, 112035.	2.9	3
31115	Recent advances in the area of plant-based anti-cancer drug discovery using computational approaches. <i>Molecular Diversity</i> , 0, , .	2.1	7
31116	Identification and Functional Prediction of Long Non-Coding RNA in Longissimus Dorsi Muscle of Queshan Black and Large White Pigs. <i>Genes</i> , 2023, 14, 197.	1.0	3
31117	Isomeric Activity Cliffsâ€™A Case Study for Fluorine Substitution of Aminergic G Protein-Coupled Receptor Ligands. <i>Molecules</i> , 2023, 28, 490.	1.7	2
31119	A Group of Tumor-Suppressive micro-RNAs Changes Expression Coordinately in Colon Cancer. <i>Current Issues in Molecular Biology</i> , 2023, 45, 975-989.	1.0	0
31120	Whole-transcriptome profiling across different developmental stages of <i>Aedes albopictus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 networks. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	4
31121	Systems level analysis of sex-dependent gene expression changes in Parkinsonâ€™s disease. <i>Npj Parkinson's Disease</i> , 2023, 9, .	2.5	6
31123	Genome-wide in silico identification of glutathione S-transferase (GST) gene family members in fig ( <i>Ficus carica</i> L.) and expression characteristics during fruit color development. <i>PeerJ</i> , 0, 11, e14406.	0.9	1
31124	CpH methylome analysis in human cortical neurons identifies novel gene pathways and drug targets for opioid use disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	7
31125	Parkinsonâ€™s Disease Gene Biomarkers Screened by the LASSO and SVM Algorithms. <i>Brain Sciences</i> , 2023, 13, 175.	1.1	4
31126	Identification of the potential biomarkers associated with circadian rhythms in heart failure. <i>PeerJ</i> , 0, 11, e14734.	0.9	1
31127	Analysis of dog breed diversity using a composite selection index. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
31128	A targeted multi-proteomics approach generates a blueprint of the ciliary ubiquitinome. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	11
31129	High Expression of DLGAP5 Indicates Poor Prognosis and Immunotherapy in Lung Adenocarcinoma and Promotes Proliferation through Regulation of the Cell Cycle. <i>Disease Markers</i> , 2023, 2023, 1-20.	0.6	4
31130	Molecular Networking Revealed Unique UV-Absorbing Phospholipids: Favilipids from the Marine Sponge <i>Clathria faviformis</i> . <i>Marine Drugs</i> , 2023, 21, 58.	2.2	2
31134	Integrated multiomics analysis to infer COVID-19 biological insights. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
31136	From big data to complex network: a navigation through the maze of drugâ€™target interaction. , 2023, , 407-436.		0

#	ARTICLE	IF	CITATIONS
31137	Identification of Potential Hub Genes Related to Aflatoxin B1, Liver Fibrosis and Hepatocellular Carcinoma via Integrated Bioinformatics Analysis. <i>Biology</i> , 2023, 12, 205.	1.3	3
31138	Gene coexpression analysis reveals key pathways and hub genes related to late-acting self-incompatibility in <i>Camellia oleifera</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
31139	Identification and verification of FN1, P4HA1 and CREBBP as potential biomarkers in human atrial fibrillation. <i>Mathematical Biosciences and Engineering</i> , 2023, 20, 6947-6965.	1.0	0
31140	Transcriptomic changes associated with maternal care in the brain of mouthbrooding cichlid <i>Astatotilapia burtoni</i> reflect adaptation to self-induced metabolic stress. <i>Journal of Experimental Biology</i> , 2023, 226, .	0.8	2
31141	Network analyses of upper and lower airway transcriptomes identify shared mechanisms among children with recurrent wheezing and school-age asthma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
31142	Abscisic acid mediated strawberry receptacle ripening involves the interplay of multiple phytohormone signaling networks. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31143	Comparative proteomic analysis identified proteins and the phenylpropanoid biosynthesis pathway involved in the response to ABA treatment in cotton fiber development. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
31144	Comparative Proteomic Analysis Provides New Insights into the Molecular Basis of Thermal-Induced Parthenogenesis in Silkworm ( <i>Bombyx mori</i> ). <i>Insects</i> , 2023, 14, 134.	1.0	2
31145	Cell-Type-Specific Signalling Networks Impacted by Prostate Epithelial-Stromal Intercellular Communication. <i>Cancers</i> , 2023, 15, 699.	1.7	1
31147	Identification of drug and protein-protein interaction network among stress and depression: A bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2023, 37, 101174.	1.9	7
31148	Genome-wide characterization of phospholipase D family genes in allotetraploid peanut and its diploid progenitors revealed their crucial roles in growth and abiotic stress responses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
31149	A Four-Step Platform to Optimize Growth Conditions for High-Yield Production of Siderophores in Cyanobacteria. <i>Metabolites</i> , 2023, 13, 154.	1.3	2
31150	scm6A-seq reveals single-cell landscapes of the dynamic m6A during oocyte maturation and early embryonic development. <i>Nature Communications</i> , 2023, 14, .	5.8	21
31151	<i>GATA6-AS1</i> Regulates Intestinal Epithelial Mitochondrial Functions, and its Reduced Expression is Linked to Intestinal Inflammation and Less Favourable Disease Course in Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2023, 17, 960-971.	0.6	8
31152	Identifying colon cancer stage related genes and their cellular pathways. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31153	Microbial Interactions Related to N <sub>2</sub> O Emissions and Temperature Sensitivity from Rice Paddy Fields. <i>MBio</i> , 2023, 14, .	1.8	4
31154	Investigating nicotine pathway-related long non-coding RNAs in tobacco. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
31155	Genetic dissection reveals the complex architecture of amino acid composition in soybean seeds. <i>Theoretical and Applied Genetics</i> , 2023, 136, 1-15.	1.8	0

#	ARTICLE	IF	CITATIONS
31156	The structure and diversity of microbial communities in <i>Paederus fuscipes</i> (Coleoptera: Staphylinidae): from ecological paradigm to pathobiome. <i>Microbiome</i> , 2023, 11, .	4.9	5
31157	Harnessing Novel Soil Bacteria for Beneficial Interactions with Soybean. <i>Microorganisms</i> , 2023, 11, 300.	1.6	2
31159	Towards a structurally resolved human protein interaction network. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 216-225.	3.6	74
31160	FAS-mediated circRNA-miRNA-mRNA Crosstalk Network Regulates Immune Cell Infiltration in Cerebral Infarction. <i>Journal of Molecular Neuroscience</i> , 0, , .	1.1	1
31161	Detection of key mRNAs in liver tissue of hepatocellular carcinoma patients based on machine learning and bioinformatics analysis. <i>MethodsX</i> , 2023, 10, 102021.	0.7	2
31162	A compendium of mucosal molecular characteristics provides novel perspectives on the treatment of ulcerative colitis. <i>Journal of Crohn's and Colitis</i> , 0, , .	0.6	0
31164	Antithymocyte Globulin Inhibits CD8+ T Cell Effector Functions via the Paracrine Induction of PDL-1 on Monocytes. <i>Cells</i> , 2023, 12, 382.	1.8	2
31165	Potential Pharmacological Mechanism of Action Mechanism of <i>Spica prunellae</i> in Treating Thyroid Nodule. <i>Advances in Clinical Medicine</i> , 2023, 13, 1128-1138.	0.0	0
31166	PARP1 Inhibition and Effect on Burn Injury-Induced Inflammatory Response and Cardiac Function. <i>Journal of the American College of Surgeons</i> , 2023, 236, 783-802.	0.2	0
31167	Algal rhodopsins encoding diverse signal sequence holds potential for expansion of organelle optogenetics. <i>Biophysics and Physicobiology</i> , 2023, 20, n/a.	0.5	2
31168	RALF peptides modulate immune response in the moss <i>Physcomitrium patens</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
31169	Genome-Wide Characterization of HSP90 Gene Family in Chinese Pumpkin ( <i>Cucurbita moschata</i> Duch.) and Their Expression Patterns in Response to Heat and Cold Stresses. <i>Agronomy</i> , 2023, 13, 430.	1.3	0
31171	Impaired Function of Solute Carrier Family 19 Leads to Low Folate Levels and Lipid Droplet Accumulation in Hepatocytes. <i>Biomedicines</i> , 2023, 11, 337.	1.4	0
31172	Exploring the shared molecular mechanism of microvascular and macrovascular complications in diabetes: Seeking the hub of circulatory system injury. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	1
31173	A usage-based diachronic study of translated terminology. <i>Terminology</i> , 0, , .	2.9	0
31174	Genome-Wide Identification of BTB Domain-Containing Gene Family in Grapevine ( <i>Vitis vinifera</i> L.). <i>Agriculture (Switzerland)</i> , 2023, 13, 252.	1.4	1
31175	Analysis of affinity purification-related proteomic data for studying proteinâ€“protein interaction networks in cells. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
31176	In Silico Study on the Interactions, Molecular Docking, Dynamics and Simulation of Potential Compounds from <i>Withania somnifera</i> (L.) Dunal Root against Cancer by Targeting KAT6A. <i>Molecules</i> , 2023, 28, 1117.	1.7	6

#	ARTICLE	IF	CITATIONS
31177	Integrative analysis of the expression profiles of whole coding and non-coding RNA transcriptomes and construction of the competing endogenous RNA networks for chronic obstructive pulmonary disease. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	4
31179	When type 2 diabetes mellitus meets COVID-19 Identification of the shared gene signatures and biological mechanism between the two diseases. <i>European Journal of Clinical Investigation</i> , 2023, 53, .	1.7	1
31180	Stress-Induced Transcriptomic Changes in Females with Myalgic Encephalomyelitis/Chronic Fatigue Syndrome Reveal Disrupted Immune Signatures. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2698.	1.8	7
31182	Sex-dimorphic and age-dependent organization of 24-hour gene expression rhythms in humans. <i>Science</i> , 2023, 379, 478-483.	6.0	52
31183	Co-expression network of heat-response transcripts: A glimpse into how splicing factors impact rice basal thermotolerance. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	1
31184	SIRT6 is a key regulator of mitochondrial function in the brain. <i>Cell Death and Disease</i> , 2023, 14, .	2.7	12
31185	The Role of Mitotic Slippage in Creating a "Female Pregnancy-like System" in a Single Polyploid Giant Cancer Cell. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3237.	1.8	2
31186	Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. <i>Nature Communications</i> , 2023, 14, .	5.8	11
31187	Uncovering the Oxidative Stress Mechanisms and Targets in Alzheimer's Disease by Integrating Phenotypic Screening Data and Polypharmacology Networks. <i>Journal of Alzheimer's Disease</i> , 2023, , 1-18.	1.2	3
31188	The dynamics of the microbial community in fall armyworm ( <i>Spodoptera frugiperda</i> ) during a life cycle. <i>Entomologia Experimentalis Et Applicata</i> , 2023, 171, 502-513.	0.7	4
31189	Quantitative Proteomics of Human Retinal Pigment Epithelium Reveals Key Regulators for the Pathogenesis of Age-Related Macular Degeneration. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3252.	1.8	4
31190	A systematic review and meta-analysis of inflammatory biomarkers in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2023, 9, .	2.5	18
31191	Integrative pathway and network analysis provide insights on flooding-tolerance genes in soybean. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31192	Novel Prognostic Biomarkers for Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (CESC) Patients via Analysis of Competing Endogenous RNA (ceRNA) Network. <i>Disease Markers</i> , 2023, 2023, 1-12.	0.6	2
31193	Comparative transcriptomics and co-expression networks reveal cultivar-specific molecular signatures associated with reproductive-stage cold stress in rice. <i>Plant Cell Reports</i> , 2023, 42, 707-722.	2.8	2
31194	Network Pharmacology Analysis and Experimental Pharmacology Study Explore the Mechanism of Asparagus against Glioblastoma. <i>Journal of Food Biochemistry</i> , 2023, 2023, 1-11.	1.2	1
31196	Pathway network-based quantitative modeling of the time-dependent and dose-response anti-inflammatory effect of Reduning Injection. <i>Journal of Ethnopharmacology</i> , 2023, 307, 116216.	2.0	0
31197	Land use effects on soil protists and their top-down regulation on bacteria and fungi in soil profiles. <i>Applied Soil Ecology</i> , 2023, 185, 104799.	2.1	7

#	ARTICLE	IF	CITATIONS
31198	Therapeutic effects and mechanisms of Ku-Gan formula on atopic dermatitis: A pilot clinical study and modular pharmacology analysis with animal validation. <i>Journal of Ethnopharmacology</i> , 2023, 307, 116194.	2.0	3
31199	Recursos naturales, diversificación y crecimiento regional en el Perú. <i>Economía</i> , 2015, 38, 41-100.	0.2	0
31200	Exploration of genetic basis of differential immune response to CSF vaccination in desi (indigenous) piglets using RNA-Seq approach. <i>Indian Journal of Animal Sciences</i> , 2017, 87, .	0.1	0
31201	miR-let-7a-2, miR103a-2 and CREB1-TF as therapeutic targets to regulate the transcription of DISC1 and PDE4D in the transcriptional regulation pathway by DISC1/ATF4 complex. , 2022, , .		0
31202	Metabolomic analysis-identified 2-hydroxybutyric acid might be a key metabolite of severe preeclampsia. <i>Open Life Sciences</i> , 2023, 18, .	0.6	1
31203	All-in-One digital microfluidics pipeline for proteomic sample preparation and analysis. <i>Chemical Science</i> , 2023, 14, 2887-2900.	3.7	11
31204	Deciphering Macromolecular Interactions Involved in Abiotic Stress Signaling: A Review of Bioinformatics Analysis. <i>Methods in Molecular Biology</i> , 2023, , 257-294.	0.4	2
31205	What transcriptomics and proteomics can tell us about a high borate perturbed boron tolerant Bacilli strain. <i>Molecular Omics</i> , 2023, 19, 370-382.	1.4	1
31206	NF- $\kappa$ B Pathway Analysis and Biomarker Identification in Nasopharyngeal Carcinoma. <i>Re:GEN Open</i> , 2023, 3, 11-20.	0.7	0
31207	Identification of Potential Diagnostic and Prognostic Biomarkers for Gastric Cancer Based on Bioinformatic Analysis. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2023, , .	0.6	0
31208	Generation of Red Blood Cell Nanovesicles as a Delivery Tool. <i>Methods in Molecular Biology</i> , 2023, , 321-336.	0.4	2
31209	Phosphoproteomic analysis of metformin signaling in colorectal cancer cells elucidates mechanism of action and potential therapeutic opportunities. <i>Clinical and Translational Medicine</i> , 2023, 13, .	1.7	7
31210	Gene Structural Specificity and Expression of MADS-Box Gene Family in <i>Camellia chekiangoleosa</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3434.	1.8	4
31211	Differential lncRNA/mRNA expression profiling and ceRNA network analyses in amniotic fluid from fetuses with ventricular septal defects. <i>PeerJ</i> , 0, 11, e14962.	0.9	1
31212	A Novel Molecular Analysis Approach in Colorectal Cancer Suggests New Treatment Opportunities. <i>Cancers</i> , 2023, 15, 1104.	1.7	1
31213	Time-Course Transcriptome Analysis of the Lungs of Mice Challenged with Aerosols of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Clone Reveals Inflammatory Balance. <i>Biomolecules</i> , 2023, 13, 347.	1.8	1
31214	The Hyphosphere of Leaf-Cutting Ant Cultivars Is Enriched with Helper Bacteria. <i>Microbial Ecology</i> , 2023, 86, 1773-1788.	1.4	3
31215	Global hypomethylation in childhood asthma identified by genome-wide DNA methylation sequencing preferentially affects enhancer regions. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2023, 78, 1489-1506.	2.7	5



#	ARTICLE	IF	CITATIONS
31216	Multi-Tissue Transcriptome Study of Innate Immune Gene Expression Profiling Reveals Negative Energy Balance Altered the Defense and Promoted System Inflammation of Dairy Cows. <i>Veterinary Sciences</i> , 2023, 10, 107.	0.6	1
31218	Interaction between Microbes and Host in Sow Vaginas in Early Pregnancy. <i>MSystems</i> , 0, , .	1.7	1
31219	Recognition of Differentially Expressed Molecular Signatures and Pathways Associated with COVID-19 Poor Prognosis in Glioblastoma Patients. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3562.	1.8	4
31220	Rapid remodeling of the soil lipidome in response to a drying-rewetting event. <i>Microbiome</i> , 2023, 11, .	4.9	3
31221	Quantitative proteomics of sperm tail in asthenozoospermic patients: exploring the molecular pathways affecting sperm motility. <i>Cell and Tissue Research</i> , 2023, 392, 793-810.	1.5	1
31222	RNA-Sequencing Reveals the Involvement of Sesquiterpene Biosynthesis Genes and Transcription Factors during an Early Response to Mechanical Wounding of <i>Aquilaria sinensis</i> . <i>Genes</i> , 2023, 14, 464.	1.0	3
31226	mNeuCode Empowers Targeted Proteome Analysis of Arginine Dimethylation. <i>Analytical Chemistry</i> , 2023, 95, 3684-3693.	3.2	2
31227	EWI2 and its relatives in Tetraspanin-enriched membrane domains regulate malignancy. <i>Oncogene</i> , 2023, 42, 861-868.	2.6	2
31228	Markers of aging: Unsupervised integrated analyses of the human plasma proteome. <i>Frontiers in Aging</i> , 0, 4, .	1.2	4
31229	The Identification and Characteristics of miRNAs Related to Cashmere Fiber Traits in Skin Tissue of Cashmere Goats. <i>Genes</i> , 2023, 14, 473.	1.0	0
31230	Identification and Functional Characterization of WRKY, PHD and MYB Three Salt Stress Responsive Gene Families in Mungbean ( <i>Vigna radiata</i> L.). <i>Genes</i> , 2023, 14, 463.	1.0	1
31231	Altered Faecal Microbiota Composition and Structure of Ghanaian Children with Acute Gastroenteritis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3607.	1.8	4
31232	Germline VWF/MPRIIP and somatoplasm FGA variants synergically confer susceptibility to non-traumatic osteonecrosis of the femoral head. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31233	Identification and verification of a BMPs-related gene signature for osteosarcoma prognosis prediction. <i>BMC Cancer</i> , 2023, 23, .	1.1	0
31234	Biosynthetic Gene Clusters from Swine Gut Microbiome. <i>Microorganisms</i> , 2023, 11, 434.	1.6	3
31235	Knockout of AMD-associated gene POLDIP2 reduces mitochondrial superoxide in human retinal pigment epithelial cells. <i>Aging</i> , 2023, 15, 1713-1733.	1.4	1
31236	Mitochondrial control of microglial phagocytosis by the translocator protein and hexokinase 2 in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	22
31238	Mitochondrial DNA Deficiency and Supplementation in <i>Sus scrofa</i> Oocytes Influence Transcriptome Profiles in Oocytes and Blastocysts. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3783.	1.8	3

#	ARTICLE	IF	CITATIONS
31240	Hippo pathway and Bonus control developmental cell fate decisions in the Drosophila eye. <i>Developmental Cell</i> , 2023, 58, 416-434.e12.	3.1	5
31241	Gene Co-Expression Network Analysis Reveals the Hub Genes and Key Pathways Associated with Resistance to Salmonella Enteritidis Colonization in Chicken. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4824.	1.8	0
31242	Identification of a novel Immune-Related prognostic model for patients with colorectal cancer based on 3 subtypes. <i>Immunobiology</i> , 2023, 228, 152352.	0.8	0
31243	Unique alcohol dehydrogenases involved in algal sugar utilization by marine bacteria. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 2363-2384.	1.7	1
31244	Genome-wide analysis of the laccase (LAC) gene family in <i>Aeluropus littoralis</i> : A focus on identification, evolution and expression patterns in response to abiotic stresses and ABA treatment. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	17
31246	Sweetener System Intervention Shifted Neutrophils from Homeostasis to Priming. <i>Nutrients</i> , 2023, 15, 1260.	1.7	2
31247	Time-Series Expression Profile Analysis of Post-Traumatic Joint Contracture in Rats at the Early Stages of the Healing Process. <i>Journal of Inflammation Research</i> , 0, Volume 16, 1169-1181.	1.6	0
31249	Translating desktop success to the web in the cytoscape project. <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	0
31250	Diapause-Linked Gene Expression Pattern and Related Candidate Duplicated Genes of the Mountain Butterfly <i>Parnassius glacialis</i> (Lepidoptera: Papilionidae) Revealed by Comprehensive Transcriptome Profiling. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5577.	1.8	1
31251	Integration of the Microbiome, Metabolome and Transcriptome Reveals <i>Escherichia coli</i> F17 Susceptibility of Sheep. <i>Animals</i> , 2023, 13, 1050.	1.0	1
31252	The effect of GOS2 on insulin sensitivity: A proteomic analysis in a GOS2-overexpressed high-fat diet mouse model. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	1
31253	Effects of donkey milk on UVB-induced skin barrier damage and melanin pigmentation: A network pharmacology and experimental validation study. <i>Frontiers in Nutrition</i> , 0, 10, .	1.6	1
31254	Evolutionary Analysis of the Melon ( <i>Cucumis melo</i> L.) GH3 Gene Family and Identification of GH3 Genes Related to Fruit Growth and Development. <i>Plants</i> , 2023, 12, 1382.	1.6	2
31255	Molecular Networking-Guided Isolation of a Phenolic Constituent from <i>Prunus mume</i> Seed and Its Antioxidant and Anti-Inflammatory Activities. <i>Foods</i> , 2023, 12, 1146.	1.9	3
31256	Plant species shape the bacterial communities on the phyllosphere in a hyper-arid desert. <i>Microbiological Research</i> , 2023, 269, 127314.	2.5	4
31259	Emergent patterns in global health diplomacy: a network analysis of the resolutions adopted by the World Health Assembly from 1948 to 2022. <i>BMJ Global Health</i> , 2023, 8, e011211.	2.0	2
31260	IDENTIFICATION AND CLINICAL VALIDATION OF HYPOXIA-INDUCIBLE FACTOR 1 $\pm$ PROTEIN AS THE POTENTIAL BIOMARKER IN PATIENTS WITH SEPSIS. <i>Shock</i> , 2023, 59, 855-863.	1.0	5
31261	Widely targeted metabolomic, transcriptomic, and metagenomic profiling reveal microbeâ€œplantâ€œmetabolic reprogramming patterns mediated by <i>Streptomyces pactum</i> Act12 enhance the fruit quality of <i>Capsicum annuum</i> L. <i>Food Research International</i> , 2023, 166, 112587.	2.9	6

#	ARTICLE	IF	CITATIONS
31262	Analyses of a chromosome-scale genome assembly reveal the origin and evolution of cultivated chrysanthemum. <i>Nature Communications</i> , 2023, 14, .	5.8	25
31263	PGC-1s shape epidermal physiology by modulating keratinocyte proliferation and terminal differentiation. <i>iScience</i> , 2023, 26, 106314.	1.9	3
31264	Comparative transcriptomic analysis of germinating rice seedlings to individual and combined anaerobic and cold stress. <i>BMC Genomics</i> , 2023, 24, .	1.2	5
31265	RNA-Sequencing Reveals Gene Expression and Pathway Signatures in Umbilical Cord Blood Affected by Birth Delivery Mode. <i>Phenomics</i> , 2023, 3, 228-242.	0.9	2
31266	Effects of heat and hyposalinity on the gene expression in <i>Acropora pruinosa</i> larvae. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	2
31267	Transcriptomics of Hirschsprung disease patient-derived enteric neural crest cells reveals a role for oxidative phosphorylation. <i>Nature Communications</i> , 2023, 14, .	5.8	6
31268	Plant growth stages covered the legacy effect of rotation systems on microbial community structure and function in wheat rhizosphere. <i>Environmental Science and Pollution Research</i> , 2023, 30, 59632-59644.	2.7	1
31269	Emodin Exerts its Therapeutic Effects Through Metabolic Remodeling in Severe Acute Pancreatitis-Related Intestinal Injury. <i>Natural Product Communications</i> , 2023, 18, 1934578X2311639.	0.2	0
31270	Molecular Mechanism of the Therapeutic Effect of Peach Blossom against Constipation: An Exploratory Study Based on Network Pharmacology Analysis and Molecular Docking Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-14.	0.5	0
31271	Identification of Inflammatory Gene in the Congenital Heart Surgery Patients following Cardiopulmonary Bypass via the Way of WGCNA and Machine Learning Algorithms. <i>Disease Markers</i> , 2023, 2023, 1-21.	0.6	0
31272	Metagenomic Insight into Microbiome and Antibiotic Resistance Genes of High Clinical Concern in Urban and Rural Hospital Wastewater of Northern India Origin: a Major Reservoir of Antimicrobial Resistance. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	7
31273	Exploration of phytochemicals and biological functions of <i>Kadsura coccinea</i> pericarpium based on LC-MS and network pharmacology analysis and experimental validation. <i>Journal of Functional Foods</i> , 2023, 103, 105493.	1.6	0
31274	Maternal Rumen Bacteriota Shapes the Offspring Rumen Bacteriota, Affecting the Development of Young Ruminants. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
31275	A conserved gene regulatory network controls root epidermal cell patterning in superrosid species. <i>New Phytologist</i> , 2023, 238, 2410-2426.	3.5	2
31276	The transcription factor PbrMYB24 regulates lignin and cellulose biosynthesis in stone cells of pear fruits. <i>Plant Physiology</i> , 2023, 192, 1997-2014.	2.3	13
31277	Bioinformatics and computational chemistry approaches to explore the mechanism of the anti-depressive effect of ligustilide. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31278	Impaired Humoral Immunity Identified in Inactivated SARS-CoV-2 Vaccine Recipients without Anti-Spike RBD Antibodies. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
31279	A single-cell landscape of triptolide-associated testicular toxicity in mice. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 880-893.	2.4	3

#	ARTICLE	IF	CITATIONS
31280	Key ingredients in <i>Verbena officinalis</i> and determination of their anti-atherosclerotic effect using a computer-aided drug design approach. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
31281	Molecular networking-based discovery of new polyketides from the deep-sea-derived fungus <i>Talaromyces indigoticus</i> FS688. <i>Tetrahedron</i> , 2023, , 133410.	1.0	1
31282	The Interaction between Intratumoral Microbiome and Immunity Is Related to the Prognosis of Ovarian Cancer. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	7
31283	<i>Akkermansia muciniphila</i> plays a neuroprotective role in HMC3 cells through the "gut-brain" axis. <i>Future Microbiology</i> , 0, , .	1.0	0
31284	Microbial life in 25-m-deep boreholes in ancient permafrost illuminated by metagenomics. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	1
31285	Decrypting drug actions and protein modifications by dose- and time-resolved proteomics. <i>Science</i> , 2023, 380, 93-101.	6.0	21
31286	Acute temperature stresses trigger liver transcriptome and microbial community remodeling in largemouth bass ( <i>Micropterus salmoides</i> ). <i>Aquaculture</i> , 2023, 573, 739573.	1.7	7
31287	Characterization of aroma differences on three drying treatments in Rucheng Baimao ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Qverlock 2.5	1.8	1
31288	SUMOylation patterns and signature characterize the tumor microenvironment and predict prognosis in lung adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
31289	MicroRNA-130a-3p inhibition suppresses cervical cancer cell progression. <i>Oncology Reports</i> , 2023, 49, .	1.2	1
31290	Proteostasis networks in aging: novel insights from text-mining approaches. <i>Biogerontology</i> , 2023, 24, 555-562.	2.0	1
31291	An integrated signature of extracellular matrix proteins and a diastolic function imaging parameter predicts post-MI long-term outcomes. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	2
31292	Use of <i>Arabidopsis thaliana</i> as a model to understand specific carcinogenic events: Comparison of the molecular machinery associated with cancer-hallmarks in plants and humans. <i>Heliyon</i> , 2023, 9, e15367.	1.4	0
31293	Mass spectrometry for mitochondrial multi-omics. <i>TrAC - Trends in Analytical Chemistry</i> , 2023, 163, 117063.	5.8	0
31294	Integration of text mining and biological network analysis: Identification of essential genes in sulfate-reducing bacteria. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
31295	Identification and Validation of Cyclin A2 and Cyclin E2 as Potential Biomarkers in Small Cell Lung Cancer. <i>Oncology Research and Treatment</i> , 2023, 46, 246-258.	0.8	3
31296	Comprehensive analysis of bZIP transcription factors in passion fruit. <i>IScience</i> , 2023, 26, 106556.	1.9	2
31297	Responses of root architecture and the rhizosphere microbiome assembly of maize ( <i>Zea mays</i> L.) to a soil texture gradient. <i>Soil Biology and Biochemistry</i> , 2023, 181, 109026.	4.2	3

#	ARTICLE	IF	CITATIONS
31298	CRISPR-resolved virus-host interactions in a municipal landfill include non-specific viruses, hyper-targeted viral populations, and interviral conflicts. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
31299	Multi-omics analysis of the Indian ovarian cancer cohort revealed histotype-specific mutation and gene expression patterns. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31300	Analysing and Transforming Graph Structures: The Graph Transformation Framework. , 2023, 2, 218-233.		1
31301	Single-cell RNA sequencing and transcriptomic analysis reveal key genes and regulatory mechanisms in sepsis. <i>Biotechnology and Genetic Engineering Reviews</i> , 0, , 1-23.	2.4	0
31302	Altered trafficking of miRNAs at mitochondria modulates mitochondrial functions and cell death in brain ischemia. <i>Free Radical Biology and Medicine</i> , 2023, 199, 26-33.	1.3	0
31303	Predicting the evolution of scientific communities by interpretable machine learning approaches. <i>Journal of Informetrics</i> , 2023, 17, 101399.	1.4	1
31304	miR-9a-5p expression is decreased in the hippocampus of rats resistant to lamotrigine: A behavioural, molecular and bioinformatics assessment. <i>Neuropharmacology</i> , 2023, 227, 109425.	2.0	3
31305	High expression of the RET receptor tyrosine kinase and its ligand GDNF identifies a high-risk subset of estrogen receptor positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2023, 199, 589-601.	1.1	1
31306	Sequencing the genomes of LPP-1, the first isolated cyanophage, and its relative LPP-2 reveal different integration mechanisms in closely related phages. <i>Harmful Algae</i> , 2023, 124, 102409.	2.2	2
31308	Gene network interaction analysis to elucidate the antimicrobial resistance mechanisms in the <i>Clostridium difficile</i> . <i>Microbial Pathogenesis</i> , 2023, 178, 106083.	1.3	3
31309	Transcriptomics analysis reveals key lncRNAs and genes related to the infection of feline kidney cell line by panleukopenia virus. <i>Research in Veterinary Science</i> , 2023, 158, 203-214.	0.9	1
31310	Coevolutionary signals in metabotropic glutamate receptors capture residue contacts and long-range functional interactions. <i>Journal of Biological Chemistry</i> , 2023, 299, 103030.	1.6	2
31311	Bioinformatics analysis of potential key ferroptosis-related genes involved in tubulointerstitial injury in patients with diabetic nephropathy. <i>Renal Failure</i> , 2023, 45, .	0.8	1
31312	Heavy metal stress induces adaptative responses in the liverwort <i>Conocephalum conicum</i> L. (Dum.): An integrated biologic and metabolomic study. <i>Environmental and Experimental Botany</i> , 2023, 209, 105292.	2.0	1
31313	The molecular mechanism of cardiac injury in SARS-CoV-2 infection: Focus on mitochondrial dysfunction. <i>Journal of Infection and Public Health</i> , 2023, 16, 746-753.	1.9	8
31314	Identification of critical autophagy-related proteins in diabetic retinopathy: A multi-dimensional computational study. <i>Gene</i> , 2023, 866, 147339.	1.0	2
31315	Sustained detoxification of 1,2-dichloroethane to ethylene by a symbiotic consortium containing <i>Dehalococcoides</i> species. <i>Environmental Pollution</i> , 2023, 325, 121443.	3.7	3
31316	Structural analysis and conformational dynamics of SOCS1 gene mutations involved in diffuse large B-cell lymphoma. <i>Gene</i> , 2023, 864, 147293.	1.0	1

#	ARTICLE	IF	CITATIONS
31317	The novel circular RNA CircMef2c is positively associated with muscle growth in Nile tilapia. <i>Genomics</i> , 2023, 115, 110598.	1.3	5
31318	Mollugin ameliorates murine allergic airway inflammation by inhibiting Th2 response and M2 macrophage activation. <i>European Journal of Pharmacology</i> , 2023, 946, 175630.	1.7	3
31319	Resveratrol improves the cytotoxic effect of CD8 <sup>+</sup> T cells in the tumor microenvironment by regulating HMMR/Ferroptosis in lung squamous cell carcinoma. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2023, 229, 115346.	1.4	10
31320	Effects of <i>Bacillus</i> strain added as initial indigenous species into the biofloc system rearing <i>Litopenaeus vannamei</i> juveniles on biofloc preformation, water quality and shrimp growth. <i>Aquaculture</i> , 2023, 569, 739375.	1.7	5
31321	Small Auxin Up RNA (SAUR) gene family identification and functional genes exploration during the floral organ and fruit developmental stages in pineapple ( <i>Ananas comosus</i> L.) and its response to salinity and drought stresses. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 124061.	3.6	4
31322	Phytochemical profiling of <i>Nothapodytes nimmoniana</i> to understand camptothecin biosynthesis using tandem mass spectrometry. <i>South African Journal of Botany</i> , 2023, 156, 169-176.	1.2	0
31323	Standardized extract of <i>Ginkgo biloba</i> enhances memory persistence over time. <i>Phytomedicine Plus</i> , 2023, 3, 100441.	0.9	3
31324	Deciphering crucial genes in multiple sclerosis pathogenesis and drug repurposing: A systems biology approach. <i>Journal of Proteomics</i> , 2023, 280, 104890.	1.2	1
31325	HPV16 status predicts potential protein biomarkers and therapeutics in head and neck squamous cell carcinoma. <i>Virology</i> , 2023, 582, 90-99.	1.1	1
31326	Machine learning based age-authentication assisted by chemo-kinetics: Case study of strong-flavor Chinese Baijiu. <i>Food Research International</i> , 2023, 167, 112594.	2.9	6
31327	Metabolomics integrated network pharmacology reveals the mechanism of Ma-Mu-Ran Antidiarrheal Capsules on acute enteritis mice. <i>Analytical Biochemistry</i> , 2023, 668, 115116.	1.1	0
31328	Proteomic and phosphoproteomic analyses of Jurkat T-cell treated with 2 $\mu$ M cGAMP reveals various signaling axes impacted by cyclic dinucleotides. <i>Journal of Proteomics</i> , 2023, 279, 104869.	1.2	0
31329	Genome-wide identification and expression profiling of the bZIP gene family in <i>Betula platyphylla</i> and the functional characterization of BpChr04G00610 under low-temperature stress. <i>Plant Physiology and Biochemistry</i> , 2023, 198, 107676.	2.8	2
31330	EPEK: Creation and analysis of an Ectopic Pregnancy Expression Knowledgebase. <i>Computational Biology and Chemistry</i> , 2023, 104, 107866.	1.1	0
31331	Paeoniflorin protects against cisplatin-induced acute kidney injury through targeting Hsp90AA1-Akt protein-protein interaction. <i>Journal of Ethnopharmacology</i> , 2023, 310, 116422.	2.0	2
31332	Metabolic engineering of low-pH-tolerant non-model yeast, <i>Issatchenkia orientalis</i> , for production of citramalate. <i>Metabolic Engineering Communications</i> , 2023, 16, e00220.	1.9	2
31333	Risk factors and actionable molecular signatures in COVID-19-associated lung adenocarcinoma and lung squamous cell carcinoma patients. <i>Computers in Biology and Medicine</i> , 2023, 158, 106855.	3.9	0
31334	Using feature selection and Bayesian network identify cancer subtypes based on proteomic data. <i>Journal of Proteomics</i> , 2023, 280, 104895.	1.2	3



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31335	Molecular level insight of thiocyanate degradation by <i>Pseudomonas putida</i> TDB-1 under a high arsenic and alkaline condition. <i>Science of the Total Environment</i> , 2023, 874, 162578.	3.9	2
31336	Competitive endogenous RNA-mediated upregulation of PLOD2 expression correlates with poor prognosis and tumor immune infiltration of head and neck squamous cell carcinoma. , 2023, 6, 100026.		0
31337	Proteomic and toxicological analysis of the response of dinoflagellate <i>Alexandrium catenella</i> to changes in NaNO <sub>3</sub> concentration. <i>Harmful Algae</i> , 2023, 125, 102428.	2.2	0
31338	Integrating transcriptome and phytohormones analysis provided insights into plant height development in sesame. <i>Plant Physiology and Biochemistry</i> , 2023, 198, 107695.	2.8	4
31339	Identification of circular RNAs in tea plant during <i>Helopeltis theivora</i> infestation. <i>Plant Stress</i> , 2023, 8, 100150.	2.7	4
31340	Integrated analysis of smRNAome, transcriptome, and degradome data to decipher microRNAs regulating costunolide biosynthesis in <i>Saussurea lappa</i> . <i>Plant Science</i> , 2023, 331, 111689.	1.7	1
31341	Leaf metabolomics and molecular networking of wild type and mutant genotypes of chia ( <i>Salvia</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	1.4	3
31342	Microbial assessment of water, sanitation, and hygiene (WaSH) in temporary and permanent settlements two years after Nepal 2015 earthquake. <i>Science of the Total Environment</i> , 2023, 877, 162867.	3.9	1
31343	Identification of shared characteristics in tumor-infiltrating T <sub>H</sub> cells across 15 cancers. <i>Molecular Therapy - Nucleic Acids</i> , 2023, 32, 189-202.	2.3	3
31344	Exploring the effect of the Uyghur medicine Munziq Balam on a collagen-induced arthritis rat model by UPLC-MS/MS-based metabolomics approach. <i>Journal of Ethnopharmacology</i> , 2023, 310, 116437.	2.0	0
31345	Structural annotation, semi-quantification and toxicity prediction of pyrrolizidine alkaloids from functional food: In silico and molecular networking strategy. <i>Food and Chemical Toxicology</i> , 2023, 176, 113738.	1.8	3
31346	YBX2 modulates mRNA stability via interaction with YTHDF2 in endometrial cancer cells. <i>Experimental Cell Research</i> , 2023, 427, 113586.	1.2	1
31347	Convergent thinking and insight problem solving relate to semantic memory network structure. <i>Thinking Skills and Creativity</i> , 2023, 48, 101277.	1.9	8
31348	Integrated analysis of methylation profiles and transcriptome of Marek's disease virus-infected chicken spleens reveal hypomethylation of CD4 and HMGB1 genes might promote Marek's disease tumorigenesis. <i>Poultry Science</i> , 2023, 102, 102594.	1.5	0
31349	Metabolic regulation mechanism of <i>Trametes gibbosa</i> CB1 on lignin. <i>International Journal of Biological Macromolecules</i> , 2023, 240, 124189.	3.6	2
31350	Network pharmacology, a promising approach to reveal the pharmacology mechanism of Chinese medicine formula. <i>Journal of Ethnopharmacology</i> , 2023, 309, 116306.	2.0	89
31351	Cultural heritage adaptive reuse in Salerno: Challenges and solutions. <i>City, Culture and Society</i> , 2023, 33, 100505.	1.1	5
31352	Unveiling the role of hub proteins in controlling quorum sensing regulated virulence through analogues in <i>Pseudomonas aeruginosa</i> PAO1: A functional protein-protein network biology approach. <i>Biochemical and Biophysical Research Communications</i> , 2023, 660, 13-20.	1.0	2

#	ARTICLE	IF	CITATIONS
31353	Community structures and biodeterioration processes of epilithic biofilms imply the significance of micro-environments. <i>Science of the Total Environment</i> , 2023, 876, 162665.	3.9	4
31354	Identification of key differentially expressed genes in SARS-CoV-2 using RNA-seq analysis with a systems biology approach. <i>Cytokine</i> , 2023, 166, 156187.	1.4	0
31355	Simple identification of discriminative markers for four Citrus species using a combination of molecular networking and multivariate analysis. <i>Journal of Food Composition and Analysis</i> , 2023, 119, 105264.	1.9	3
31356	Unraveling the mechanism of action of cepharanthine for the treatment of novel coronavirus pneumonia (COVID-19) from the perspectives of systematic pharmacology. <i>Arabian Journal of Chemistry</i> , 2023, 16, 104722.	2.3	1
31357	In-depth profiling of di(2-ethylhexyl) phthalate metabolic footprints in rats using click chemistry-mass spectrometry probes. <i>Journal of Hazardous Materials</i> , 2023, 452, 131190.	6.5	0
31358	Anti-tumor potential and mode of action of karanjin against breast cancer; an in-silico approach. <i>Arabian Journal of Chemistry</i> , 2023, 16, 104778.	2.3	5
31359	Revealing the molecular mechanisms of zinc accumulation and zinc deficiency responses in quinoa, analyzed by high-throughput gene expression profiling under zinc depletion and resupply. <i>Environmental and Experimental Botany</i> , 2023, 210, 105330.	2.0	1
31360	Analysis of protein-protein interface with incorporating low-frequency molecular interactions in molecular dynamics simulation. <i>Journal of Molecular Graphics and Modelling</i> , 2023, 122, 108461.	1.3	0
31361	Weather factors, soil microbiome, and bacteria-fungi interactions as drivers of the epiphytic phyllosphere communities of romaine lettuce. <i>Food Microbiology</i> , 2023, 113, 104260.	2.1	7
31362	Profiling bacterial communities and foodborne pathogens on food-associated surface following contact with raw beef, chicken and pork using 16S amplicon metagenomics. <i>Food Control</i> , 2023, 149, 109698.	2.8	5
31363	Deterministic versus stochastic control in $\beta$ -diversity, abundance and co-occurrence patterns of a soil nematode assemblage living in a Mediterranean soil. <i>Applied Soil Ecology</i> , 2023, 188, 104879.	2.1	1
31364	Pathogenic mycoplasmas of humans regulate the long noncoding RNAs in epithelial cells. <i>Non-coding RNA Research</i> , 2023, 8, 282-293.	2.4	0
31365	Artificial intelligence-driven pan-cancer analysis reveals miRNA signatures for cancer stage prediction. <i>Human Genetics and Genomics Advances</i> , 2023, 4, 100190.	1.0	6
31366	Transcriptome and weighted gene co-expression network analysis of jujube ( <i>Ziziphus jujuba</i> Mill.) fruit reveal putative genes involved in proanthocyanin biosynthesis and regulation. <i>Food Science and Human Wellness</i> , 2023, 12, 1557-1570.	2.2	3
31367	Exploring the effective components and potential mechanisms of Zukamu granules against acute upper respiratory tract infections by UHPLC-Q-Exactive Orbitrap-MS and network pharmacology analysis. <i>Arabian Journal of Chemistry</i> , 2023, 16, 104875.	2.3	1
31368	An integrated transcriptomic and metabolomic approach to investigate the heterogeneous <i>Candida albicans</i> biofilm phenotype. <i>Biofilm</i> , 2023, 5, 100112.	1.5	1
31369	Rare microbial communities drive ecosystem multifunctionality in acidic soils of southern China. <i>Applied Soil Ecology</i> , 2023, 189, 104895.	2.1	8
31370	Microbial community and volatilome changes in brines along the spontaneous fermentation of Spanish-style and natural-style green table olives ( <i>Manzanilla</i> cultivar). <i>Food Microbiology</i> , 2023, 113, 104286.	2.1	7

#	ARTICLE	IF	CITATIONS
31371	Fibroblast exosomal TFAP2C induced by chitosan oligosaccharides promotes peripheral axon regeneration via the miR-132-5p/CAMKK1 axis. <i>Bioactive Materials</i> , 2023, 26, 249-263.	8.6	3
31372	Comprehensive characterization of the embryonic factor LEUTX. <i>IScience</i> , 2023, 26, 106172.	1.9	1
31373	Identifying developments over a decade in the digital health and telemedicine landscape in the UK using quantitative text mining. <i>Frontiers in Digital Health</i> , 0, 5, .	1.5	0
31374	Multi-omics profiling of papillary thyroid microcarcinoma reveals different somatic mutations and a unique transcriptomic signature. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	2
31375	A multi-omics integrative analysis based on CRISPR screens re-defines the pluripotency regulatory network in ESCs. <i>Communications Biology</i> , 2023, 6, .	2.0	0
31376	Emergence of terpene chemical communication in insects: Evolutionary recruitment of isoprenoid metabolism. <i>Protein Science</i> , 2023, 32, .	3.1	4
31378	METTL3-Mediated m6A Modification Controls Splicing Factor Abundance and Contributes to Aggressive CLL. <i>Blood Cancer Discovery</i> , 2023, 4, 228-245.	2.6	6
31380	The viral packaging motor potentiates Kaposi's sarcoma-associated herpesvirus gene expression late in infection. <i>PLoS Pathogens</i> , 2023, 19, e1011163.	2.1	1
31381	Study on differentially expressed genes and participating pathways of ectopic endometrium in adenomyosis patients with different data sets. <i>Genomics</i> , 2023, 115, 110619.	1.3	0
31382	Myelin basic protein recovery during PKU mice lifespan and the potential role of microRNAs on its regulation. <i>Neurobiology of Disease</i> , 2023, 180, 106093.	2.1	4
31383	Transcriptomic analysis of esophageal cancer reveals hub genes and networks involved in cancer progression. <i>Computers in Biology and Medicine</i> , 2023, 159, 106944.	3.9	1
31384	MicroRNA mediated gene regulatory circuits leads to machine learning based preliminary detection of acute myeloid leukemia. <i>Computational Biology and Chemistry</i> , 2023, 104, 107859.	1.1	1
31385	Expression and functional analysis of NAC transcription factors under five diverse growth stages reveal their regulatory roles during wood formation in Chinese cedar ( <i>Cryptomeria fortunei</i> ) <a href="https://doi.org/10.1016/j.tbi.2023.101527">https://doi.org/10.1016/j.tbi.2023.101527</a>	0.0	0
31386	Comprehensive metabolomics reveals correlation between sophorolipid biosynthesis and autophagy. <i>New Biotechnology</i> , 2023, 75, 1-12.	2.4	1
31387	New insights into aroma regulation in pear peel and flesh under methyl jasmonate treatment obtained by metabolite and whole-transcriptome RNA sequencing analyses. <i>Postharvest Biology and Technology</i> , 2023, 201, 112347.	2.9	3
31388	Metaviromic analyses of DNA virus community from sediments of the N-Choe stream, North India. <i>Virus Research</i> , 2023, 330, 199110.	1.1	0
31395	A detailed multi-omics analysis of GNB2 gene in human cancers. <i>Brazilian Journal of Biology</i> , 0, 84, .	0.4	1
31416	Dry tobacco leaves: an <i>in vivo</i> and <i>in silico</i> approach to the consequences of occupational exposure. <i>Mutagenesis</i> , 0, , .	1.0	0

#	ARTICLE	IF	CITATIONS
31417	MiRNA Differences Related to Treatment-Resistant Schizophrenia. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1891.	1.8	3
31418	Disulfiram reduces the severity of mouse acute pancreatitis by inhibiting RIPK1-dependent acinar cell necrosis. <i>Bioorganic Chemistry</i> , 2023, 133, 106382.	2.0	4
31419	LPS-induced acute neuroinflammation, involving interleukin-1 beta signaling, leads to proteomic, cellular, and network-level changes in the prefrontal cortex of mice. <i>Brain, Behavior, &amp; Immunity - Health</i> , 2023, 28, 100594.	1.3	6
31420	Decoding transcriptional regulation via a human gene expression predictor. <i>Journal of Genetics and Genomics</i> , 2023, , .	1.7	1
31421	Rewiring of hormones and light response pathways underlies the inhibition of stomatal development in an amphibious plant <i>Rorippa aquatica</i> underwater. <i>Current Biology</i> , 2023, 33, 543-556.e4.	1.8	4
31423	Time-course RNA-sequencing and Co-expression Modules Revealed a Critical Salt Response Regulatory Network in Apple. <i>Journal of the American Society for Horticultural Science</i> , 2023, 148, 53-63.	0.5	0
31424	Identification and Functional Prediction of CircRNAs in Leaves of F1 Hybrid Poplars with Different Growth Potential and Their Parents. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2284.	1.8	2
31425	diffeRenTES: An R package for computing cell differentiation trees from Boolean networks. <i>Software Impacts</i> , 2023, 15, 100470.	0.8	0
31426	Genome-wide transcriptome analysis uncovers gene networks regulating fruit quality and volatile compounds in mango cultivar 'Tainong' during postharvest. <i>Food Research International</i> , 2023, 165, 112531.	2.9	2
31427	Systematic analysis reveals novel insight into the molecular determinants of function, diversity and evolution of sweet taste receptors T1R2/T1R3 in primates. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	1
31428	Identification of mosquito proteins that differentially interact with alphavirus nonstructural protein 3, a determinant of vector specificity. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011028.	1.3	0
31429	Evaluation of differentially expressed genes during replication using gene expression landscape of monkeypox-infected MK2 cells: A bioinformatics and systems biology approach to understanding the genomic pattern of viral replication. <i>Journal of Infection and Public Health</i> , 2023, 16, 399-409.	1.9	4
31430	Differential proteomic patterns of plasma extracellular vesicles show potential to discriminate $\beta^2$ -thalassemia subtypes. <i>IScience</i> , 2023, 26, 106048.	1.9	3
31432	Network pharmacology and experimental validation to identify the potential mechanism of <i>Hedyotis diffusa</i> Willd against rheumatoid arthritis. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
31433	Annelid functional genomics reveal the origins of bilaterian life cycles. <i>Nature</i> , 2023, 615, 105-110.	13.7	34
31434	Multi-breed genomic predictions and functional variants for fertility of tropical bulls. <i>PLoS ONE</i> , 2023, 18, e0279398.	1.1	2
31435	A comparative study of COVID-19 transcriptional signatures between clinical samples and preclinical cell models in the search for disease master regulators and drug repositioning candidates. <i>Virus Research</i> , 2023, 326, 199053.	1.1	2
31436	Identifying molecular targets of Aspiletrein-derived steroidal saponins in lung cancer using network pharmacology and molecular docking-based assessments. <i>Scientific Reports</i> , 2023, 13, .	1.6	7

#	ARTICLE	IF	CITATIONS
31437	Cell wall disassembly, metabolome and transcriptome analysis in sweet cherry fruit with induced surface pitting. <i>Postharvest Biology and Technology</i> , 2023, 198, 112262.	2.9	0
31438	GENOME-WIDE IDENTIFICATION OF NICOTIANA TABACUM MIRNAS AND THEIR ROLE IN HUMAN HEALTH – A COMPUTATIONAL GENOMICS ASSESSMENT. <i>Towards Excellence</i> , 0, , 1560-1570.	0.0	0
31439	Integrated transcriptomic and metabolomic analyses reveal key genes controlling flavonoid biosynthesis in <i>Citrus grandis</i> ‘Tomentosa’™ fruits. <i>Plant Physiology and Biochemistry</i> , 2023, 196, 210-221.	2.8	6
31440	RHOA Therapeutic Targeting in Hematological Cancers. <i>Cells</i> , 2023, 12, 433.	1.8	7
31441	Differentially regulated targets in the fast-acting antidepressant effect of (R)-ketamine: A systems biology approach. <i>Pharmacology Biochemistry and Behavior</i> , 2023, 223, 173523.	1.3	4
31443	High expression level of the FTH1 gene is associated with poor prognosis in children with non-M3 acute myeloid leukemia. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
31444	Genomic Analysis of the Rare Slightly Halophilic Myxobacterium ‘Paraliomyxa’ miuraensis SMH-27-4, the Producer of the Antibiotic Miuraenamides. <i>Microorganisms</i> , 2023, 11, 371.	1.6	3
31445	CP204L Is a Multifunctional Protein of African Swine Fever Virus That Interacts with the VPS39 Subunit of the Homotypic Fusion and Vacuole Protein Sorting Complex and Promotes Lysosome Clustering. <i>Journal of Virology</i> , 2023, 97, .	1.5	2
31447	Systematic approach to identify therapeutic targets and functional pathways for the cervical cancer. <i>Journal of Genetic Engineering and Biotechnology</i> , 2023, 21, 10.	1.5	1
31448	Biomarkers Associated with Immune Checkpoint, N6-Methyladenosine, and Ferroptosis in Patients with Restenosis. <i>Journal of Inflammation Research</i> , 0, Volume 16, 407-420.	1.6	1
31449	Systems biology approach to understand the interplay between <i>Bacillus anthracis</i> and human host genes that leads to CVDs. <i>Microbial Pathogenesis</i> , 2023, 176, 106019.	1.3	0
31450	Deciphering sperm functions using biological networks. <i>Biotechnology and Genetic Engineering Reviews</i> , 0, , 1-25.	2.4	0
31453	Rhizosphere phage communities drive soil suppressiveness to bacterial wilt disease. <i>Microbiome</i> , 2023, 11, .	4.9	15
31455	Successional and phenological effects on plant-floral visitor interaction networks of a tropical dry forest. <i>Journal of Ecology</i> , 2023, 111, 927-942.	1.9	2
31457	Pan-cancer chemoresistance-associated genes, affected pathways and potential therapeutic targets. , 2023, 35, 201151.		0
31458	Levofloxacin induces differential effects in the transcriptome between the gut, peripheral and axial joints in the Spondyloarthritis DBA/1 mice: Improvement of intestinal dysbiosis and the overall inflammatory process. <i>PLoS ONE</i> , 2023, 18, e0281265.	1.1	3
31459	Genome-wide analysis of Catalase gene family reveal insights into abiotic stress response mechanism in <i>Brassica juncea</i> and <i>B. rapa</i> .. <i>Plant Science</i> , 2023, 330, 111620.	1.7	7
31460	In silico Identification of miRNA as possible therapeutic targets for Micro Invasive Bladder Cancer (MIBC) treatment. , 2022, , .		0

#	ARTICLE	IF	CITATIONS
31461	The human microbial exposome: expanding the Exposome-Explorer database with gut microbial metabolites. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
31462	Screening of Key Genes in Retinoblastoma and Construction of ceRNA Regulatory Network. <i>Lecture Notes in Computer Science</i> , 2023, , 147-168.	1.0	0
31463	Towards the Understanding of the Function of Lanthipeptide and TOMM-Related Genes in <i>Haloferax mediterranei</i> . <i>Biology</i> , 2023, 12, 236.	1.3	1
31464	miR-124-2, miR-92-A1 and miR-372 regulate differential gene expression in a mathematical model of the progression of ductal carcinoma in situ (DCIS) to microinvasive breast cancer (MIBC). , 2022, , .		0
31465	Metabolomics Reveals a Trimeric Actinorhodin from <i>Streptomyces coelicolor</i> M145. <i>ChemBioChem</i> , 2023, 24, .	1.3	0
31466	Exosomes of Adipose Tissue-Derived Stem Cells Promote Wound Healing by Sponging miR-17-5p and Inducing Autophagy Protein Ulk1. <i>Plastic and Reconstructive Surgery</i> , 2023, 151, 1016-1028.	0.7	2
31467	Gene expression analyses of gingival tissue of patients with periodontitis using public transcriptomic data. , 2022, , .		0
31468	Inactivation of <i>Exosc10</i> in the oocyte impairs oocyte development and maturation, leading to a depletion of the ovarian reserve in mice. <i>International Journal of Biological Sciences</i> , 2023, 19, 1080-1093.	2.6	0
31469	3-Mercaptopyruvate sulfur transferase is a protein persulfidase. <i>Nature Chemical Biology</i> , 2023, 19, 507-517.	3.9	16
31470	Identifying miRNA biomarkers of polycystic ovary syndrome through text mining. <i>Reproductive and Developmental Medicine</i> , 2023, 7, 96-101.	0.2	0
31471	Integrative in situ mapping of single-cell transcriptional states and tissue histopathology in a mouse model of Alzheimer's disease. <i>Nature Neuroscience</i> , 0, , .	7.1	21
31472	Global transcriptome and gene co-expression network analyses reveal regulatory and non-additive effects of drought and heat stress in grapevine. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	10
31473	Computer-Aided Screening and Revealing Action Mechanism of Green Tea Polyphenols Intervention in Alzheimer's Disease. <i>Foods</i> , 2023, 12, 635.	1.9	2
31474	Analysis of bulk RNA-seq data from sepsis patients reveals sepsis-associated lncRNAs and targeted cell death-related genes contributing to immune microenvironment regulation. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
31475	Renal control of life-threatening malarial anemia. <i>Cell Reports</i> , 2023, 42, 112057.	2.9	4
31477	Pyridoxal 5-phosphate synthesis and salvage in Bacteria and Archaea: predicting pathway variant distributions and holes. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
31478	Functionality of methane cycling microbiome during methane flux hot moments from riparian buffer systems. <i>Science of the Total Environment</i> , 2023, 870, 161921.	3.9	3
31479	Toxicological impacts and likely protein targets of bisphenol a in <i>Paramecium caudatum</i> . <i>European Journal of Protistology</i> , 2023, 88, 125958.	0.5	0



#	ARTICLE	IF	CITATIONS
31480	Integrative miRNA-mRNA profiling of human epidermis: unique signature of SCN9A painful neuropathy. <i>Brain</i> , 0, , .	3.7	1
31481	Genome-Wide Analysis of the AP2/ERF Family in Oily Persimmon ( <i>Diospyros oleifera</i> ) and Their Preliminary Roles Exploration in Response to Polyamines for Adventitious Root Formation in Cultivated Persimmon ( <i>D. kaki</i> ). <i>Horticulturae</i> , 2023, 9, 191.	1.2	4
31482	A strategy combining chemical analysis and network pharmacology to investigate the mechanism of Xiaohu'er Qingre Zhike Oral solution in cough. <i>Biomedical Chromatography</i> , 2023, 37, .	0.8	0
31483	Proteomic analysis of fetal skin by iTRAQ reveals molecular signals underlying Inner Mongolia Cashmere goat hair follicle initiation. <i>International Journal of Transgender Health</i> , 2023, 16, .	1.1	1
31484	Protein Therapeutic Target Candidates Against <i>Acinetobacter baumannii</i> , a Pathogen of Concern to Planetary Health: A Network-Based Integrative Omics Drug Discovery Approach. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 62-74.	1.0	0
31485	RNA-seq analysis reveals the critical role of the novel lncRNA BIANCR in intramuscular adipogenesis through the ERK1/2 signaling pathway. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	7
31486	Antinociceptive Activity of Vanilloids in <i>Caenorhabditis elegans</i> is Mediated by the Desensitization of the TRPV Channel OCR-2 and Specific Signal Transduction Pathways. <i>Neurochemical Research</i> , 2023, 48, 1900-1911.	1.6	2
31488	VEGF-A enhances the cytotoxic function of CD4+ cytotoxic T cells via the VEGF-receptor 1/VEGF-receptor 2/AKT/mTOR pathway. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	5
31489	Identification and verification of m7G-Related genes as biomarkers for prognosis of sarcoma. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31490	Microorganisms carrying nosZ I and nosZ II share similar ecological niches in a subtropical coastal wetland. <i>Science of the Total Environment</i> , 2023, 870, 162008.	3.9	2
31491	Landscape of immunocytes infiltration and prognostic immune-related genes in hepatocellular carcinoma. <i>Asian Journal of Surgery</i> , 2023, 46, 4251-4260.	0.2	0
31493	Metabolomic Strategies to Improve Chemical Information from OSMAC Studies of Endophytic Fungi. <i>Metabolites</i> , 2023, 13, 236.	1.3	3
31494	Investigation of the Pathogenic Mechanism of Ciprofloxacin in Aortic Aneurysm and Dissection by an Integrated Proteomics and Network Pharmacology Strategy. <i>Journal of Clinical Medicine</i> , 2023, 12, 1270.	1.0	1
31495	FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3181.	1.8	6
31496	Potential determinants of low circulating glucagon-like peptide 2 concentrations in Zambian children with non-responsive stunting. <i>Experimental Physiology</i> , 2023, 108, 568-580.	0.9	0
31497	Blood transcriptome reveals immune and metabolic-related genes involved in growth of pasteurized colostrum-fed calves. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31498	An actin remodeling role for <i>Arabidopsis</i> processing bodies revealed by their proximity interactome. <i>EMBO Journal</i> , 2023, 42, .	3.5	9
31499	Candidate genes potentially involved in molting and body size reduction in the male of the horned gall aphid, <i>Schlechtendalia chinensis</i> . <i>Frontiers in Physiology</i> , 0, 14, .	1.3	1

#	ARTICLE	IF	CITATIONS
31500	Genome-wide identification, characterization, and expression pattern of the late embryogenesis abundant (LEA) gene family in <i>Juglans regia</i> and its wild relatives <i>J. mandshurica</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
31501	Expanding the Disease Network of Glioblastoma Multiforme via Topological Analysis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3075.	1.8	0
31502	Role of miRNAs in the regulation of proanthocyanidin biosynthesis in the legume <i>Psophocarpus tetragonolobus</i> (L.) DC.. <i>Plant Growth Regulation</i> , 2024, 102, 23-38.	1.8	0
31503	Comparative Analyses of Soil Bacterial Colonies of Two Types of Chinese Ginger after a Major Flood Disaster. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
31504	Guild-Level Microbiome Signature Associated with COVID-19 Severity and Prognosis. <i>MBio</i> , 2023, 14, .	1.8	6
31505	Comprehensive Kinase Activity Profiling Revealed the Kinase Activity Patterns Associated with the Effects of EGFR Tyrosine Kinase Inhibitor Therapy in Advanced Non-Small-Cell Lung Cancer Patients with Sensitizing EGFR Mutations. <i>Proteomes</i> , 2023, 11, 6.	1.7	1
31506	Rac1 and Rac3 GTPases and TPC2 are required for axonal outgrowth and migration of cortical interneurons. <i>Journal of Cell Science</i> , 2023, 136, .	1.2	2
31507	Gene expression pattern and molecular mechanisms involved in Shal and Sangsari sheep fertility using $\text{scRNA-Seq}$ . <i>Reproduction in Domestic Animals</i> , 2023, 58, 548-559.	0.6	2
31508	SMYD Family Members Serve as Potential Prognostic Markers and Correlate with Immune Infiltrates in Gastric Cancer. <i>Journal of Oncology</i> , 2023, 2023, 1-16.	0.6	4
31509	Construction of a three-component regulatory network of transcribed ultraconserved regions for the identification of prognostic biomarkers in gastric cancer. <i>Journal of Cellular Biochemistry</i> , 2023, 124, 396-408.	1.2	3
31510	Effect of Shan Zha ( <i>Hawthorn</i> or <i>Crataegus</i> ) on gastrointestinal cancer: A network pharmacology and molecular docking study. , 2023, 1, 229-237.		3
31511	Toxicoproteomics of Mono(2-ethylhexyl) phthalate and Perfluorooctanesulfonic Acid in Models of Prostatic Diseases. <i>Chemical Research in Toxicology</i> , 2023, 36, 251-259.	1.7	3
31512	Myocardial Infarction-Induced INSL6 Decrease Contributes to Breast Cancer Progression. <i>Disease Markers</i> , 2023, 2023, 1-33.	0.6	1
31513	Interaction network among <i>de novo</i> purine nucleotide biosynthesis enzymes in <i>Escherichia coli</i> . <i>FEBS Journal</i> , 2023, 290, 3165-3184.	2.2	3
31514	The Arabidopsis transcription factor NLP2 regulates early nitrate responses and integrates nitrate assimilation with energy and carbon skeleton supply. <i>Plant Cell</i> , 2023, 35, 1429-1454.	3.1	17
31515	Bioinformatics and Next-Generation Data Analysis for Identification of Genes and Molecular Pathways Involved in Subjects with Diabetes and Obesity. <i>Medicina (Lithuania)</i> , 2023, 59, 309.	0.8	8
31516	Zygomatic Implants Research: A Scientometric Analysis from 1990 to 2021. <i>Prosthesis</i> , 2023, 5, 208-220.	1.1	1
31517	Identification of candidate genes and pathways associated with juvenile idiopathic arthritis by integrative transcriptome-wide association studies and mRNA expression profiles. <i>Arthritis Research and Therapy</i> , 2023, 25, .	1.6	2

#	ARTICLE	IF	CITATIONS
31518	Competing endogenous RNA network analysis of the molecular mechanisms of ischemic stroke. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
31519	Novel microRNAs associated with the immune response to cucumber mosaic virus in hot pepper ( <i>Capsicum annuum</i> L.). <i>Physiological and Molecular Plant Pathology</i> , 2023, 124, 101963.	1.3	2
31520	Systematic investigation of the multi-scale mechanisms of herbal medicine on treating ventricular remodeling: Theoretical and experimental studies. <i>Phytomedicine</i> , 2023, 112, 154706.	2.3	2
31521	Visualising disease trajectories from population-wide data. <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	0
31522	The Application of Cinnamon Twig Extract as an Inhibitor of Listeriolysin O against <i>Listeria monocytogenes</i> Infection. <i>Molecules</i> , 2023, 28, 1625.	1.7	3
31523	A Tale of Two Seasons: Distinct Seasonal Viral Communities in a Thermokarst Lake. <i>Microorganisms</i> , 2023, 11, 428.	1.6	2
31524	In silico study of molecular mimicry between SARS-CoV-2 and neutrophil extracellular traps composition in granulocyte-rich supernatants of patients with systemic lupus erythematosus and lupus nephritis. , 2023, , 199-274.		0
31525	Targeting Glutaminolysis Shows Efficacy in Both Prednisolone-Sensitive and in Metabolically Rewired Prednisolone-Resistant B-Cell Childhood Acute Lymphoblastic Leukaemia Cells. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3378.	1.8	2
31526	Role of Senescence-Resumed Proliferation in Keloid Pathogenesis. <i>Future Pharmacology</i> , 2023, 3, 198-212.	0.6	1
31527	EVI2B Is a Prognostic Biomarker and Is Correlated with Monocyte and Macrophage Infiltration in Osteosarcoma Based on an Integrative Analysis. <i>Biomolecules</i> , 2023, 13, 327.	1.8	1
31528	Virtual Screening and Multi-targets Investigation of Novel Diazine Derivatives as Potential Xanthine Oxidase Inhibitors Based on QSAR, Molecular Docking, ADMET Properties, Dynamics Simulation and Network Pharmacology. <i>Medicinal Chemistry</i> , 2023, 19, 704-716.	0.7	2
31530	589. Host transcriptome response of meat-type chickens infected with <i>Eimeria maxima</i> and reared under heat stress environment. , 2022, , .		0
31531	IL-1 receptor-associated kinase-3 acts as an immune checkpoint in myeloid cells to limit cancer immunotherapy. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	5
31532	781. Unravelling the genetic basis governing the porcine metabolism. , 2022, , .		0
31533	Mechanism of anti-hyperuricemia of isobavachin based on network pharmacology and molecular docking. <i>Computers in Biology and Medicine</i> , 2023, 155, 106637.	3.9	2
31534	Integration of miRNA and mRNA expression profiles in Asian spongy moth <i>Lymantria dispar</i> in response to cyantraniliprole. <i>Pesticide Biochemistry and Physiology</i> , 2023, 191, 105364.	1.6	5
31535	Investigation of the Underlying Mechanism of Huangqi-Dangshen for Myasthenia Gravis Treatment via Molecular Docking and Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-18.	0.5	1
31537	Grain shattering by cell death and fracture in <i>Eragrostis tef</i> . <i>Plant Physiology</i> , 0, , .	2.3	1

#	ARTICLE	IF	CITATIONS
31538	Identification of lncRNAs associated with the progression of acute lymphoblastic leukemia using a competing endogenous RNAs network. <i>Oncology Research</i> , 2022, 30, 259-268.	0.6	2
31539	Potential role of Bavachin in Rheumatoid arthritis: Informatics approach for rational based selection of phytoestrogen. <i>Journal of Herbal Medicine</i> , 2023, 38, 100640.	1.0	0
31540	The cecal ecosystem is a great contributor to intramuscular fat deposition in broilers. <i>Poultry Science</i> , 2023, 102, 102568.	1.5	5
31541	Regulatory network characterization of anthocyanin metabolites in purple sweetpotato via joint transcriptomics and metabolomics. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
31542	Integrated Transcriptome and Metabolome Analyses Provide Insights into the Coloring Mechanism of Dark-red and Yellow Fruits in Chinese Cherry [ <i>Cerasus pseudocerasus</i> (Lindl.) G. Don]. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3471.	1.8	7
31543	MIF Variant rs755622 Is Associated with Severe Crohn's Disease and Better Response to Anti-TNF Adalimumab Therapy. <i>Genes</i> , 2023, 14, 452.	1.0	2
31544	Splicing factor SRSF1 deficiency in the liver triggers NASH-like pathology and cell death. <i>Nature Communications</i> , 2023, 14, .	5.8	8
31545	Molecular Modeling and In Vitro Evaluation of Piplartine Analogs against Oral Squamous Cell Carcinoma. <i>Molecules</i> , 2023, 28, 1675.	1.7	2
31546	Biomolecular Network-based Study of a Parasitic Disease and Therapeutic Drugs. , 2022, 1, 22-34.		0
31548	Multilingual translation for zero-shot biomedical classification using BioTranslator. <i>Nature Communications</i> , 2023, 14, .	5.8	4
31549	Diversity and Potential Interactions of Soil Viruses and Host Bacteria under Different Land Use Patterns. <i>Forests</i> , 2023, 14, 342.	0.9	0
31550	Candidate genes for mastitis resistance in dairy cattle: a data integration approach. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	3
31551	Five-hub genes identify potential mechanisms for the progression of asthma to lung cancer. <i>Medicine (United States)</i> , 2023, 102, e32861.	0.4	0
31552	Bioinformatics Analysis Reveals a Shared Pathway for Common Forms of Adult Nephrotic Syndrome. <i>Kidney360</i> , 2023, Publish Ahead of Print, .	0.9	0
31553	Insights into the substrate specificity, structure, and dynamics of plant histidinol-phosphate aminotransferase (HISN6). <i>Plant Physiology and Biochemistry</i> , 2023, 196, 759-773.	2.8	1
31554	Integrative competing endogenous RNA network analyses identify novel lncRNA and genes implicated in metastatic breast cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31555	Establishment of Ferroptosis-Related Key Gene Signature and Its Validation in Compression-Induced Intervertebral Disc Degeneration Rats. <i>Oxidative Medicine and Cellular Longevity</i> , 2023, 2023, 1-20.	1.9	1
31556	Dissecting the microbial community structure of internal organs during the early postmortem period in a murine corpse model. <i>BMC Microbiology</i> , 2023, 23, .	1.3	2

#	ARTICLE	IF	CITATIONS
31557	MiR-190a regulates milk protein biosynthesis through the mTOR and JAK2-STAT5 signaling pathways by targeting PTHLH in buffalo mammary epithelial cells. <i>Journal of Functional Foods</i> , 2023, 102, 105451.	1.6	0
31559	Investigating the chemical profile of Rheum lhasaense and its main ingredient of piceatannol-3-O- $\beta$ -D-glucopyranoside on ameliorating cognitive impairment. <i>Biomedicine and Pharmacotherapy</i> , 2023, 160, 114394.	2.5	0
31560	Sp3 is essential for normal lung morphogenesis and cell cycle progression during mouse embryonic development. <i>Development (Cambridge)</i> , 2023, 150, .	1.2	2
31561	Pan-cancer pseudogene RNA analysis reveals a regulatory network promoting cancer cell proliferation. <i>Genome Instability &amp; Disease</i> , 2023, 4, 85-97.	0.5	1
31562	Bioinformatics analyses of combined databases identify shared differentially expressed genes in cancer and autoimmune disease. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	4
31563	Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in <i>Gossypium bickii</i> . <i>Molecular Plant</i> , 2023, 16, 694-708.	3.9	12
31564	Integrated miRNA-mRNA analysis reveals candidate miRNA family regulating arbuscular mycorrhizal symbiosis of <i>Poncirus trifoliata</i> . <i>Plant, Cell and Environment</i> , 2023, 46, 1805-1821.	2.8	3
31565	Identification of androgen response-related lncRNAs in prostate cancer. <i>Prostate</i> , 2023, 83, 590-601.	1.2	2
31566	Mixed Origins: HIV gp120-Specific Memory Develops from Pre-Existing Memory and Naive B Cells Following Vaccination in Humans. <i>AIDS Research and Human Retroviruses</i> , 2023, 39, 350-366.	0.5	2
31567	Integration of single sample and population analysis for understanding immune evasion mechanisms of lung cancer. <i>Npj Systems Biology and Applications</i> , 2023, 9, .	1.4	0
31568	TAP1, a potential immune-related prognosis biomarker with functional significance in uveal melanoma. <i>BMC Cancer</i> , 2023, 23, .	1.1	1
31569	Human cytomegalovirus infection perturbs neural progenitor cell fate via the expression of viral microRNAs. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	3
31570	Integrative proteomic characterization of adenocarcinoma of esophagogastric junction. <i>Nature Communications</i> , 2023, 14, .	5.8	10
31571	Integrated bioinformatics analyses identifying key transcriptomes correlated with prognosis and immune infiltrations in lung squamous cell carcinoma. <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103596.	1.8	2
31573	Diverse DNA virus genomes identified in fecal samples of Mexican free-tailed bats ( <i>Tadarida</i> ). <i>Journal of Virology</i> , 2023, 97, 1011-1022.	1.1	2
31574	Untargeted metabolomics revealed essential biochemical rearrangements towards combined heat and drought stress acclimatization in <i>Pinus pinaster</i> . <i>Environmental and Experimental Botany</i> , 2023, 208, 105261.	2.0	2
31575	Ferroptosis is the key cellular process mediating Bisphenol A responses in <i>Chlamydomonas</i> and a promising target for enhancing microalgae-based bioremediation. <i>Journal of Hazardous Materials</i> , 2023, 448, 130997.	6.5	7
31577	Integrated transcriptomic and metabolomic analyses reveal key metabolic pathways in response to potassium deficiency in coconut ( <i>Cocos nucifera</i> L.) seedlings. <i>Frontiers in Plant Science</i> , 2023, 14, .	1.7	3

#	ARTICLE	IF	CITATIONS
31579	Combined proliferation and apoptosis index provides better risk stratification in breast cancer. <i>Histopathology</i> , 0, , .	1.6	0
31580	Bacterial composition along the digestive tract of the Horned Screamer ( <i>Anhima cornuta</i> ), a tropical herbivorous bird. <i>PeerJ</i> , 0, 11, e14805.	0.9	1
31581	Insights on the particle-attached riverine archaeal community shifts linked to seasons and to multipollution during a Mediterranean extreme storm event. <i>Environmental Science and Pollution Research</i> , 2023, 30, 49685-49702.	2.7	1
31582	Molecular characterization of physis tissue and hormonal profiles of female rats neonatally exposed to low-dose bisphenol A. <i>Toxicology and Industrial Health</i> , 2023, 39, 146-157.	0.6	0
31583	gutSMASH predicts specialized primary metabolic pathways from the human gut microbiota. <i>Nature Biotechnology</i> , 2023, 41, 1416-1423.	9.4	24
31584	The positive feedback loop of MAD2L1/TYK2/STAT3 induces progression in B-cell acute lymphoblastic leukaemia. <i>Journal of Cancer Research and Clinical Oncology</i> , 0, , .	1.2	0
31585	<i>Funneliformis mosseae</i> induced changes of rhizosphere microbial community structure enhance <i>Capsicum annuum</i> L. plant growth and fruit yield. <i>Soil Science Society of America Journal</i> , 2023, 87, 843-855.	1.2	1
31586	Molecular dynamics simulations reveal the effect of mutations in the RING domains of BRCA1-BARD1 complex and its relevance to the prognosis of breast cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 12734-12752.	2.0	1
31588	HIV-1 release requires Nef-induced caspase activation. <i>PLoS ONE</i> , 2023, 18, e0281087.	1.1	1
31589	Expansion of Kuravirus-like Phage Sequences within the Past Decade, including Escherichia Phage YF01 from Japan, Prompt the Creation of Three New Genera. <i>Viruses</i> , 2023, 15, 506.	1.5	4
31592	Impact of diet and host genetics on the murine intestinal mycobiome. <i>Nature Communications</i> , 2023, 14, .	5.8	3
31593	Exploration of the anti-liver injury active components of Shaoyao Gancao decoction by network pharmacology and experiments in vivo. <i>Phytomedicine</i> , 2023, 112, 154717.	2.3	3
31594	Co-Expression Analysis of Airway Epithelial Transcriptome in Asthma Patients with Eosinophilic vs. Non-Eosinophilic Airway Infiltration. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3789.	1.8	1
31596	Bioinformatics-based analysis of the roles of sex hormone receptors in endometriosis development. <i>International Journal of Medical Sciences</i> , 2023, 20, 415-428.	1.1	1
31597	Tundra Soil Viruses Mediate Responses of Microbial Communities to Climate Warming. <i>MBio</i> , 2023, 14, .	1.8	5
31598	DNA methylation in cocaine use disorder—An epigenome-wide approach in the human prefrontal cortex. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	4
31600	Identification of Hub Genes Associated with Breast Cancer Using Integrated Gene Expression Data with Protein-Protein Interaction Network. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 2403.	1.3	4
31601	Molecular and cellular evolution of the amygdala across species analyzed by single-nucleus transcriptome profiling. <i>Cell Discovery</i> , 2023, 9, .	3.1	14



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31602	Virtual screening of bioactive anti-SARS-CoV natural products and identification of 3Î²,12-diacetoxylabieta-6,8,11,13-tetraene as a potential inhibitor of SARS-CoV-2 virus and its infection related pathways by MD simulation and network pharmacology. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 13923-13936.	2.0	1
31603	Protocol for comparing gene-level selection on coding mutations between two groups of samples with Coselens. <i>STAR Protocols</i> , 2023, 4, 102117.	0.5	0
31604	A human antibody epitope map of Pfs230D1 derived from analysis of individuals vaccinated with a malaria transmission-blocking vaccine. <i>Immunity</i> , 2023, 56, 433-443.e5.	6.6	10
31605	Inflammation modulates intercellular adhesion and mechanotransduction in human epidermis via ROCK2. <i>IScience</i> , 2023, 26, 106195.	1.9	0
31607	Impact of National Institutes of Health and Food and Drug Administration Tobacco Research Funding: A Bibliometrics Analyses. <i>Nicotine and Tobacco Research</i> , 2023, 25, 1082-1089.	1.4	2
31609	A Capsid Protein Fragment of a Fusagra-like Virus Found in <i>Carica papaya</i> Latex Interacts with the 50S Ribosomal Protein L17. <i>Viruses</i> , 2023, 15, 541.	1.5	1
31610	Network-medicine approach for the identification of genetic association of parathyroid adenoma with cardiovascular disease and type-2 diabetes. <i>Briefings in Functional Genomics</i> , 0, , .	1.3	1
31612	Characterization of a unique polysaccharide monooxygenase from the plant pathogen <i>Magnaporthe oryzae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	4
31613	Plant colonization mediates the microbial community dynamics in glacier forelands of the Tibetan Plateau. , 2023, 2, .		5
31614	Phylogeny, transcriptional profile, and auxin-induced phosphorylation modification characteristics of conserved PIN proteins in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123671.	3.6	6
31615	Correlating Basal Gene Expression across Chemical Sensitivity Data to Screen for Novel Synergistic Interactors of HDAC Inhibitors in Pancreatic Carcinoma. <i>Pharmaceuticals</i> , 2023, 16, 294.	1.7	1
31616	Quantitative phosphoproteome analysis reveals differential whey phosphoproteins of bovine milk during lactation. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123681.	3.6	4
31617	Antibodies to repeat-containing antigens in <i>Plasmodium falciparum</i> are exposure-dependent and short-lived in children in natural malaria infections. <i>ELife</i> , 0, 12, .	2.8	8
31618	Global Responses of Autopolyploid Sugarcane <i>Badila</i> ( <i>Saccharum officinarum</i> L.) to Drought Stress Based on Comparative Transcriptome and Metabolome Profiling. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3856.	1.8	4
31619	Dysfunction of Prkcaa Links Social Behavior Defects with Disturbed Circadian Rhythm in Zebrafish. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3849.	1.8	1
31620	Artificial intelligence assessment of the potential of tocilizumab along with corticosteroids therapy for the management of COVID-19 evoked acute respiratory distress syndrome. <i>PLoS ONE</i> , 2023, 18, e0280677.	1.1	2
31621	Differentially Expressed Genes and Molecular Susceptibility to Human Age-Related Diseases. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3996.	1.8	3
31623	Whole Exome Sequencing Reveals Novel Candidate Genes in Familial Forms of Glaucomatous Neurodegeneration. <i>Genes</i> , 2023, 14, 495.	1.0	0

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31624	Taxonomically Restricted Genes in <i>Bacillus</i> may Form Clusters of Homologs and Can be Traced to a Large Reservoir of Noncoding Sequences. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4
31625	Pentacyclic triterpenoids saponins pannosides A-E from <i>Tripolium pannonicum</i> . <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
31626	Identification and validation of a novel ubiquitination-related gene UBE2T in Ewing's sarcoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	0
31627	Comprehensive analysis illustrating the role of PANoptosis-related genes in lung cancer based on bioinformatic algorithms and experiments. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	3
31628	Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S rRNA gene-based co-occurrence networks. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
31629	Network-based multi-omics integration reveals metabolic at-risk profile within treated HIV-infection. <i>ELife</i> , 0, 12, .	2.8	5
31631	Network and pathway-based analysis of candidate genes associated with esophageal adenocarcinoma. <i>Journal of Gastrointestinal Oncology</i> , 2023, 14, 40-53.	0.6	1
31632	Molecular features and predictive models identify the most lethal subtype and a therapeutic target for osteosarcoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
31633	The SAGA histone acetyltransferase module targets SMC5/6 to specific genes. <i>Epigenetics and Chromatin</i> , 2023, 16, .	1.8	4
31634	lncRNA-associated ceRNA network revealing the potential regulatory roles of ferroptosis and immune infiltration in Alzheimer's disease. <i>Frontiers in Aging Neuroscience</i> , 0, 15, .	1.7	5
31635	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, <i>Quercus dentata</i> . <i>New Phytologist</i> , 2023, 238, 2016-2032.	3.5	13
31636	Subgingival microbiome in periodontal health, gingivitis and different stages of periodontitis. <i>Journal of Clinical Periodontology</i> , 2023, 50, 905-920.	2.3	8
31637	Transcriptome profiling reveals a global response in harmful dinoflagellate <i>Karlodinium veneficum</i> to naturally-occurring bacterial algicides. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
31638	Systematic investigation of the mechanism of herbal medicines for the treatment of prostate cancer. <i>Aging</i> , 0, , .	1.4	0
31640	IRF4 as a novel target involved in malignant transformation of oral submucous fibrosis into oral squamous cell carcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31641	In silico analysis to identify novel ceRNA regulatory axes associated with gallbladder cancer. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31642	Understanding the molecular mechanism of <i>Ginkgo Folium-Forsythiae Fructus</i> for cerebral atherosclerosis treatment using network pharmacology and molecular docking. <i>Medicine (United States)</i> , 2023, 102, 101401.	0.4	0
31643	The sperm-interacting proteome in the bovine isthmus and ampulla during the periovulatory period. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	3

#	ARTICLE	IF	CITATIONS
31644	MetaboDirect: an analytical pipeline for the processing of FT-ICR MS-based metabolomic data. <i>Microbiome</i> , 2023, 11, .	4.9	8
31645	Bioactivity Profiling and Untargeted Metabolomics of Microbiota Associated with Mesopelagic Jellyfish <i>Periphylla Periphylla</i> . <i>Marine Drugs</i> , 2023, 21, 129.	2.2	2
31646	Synthetic Cinnamides and Cinnamates: Antimicrobial Activity, Mechanism of Action, and In Silico Study. <i>Molecules</i> , 2023, 28, 1918.	1.7	5
31647	Genome-wide analysis of 14-3-3 gene family in four gramineae and its response to mycorrhizal symbiosis in maize. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
31648	Genome-Wide Gene-Set Analysis Identifies Molecular Mechanisms Associated with ALS. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4021.	1.8	1
31649	Exploration of Blood Metabolite Signatures of Colorectal Cancer and Polyposis through Integrated Statistical and Network Analysis. <i>Metabolites</i> , 2023, 13, 296.	1.3	0
31650	Reverse predictive analysis of <i>Rhizoma Pinelliae</i> and <i>Rhizoma Coptidis</i> on differential miRNA target genes in lung adenocarcinoma. <i>Medicine (United States)</i> , 2023, 102, e32999.	0.4	1
31651	Association study to evaluate <i>Foxo1</i> and <i>Foxo3</i> gene polymorphisms in polycystic ovary syndrome: a preliminary case-control study and in silico analysis. <i>Molecular Biology Reports</i> , 2023, 50, 3569-3580.	1.0	1
31652	Can biomarkers identified from the uterine fluid transcriptome be used to establish a noninvasive endometrial receptivity prediction tool? A proof-of-concept study. <i>Reproductive Biology and Endocrinology</i> , 2023, 21, .	1.4	3
31653	Conditioned place avoidance is associated with a distinct hippocampal phenotype, partly preserved pattern separation, and reduced reactive oxygen species production after stress. <i>Genes, Brain and Behavior</i> , 2023, 22, .	1.1	2
31654	Diverse Marine T4-like Cyanophage Communities Are Primarily Comprised of Low-Abundance Species Including Species with Distinct Seasonal, Persistent, Occasional, or Sporadic Dynamics. <i>Viruses</i> , 2023, 15, 581.	1.5	3
31655	Analysis of gene expression profile for identification of novel gene signatures during dengue infection. , 2023, 2, 19-30.		0
31656	Proximity labeling reveals a new in vivo network of interactors for the histone demethylase KDM5. <i>Epigenetics and Chromatin</i> , 2023, 16, .	1.8	4
31657	Enzalutamide-induced signatures revealed by epigenetic plasticity using single-cell multi-omics sequencing in prostate cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2023, 31, 648-661.	2.3	2
31658	Dynamic network biomarker to determine the critical point of breast cancer stage progression. <i>Breast Cancer</i> , 2023, 30, 453-465.	1.3	1
31659	Analysis of the Genetic Relationship between Atherosclerosis and Non-Alcoholic Fatty Liver Disease through Biological Interaction Networks. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4124.	1.8	3
31660	Potential Early Markers for Breast Cancer: A Proteomic Approach Comparing Saliva and Serum Samples in a Pilot Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4164.	1.8	5
31661	Prognostic values of long noncoding RNA in bone metastasis of prostate cancer: A systematic review and meta-analysis. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	0

#	ARTICLE	IF	CITATIONS
31662	Designing a Novel Monitoring Approach for the Effects of Space Travel on Astronauts' Health. <i>Life</i> , 2023, 13, 576.	1.1	2
31663	Roe Deer Produce Less Methane and Harbor Distinct Gut Microbiota. <i>Fermentation</i> , 2023, 9, 186.	1.4	0
31664	Therapeutic Effect of Costunolide in Autoimmune Hepatitis: Network Pharmacology and Experimental Validation. <i>Pharmaceuticals</i> , 2023, 16, 316.	1.7	2
31665	Polypharmacology-Labeled Molecular Networking: An Analytical Technology Workflow for Accelerated Identification of Multiple Bioactive Constituents in Complex Extracts. <i>Analytical Chemistry</i> , 2023, 95, 4381-4389.	3.2	4
31666	Structural screens identify candidate human homologs of insect chemoreceptors and cryptic <i>Drosophila</i> gustatory receptor-like proteins. <i>ELife</i> , 0, 12, .	2.8	4
31667	UPLC-MS based integrated plasma proteomic and metabolomic profiling of TSC-RAML and its relationship with everolimus treatment. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	0
31670	Dapagliflozin alleviates myocardial ischemia/reperfusion injury by reducing ferroptosis via MAPK signaling inhibition. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	13
31671	Comparison of genomic and transcriptional microbiome analysis in gastric cancer patients and healthy individuals. <i>World Journal of Gastroenterology</i> , 0, 29, 1202-1218.	1.4	7
31672	Comprehensive analysis of cuproptosis-related prognostic gene signature and tumor immune microenvironment in HCC. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
31673	Combining Selective Enrichment and a Boosting Approach to Globally and Site-Specifically Characterize Protein Co-translational <i>O</i> -GlcNAcylation. <i>Analytical Chemistry</i> , 2023, 95, 4371-4380.	3.2	4
31674	Transcriptomic Responses to Polymyxin B and Analogues in Human Kidney Tubular Cells. <i>Antibiotics</i> , 2023, 12, 415.	1.5	0
31675	Exercise-acclimated microbiota improves skeletal muscle metabolism via circulating bile acid deconjugation. <i>IScience</i> , 2023, 26, 106251.	1.9	4
31676	Genome-wide analysis of MYB family in <i>Nicotiana benthamiana</i> and the functional role of the key members in resistance to <i>Bemisia tabaci</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 235, 123759.	3.6	3
31677	Bat pluripotent stem cells reveal unusual entanglement between host and viruses. <i>Cell</i> , 2023, 186, 957-974.e28.	13.5	17
31678	Active substances and molecular mechanisms of the anti-myocardial ischemia effects of <i>Carthami flos</i> by network pharmacology and in vitro experiments. <i>Heliyon</i> , 2023, 9, e13877.	1.4	0
31679	Nuclear High Mobility Group A2 (HMGA2) Interactome Revealed by Biotin Proximity Labeling. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4246.	1.8	1
31680	Bioinformatics Analysis of Next Generation Sequencing Data Identifies Molecular Biomarkers Associated With Type 2 Diabetes Mellitus. <i>Clinical Medicine Insights: Endocrinology and Diabetes</i> , 2023, 16, 117955142311556.	1.0	9
31681	A proteomics approach to identify COPD-related changes in lung fibroblasts. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2023, 324, L521-L535.	1.3	1

#	ARTICLE	IF	CITATIONS
31682	Microbial community dynamics of a sequentially fed anaerobic digester treating solid organic waste. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	1.3	3
31683	Elevated atmospheric CO <sub>2</sub> concentrations caused a shift of the metabolically active microbiome in vineyard soil. <i>BMC Microbiology</i> , 2023, 23, .	1.3	1
31684	Chemical composition and sensory profile of the Italian espresso coffee powder and beverage under different roasting conditions. <i>European Food Research and Technology</i> , 2023, 249, 1287-1301.	1.6	2
31685	Pan-Cancer Analysis of the Oncogenic and Prognostic Role of PKM2: A Potential Target for Survival and Immunotherapy. <i>BioMed Research International</i> , 2023, 2023, 1-14.	0.9	1
31686	tRF-20-S998LO9D inhibits endometrial carcinoma by upregulating SESN2. <i>Epigenomics</i> , 2022, 14, 1563-1577.	1.0	3
31687	A molecular atlas reveals the tri-sectional spinning mechanism of spider dragline silk. <i>Nature Communications</i> , 2023, 14, .	5.8	2
31688	Escape from X-inactivation in twins exhibits intra- and inter-individual variability across tissues and is heritable. <i>PLoS Genetics</i> , 2023, 19, e1010556.	1.5	8
31689	Studying the connection between SF3B1 and four types of cancer by analyzing networks constructed based on published research. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31690	Inhibition of SUMOylation enhances DNA hypomethylating drug efficacy to reduce outgrowth of hematopoietic malignancies. <i>Leukemia</i> , 2023, 37, 864-876.	3.3	3
31692	Short-chain fatty acids improve inflamm-aging and acute lung injury in old mice. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2023, 324, L480-L492.	1.3	4
31693	Occurrence and distribution of pineapple mealybug wilt-associated viruses (PMWaVs) in MD2 pineapple fields in the Valle del Cauca Department, Colombia. <i>Tropical Plant Pathology</i> , 2023, 48, 217-225.	0.8	1
31694	Expression of EMT-related genes in lymph node metastasis in endometrial cancer: a TCGA-based study. <i>World Journal of Surgical Oncology</i> , 2023, 21, .	0.8	4
31696	Exploring Core Genes by Comparative Transcriptomics Analysis for Early Diagnosis, Prognosis, and Therapies of Colorectal Cancer. <i>Cancers</i> , 2023, 15, 1369.	1.7	4
31697	New Phenylspirodrimanes from the Sponge-Associated Fungus <i>Stachybotrys chartarum</i> MUT 3308. <i>Marine Drugs</i> , 2023, 21, 135.	2.2	2
31698	Identification of Parkinson's disease-associated chromatin regulators. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31699	Fecal Microbiota, Forage Nutrients, and Metabolic Responses of Horses Grazing Warm- and Cool-Season Grass Pastures. <i>Animals</i> , 2023, 13, 790.	1.0	2
31700	ARPC1A correlates with poor prognosis in prostate cancer and is up-regulated by glutamine metabolism to promote tumor cell migration, invasion and cytoskeletal changes. <i>Cell and Bioscience</i> , 2023, 13, .	2.1	1
31701	Dynamics of bacterial community in the foregut and hindgut of earthworms with the nutrition supplied by kitchen waste during vermicomposting. <i>Bioresource Technology</i> , 2023, 374, 128777.	4.8	5

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31702	Proteomic Variability and Nutrient-Related Proteins across Pigmented and Non-Pigmented Rice Grains. <i>Crops</i> , 2023, 3, 63-77.	0.6	0
31703	USP15 Represses Hepatocellular Carcinoma Progression by Regulation of Pathways of Cell Proliferation and Cell Migration: A System Biology Analysis. <i>Cancers</i> , 2023, 15, 1371.	1.7	4
31704	Exploiting moderate hypoxia to benefit patients with brain disease: Molecular mechanisms and translational research in progress. , 2023, 1, 55-65.		6
31706	Pharmacology-Based Prediction of the Targets and Mechanisms for Icaritin against Myocardial Infarction. <i>Medicina (Lithuania)</i> , 2023, 59, 420.	0.8	0
31707	Epigenetic association study uncovered H3K27 acetylation enhancers and dysregulated genes in high-fat-diet-induced nonalcoholic fatty liver disease in rats. <i>Epigenomics</i> , 2022, 14, 1523-1540.	1.0	6
31708	Conserved reduction of m <sup>6</sup> A RNA modifications during aging and neurodegeneration is linked to changes in synaptic transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	20
31709	The gut microbiota in experimental abdominal aortic aneurysm. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	2
31710	Comparative transcriptome analysis of adult worker bees under short-term heat stress. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	0
31711	Coupling Environmental Whole Mixture Toxicity Screening with Unbiased RNA-Seq Reveals Site-Specific Biological Responses in Zebrafish. <i>Toxics</i> , 2023, 11, 201.	1.6	3
31712	Identification of the regulatory network and potential markers for type 2 diabetes mellitus related to internal exposure to metals in Chinese adults. <i>Environmental Geochemistry and Health</i> , 2023, 45, 6889-6902.	1.8	2
31713	Feasibility of detecting snake envenomation biomarkers from dried blood spots. <i>Analytical Science Advances</i> , 2023, 4, 26-36.	1.2	0
31714	Beyond bacteria: Reconstructing microorganism connections and deciphering the predicted mutualisms in mammalian gut metagenomes. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
31717	Skeletal dysplasia-causing TRPV4 mutations suppress the hypertrophic differentiation of human iPSC-derived chondrocytes. <i>ELife</i> , 0, 12, .	2.8	3
31718	Effects of Long-Term Physical Activity and BCAA Availability on the Subcellular Associations between Intramyocellular Lipids, Perilipins and PGC-1 $\alpha$ . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4282.	1.8	0
31719	Probing the Mechanisms of Inhibitors Binding to Presenilin Homologue Using Molecular Dynamics Simulations. <i>Molecules</i> , 2023, 28, 2076.	1.7	2
31720	Single-cell transcriptomic dissection of the cellular and molecular events underlying the triclosan-induced liver fibrosis in mice. <i>Military Medical Research</i> , 2023, 10, .	1.9	3
31721	Liquid Crystal Monomer: A Potential PPAR $\delta$ Antagonist. <i>Environmental Science &amp; Technology</i> , 2023, 57, 3758-3771.	4.6	17
31722	Exploring Myocardial Ischemia-Reperfusion Injury Mechanism of Cinnamon by Network Pharmacology, Molecular Docking, and Experiment Validation. <i>Computational and Mathematical Methods in Medicine</i> , 2023, 2023, 1-14.	0.7	1



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31723	Whole transcriptome analysis to explore the impaired immunological features in critically ill elderly patients with sepsis. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	2
31724	Anastrozole-mediated modulation of mitochondrial activity by inhibition of mitochondrial permeability transition pore opening: an initial perspective. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 14063-14079.	2.0	0
31725	Proteomic Fingerprint of Lung Fibrosis Progression and Response to Therapy in Bleomycin-Induced Mouse Model. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4410.	1.8	4
31726	IMPAT 2.0: An Enhanced and Expanded Phytochemical Atlas of Indian Medicinal Plants. <i>ACS Omega</i> , 2023, 8, 8827-8845.	1.6	29
31727	Identification of hub genes associated with osteoporosis development by comprehensive bioinformatics analysis. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31728	A comprehensive pan-cancer analysis reveals cancer-associated robust isomiR expression landscapes in miRNA arm switching. <i>Molecular Genetics and Genomics</i> , 0, , .	1.0	0
31729	Comparative and Temporal Characterization of LPS and Blue-Light-Induced TLR4 Signal Transduction and Gene Expression in Optogenetically Manipulated Endothelial Cells. <i>Cells</i> , 2023, 12, 697.	1.8	4
31730	Comprehensive analysis reveals hub genes associated with immune cell infiltration in allergic rhinitis. <i>World Journal of Otorhinolaryngology - Head and Neck Surgery</i> , 2023, 9, 340-351.	0.7	0
31731	Co-expression network of mRNA and DNA methylation in first-episode and drug-naive adolescents with major depressive disorder. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	1
31733	Discovery-Based Proteomics Identify Skeletal Muscle Mitochondrial Alterations as an Early Metabolic Defect in a Mouse Model of $\beta^2$ -Thalassemia. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4402.	1.8	0
31734	Potential diagnostic markers and therapeutic targets for rheumatoid arthritis with comorbid depression based on bioinformatics analysis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31736	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N <sub>2</sub> O cycling. <i>Communications Biology</i> , 2023, 6, .	2.0	0
31738	PI3K/AKT/SERBP-1 pathway regulates <i>Alisma orientalis</i> beverage treatment of atherosclerosis in APOE <sup>−/−</sup> high-fat diet mice. <i>Pharmaceutical Biology</i> , 2023, 61, 473-487.	1.3	4
31739	Comprehensive study of rice YABBY gene family: evolution, expression and interacting proteins analysis. <i>PeerJ</i> , 0, 11, e14783.	0.9	1
31741	Sour Orange Microbiome Is Affected by Infections of <i>Plenodomus tracheiphilus</i> Causal Agent of Citrus Mal Secco Disease. <i>Agronomy</i> , 2023, 13, 654.	1.3	2
31742	Network pharmacology and bioinformatics study on the treatment of renal fibrosis with persicae semen-carthami flos drug pair. <i>Medicine (United States)</i> , 2023, 102, e32946.	0.4	1
31743	Exploring Microbial Dysbiosis in Orchards Affected by Little Cherry Disease. <i>Phytobiomes Journal</i> , 0, , .	1.4	1
31744	Single-cell transcriptomic analysis in two patients with rare systemic autoinflammatory diseases treated with anti-TNF therapy. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0

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31748	Identifying Eukaryotes and Factors Influencing Their Biogeography in Drinking Water Metagenomes. <i>Environmental Science &amp; Technology</i> , 2023, 57, 3645-3660.	4.6	6
31749	Visualizing Semantic Web Data using Various Tools Focusing RDF, OWL and SPARQL. , 2022, , .		1
31751	Dietary intake of table olives exerts antihypertensive effects in association with changes in gut microbiota in spontaneously hypertensive rats. <i>Food and Function</i> , 2023, 14, 2793-2806.	2.1	2
31752	Phenolic acids-rich fraction from <i>Ficus drupacea</i> leaves for the prevention and treatment of ethanol-induced gastric mucosal injury in rats. <i>Inflammopharmacology</i> , 2023, 31, 1423-1436.	1.9	5
31753	A novel circRNA, hsa_circ_0069382, regulates gastric cancer progression. <i>Cancer Cell International</i> , 2023, 23, .	1.8	0
31754	Duo-role Platelet-rich Plasma: temperature-induced fibrin gel and growth factorsâ€™ reservoir for microneedles to promote hair regrowth. <i>Journal of Advanced Research</i> , 2024, 55, 89-102.	4.4	3
31755	Association of Circular RNAs levels in blood and Essential Hypertension with Carotid Plaque. <i>Clinical and Experimental Hypertension</i> , 2023, 45, .	0.5	1
31756	Construction and validation of a macrophage-related prognostic index to predict the overall survival in patients with early-stage triple-negative breast cancer. <i>Gland Surgery</i> , 2023, 12, 225-242.	0.5	1
31757	Elucidation of the Late Steps during Hexacosalactone A Biosynthesis in <i>Streptomyces samsunensis</i> OUCT16-12. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	0
31758	Identification and validation of metabolism-related hub genes in idiopathic pulmonary fibrosis. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31759	Network pharmacology and bioinformatics analysis on the underlying mechanisms of baicalein against oral squamous cell carcinoma. <i>Journal of Gene Medicine</i> , 0, , .	1.4	2
31760	Studying the mechanism underlying lipid metabolism in osteosarcoma based on transcriptomic RNA sequencing and singleâ€™cell data. <i>Journal of Gene Medicine</i> , 2023, 25, .	1.4	4
31761	Twenty Novel MicroRNAs in the Aqueous Humor of Pseudoexfoliation Glaucoma Patients. <i>Cells</i> , 2023, 12, 737.	1.8	4
31762	Comparative transcriptomic and metabolomic analyses reveal differences in flavonoid biosynthesis between PCNA and PCA persimmon fruit. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
31763	Genome-Wide Investigation of the NAC Transcription Factor Family in <i>Apocynum venetum</i> Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4578.	1.8	2
31764	Investigation on Metabolites in Structure and Biosynthesis from the Deep-Sea Sediment-Derived Actinomycete <i>Janibacter</i> sp. SCSIO 52865. <i>Molecules</i> , 2023, 28, 2133.	1.7	4
31765	Analysis of proteomesâ€™l. , 2023, , 111-138.		0
31766	CD40LG and GZMB were correlated with adipose tissue macrophage infiltration and involved in obstructive sleep apnea related metabolic dysregulation: Evidence from bioinformatics analysis. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0

#	ARTICLE	IF	CITATIONS
31767	Machine Learning Model Based on Insulin Resistance Metagenes Underpins Genetic Basis of Type 2 Diabetes. <i>Biomolecules</i> , 2023, 13, 432.	1.8	3
31768	From the Sunlit to the Aphotic Zone: Assembly Mechanisms and Co-Occurrence Patterns of Protistan-Bacterial Microbiotas in the Western Pacific Ocean. <i>MSystems</i> , 2023, 8, .	1.7	5
31769	Clear Cell Renal Cell Carcinoma: A Comprehensive in silico Study in Searching for Therapeutic Targets. <i>Kidney and Blood Pressure Research</i> , 2023, 48, 135-150.	0.9	2
31770	Integrated mRNA and miRNA expression analyses for <i>Cryptocaryon irritans</i> resistance in large yellow croaker ( <i>Larimichthys crocea</i> ). <i>Fish and Shellfish Immunology</i> , 2023, 135, 108650.	1.6	2
31771	Homocysteine impedes neurite outgrowth recovery after intracerebral haemorrhage by downregulating pCAMK2A. <i>Stroke and Vascular Neurology</i> , 2023, 8, 335-348.	1.5	1
31772	Life-Threatening Cardiogenic Shock Related to Venlafaxine Poisoning—A Case Report with Metabolomic Approach. <i>Metabolites</i> , 2023, 13, 353.	1.3	7
31773	The eukaryotic translation initiation factor <i>eIF4E</i> reprograms alternative splicing. <i>EMBO Journal</i> , 2023, 42, .	3.5	7
31774	Dynamics of extracellular vesicle-coupled microRNAs in equine follicular fluid associated with follicle selection and ovulation. <i>Molecular Human Reproduction</i> , 2023, 29, .	1.3	1
31775	Decitabine priming increases anti-PD-1 antitumor efficacy by promoting CD8+ progenitor exhausted T cell expansion in tumor models. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	8
31776	Genome-Wide Identification and Expression Analysis of RCC1 Gene Family under Abiotic Stresses in Rice ( <i>Oryza sativa</i> L.). <i>Agronomy</i> , 2023, 13, 703.	1.3	1
31778	Differential Expression Analysis of Blood MicroRNA in Identifying Potential Genes Relevant to Alzheimer's Disease Pathogenesis, Using an Integrated Bioinformatics and Machine Learning Approach. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 3071.	1.3	0
31779	Meta-Analysis of Exploring the Effect of Curcumin Supplementation with or without Other Advice on Biochemical and Anthropometric Parameters in Patients with Metabolic-Associated Fatty Liver Disease (MAFLD). <i>International Journal of Environmental Research and Public Health</i> , 2023, 20, 4266.	1.2	1
31780	Imbalanced IL-1B and IL-18 Expression in SÅ©zary Syndrome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4674.	1.8	3
31781	Integrated proteome and acetylome analyses provide novel insights into early somatic embryogenesis of <i>Dimocarpus longan</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 196, 903-916.	2.8	0
31782	Combined Multiomics and In Silico Approach Uncovers PRKAR1A as a Putative Therapeutic Target in Multi-Organ Dysfunction Syndrome. <i>ACS Omega</i> , 2023, 8, 9555-9568.	1.6	2
31784	Use of an Integrated Multi-Omics Approach To Identify Molecular Mechanisms and Critical Factors Involved in the Pathogenesis of <i>Leptospira</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
31785	Tcf21 marks visceral adipose mesenchymal progenitors and functions as a rate-limiting factor during visceral adipose tissue development. <i>Cell Reports</i> , 2023, 42, 112166.	2.9	2
31786	Bifidobacterium-derived short-chain fatty acids and indole compounds attenuate nonalcoholic fatty liver disease by modulating gut-liver axis. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	12

#	ARTICLE	IF	CITATIONS
31787	The Transcription Factor Twist1 Has a Significant Role in Mycosis Fungoides (MF) Cell Biology: An RNA Sequencing Study of 40 MF Cases. <i>Cancers</i> , 2023, 15, 1527.	1.7	0
31788	AUF1 Recognizes 8-Oxo-Guanosine Embedded in DNA and Stimulates APE1 Endoribonuclease Activity. <i>Antioxidants and Redox Signaling</i> , 2023, 39, 411-431.	2.5	3
31789	Quantitative Proteomics Reveal the Inherent Antibiotic Resistance Mechanism against Norfloxacin Resistance in <i>Aeromonas hydrophila</i> . <i>Journal of Proteome Research</i> , 2023, 22, 1193-1200.	1.8	3
31790	Microbial profiles and immune responses in seahorse gut and brood pouch under chronic exposure to environmental antibiotics. <i>Ecotoxicology and Environmental Safety</i> , 2023, 253, 114711.	2.9	3
31791	Analysis for drug metabolism-related prognostic subtypes and gene signature in liver cancer. <i>Genes and Genetic Systems</i> , 2022, 97, 271-284.	0.2	0
31792	Identification and verification of feature biomarkers associated in heart failure by bioinformatics analysis. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
31793	Identification of autophagy-related genes in neuropathic pain through bioinformatic analysis. <i>Hereditas</i> , 2023, 160, .	0.5	1
31794	Proteomic analysis identifies dysregulated proteins and associated molecular pathways in a cohort of gallbladder cancer patients of African ancestry. <i>Clinical Proteomics</i> , 2023, 20, .	1.1	3
31795	Integrated analysis of <i>Dendrobium nobile</i> extract Dendrobin A against pancreatic ductal adenocarcinoma based on network pharmacology, bioinformatics, and validation experiments. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	3
31796	A New Technique for Use in Culturing Prokaryotes Comprising the Mouse Intestinal Microbiome. <i>Advances in Microbiology</i> , 2023, 13, 119-147.	0.3	0
31797	Molecular characterization of circadian gene expression and its correlation with survival percentage in colorectal cancer patients. <i>Advances in Protein Chemistry and Structural Biology</i> , 2023, , .	1.0	0
31798	Network Pharmacology Study to reveal the mechanism of Zuogui Pill for treating osteoporosis. <i>Current Computer-Aided Drug Design</i> , 2023, 19, .	0.8	0
31799	Circular RNA Expression Signatures Provide Promising Diagnostic and Therapeutic Biomarkers for Chronic Lymphocytic Leukemia. <i>Cancers</i> , 2023, 15, 1554.	1.7	2
31800	Elucidation of Phytochemicals Affecting Platelet Responsiveness in Dangguisu-san: Active Ingredient Prediction and Experimental Research Using Network Pharmacology. <i>Plants</i> , 2023, 12, 1120.	1.6	1
31801	Involvement of 2â€²-5â€² oligoadenylate synthetase-like protein in the survival of <i>Mycobacterium tuberculosis</i> avirulent strain in macrophages. <i>Animal Diseases</i> , 2023, 3, .	0.6	0
31802	Associating brain imaging phenotypes and genetic risk factors via a hypergraph based netNMF method. <i>Frontiers in Aging Neuroscience</i> , 0, 15, .	1.7	1
31803	Identification of miR-671-5p and Its Related Pathways as General Mechanisms of Both Form-Deprivation and Lens-Induced Myopia in Mice. <i>Current Issues in Molecular Biology</i> , 2023, 45, 2060-2072.	1.0	1
31804	The IL-10 receptor inhibits cell extrinsic signals necessary for STAT1-dependent macrophage accumulation during colitis. <i>Mucosal Immunology</i> , 2023, 16, 233-249.	2.7	4

#	ARTICLE	IF	CITATIONS
31805	An updated <i>C. elegans</i> nuclear body muscle transcriptome for studies in muscle formation and function. <i>Skeletal Muscle</i> , 2023, 13, .	1.9	2
31806	Whole-transcriptome analyses identify key differentially expressed mRNAs, lncRNAs, and miRNAs associated with male sterility in watermelon. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
31807	Diversity and potential function of pig gut DNA viruses. <i>Heliyon</i> , 2023, 9, e14020.	1.4	2
31808	Network-informed discovery of multidrug combinations for ER <sup>+</sup> /HER2-/PI3K <sup>+</sup> -mutant breast cancer. <i>Cellular and Molecular Life Sciences</i> , 2023, 80, .	2.4	3
31809	CYP27A1 deficiency promoted osteoclast differentiation. <i>PeerJ</i> , 0, 11, e15041.	0.9	1
31811	Unique metabolism and protein expression signature in human decidual NK cells. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31812	Integrated Bioinformatics Analysis of Shared Genes, miRNA, Biological Pathways and Their Potential Role as Therapeutic Targets in Huntington's Disease Stages. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4873.	1.8	2
31813	A gene regulatory network for neural induction. <i>ELife</i> , 0, 12, .	2.8	9
31814	Short-term transcriptomic analysis at organ scale reveals candidate genes involved in low N responses in NUE-contrasting tomato genotypes. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
31815	A direct examination of microbial specialized metabolites associated with ocean sediments from Baffin Bay and the Gulf of Maine. <i>Canadian Journal of Microbiology</i> , 0, , .	0.8	0
31816	Transcriptome profile of skeletal muscle using different sources of dietary fatty acids in male pigs. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
31818	Single-cell sequencing reveals the evolution of immune molecules across multiple vertebrate species. <i>Journal of Advanced Research</i> , 2024, 55, 73-87.	4.4	6
31819	scRNA sequencing analysis of the <i>longissimus dorsi</i> to identify candidate genes underlying the intramuscular fat content in Anqing Sixwhite pigs. <i>Animal Genetics</i> , 2023, 54, 315-327.	0.6	4
31820	Identification of Prognostic Biomarkers for Suppressing Tumorigenesis and Metastasis of Hepatocellular Carcinoma through Transcriptome Analysis. <i>Diagnostics</i> , 2023, 13, 965.	1.3	1
31821	Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. <i>Animal Microbiome</i> , 2023, 5, .	1.5	3
31822	Experimental community coalescence sheds light on microbial interactions in soil and restores impaired functions. <i>Microbiome</i> , 2023, 11, .	4.9	10
31823	Maternal obesity and gestational diabetes reprogram the methylome of offspring beyond birth by inducing epigenetic signatures in metabolic and developmental pathways. <i>Cardiovascular Diabetology</i> , 2023, 22, .	2.7	7
31824	MAW: the reproducible Metabolome Annotation Workflow for untargeted tandem mass spectrometry. <i>Journal of Cheminformatics</i> , 2023, 15, .	2.8	12

#	ARTICLE	IF	CITATIONS
31827	The mechanism of Croci stigma in the treatment of melasma based on network pharmacology and molecular docking. <i>Journal of Cosmetic Dermatology</i> , 2023, 22, 2105-2114.	0.8	3
31828	Bioinformatics and cheminformatics approaches to identify pathways, molecular mechanisms and drug substances related to genetic basis of cervical cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-16.	2.0	2
31829	NDEx IQQuery: a multi-method network gene set analysis leveraging the Network Data Exchange. <i>Bioinformatics</i> , 2023, 39, .	1.8	7
31830	A mechanistic analysis of spontaneous cancer remission phenomenon: identification of genomic basis and effector biomolecules for therapeutic applicability. <i>3 Biotech</i> , 2023, 13, .	1.1	0
31831	Mycobiome structure does not affect field litter decomposition in Eucalyptus and Acacia plantations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
31832	miRNome and Proteome Profiling of Human Keratinocytes and Adipose Derived Stem Cells Proposed miRNA-Mediated Regulations of Epidermal Growth Factor and Interleukin 1-Alpha. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4956.	1.8	2
31833	Identification and Analysis of Necroptosis-Related Genes in COPD by Bioinformatics and Experimental Verification. <i>Biomolecules</i> , 2023, 13, 482.	1.8	0
31834	StkP- and PhpP-Mediated Posttranslational Modifications Modulate the <i>S. pneumoniae</i> Metabolism, Polysaccharide Capsule, and Virulence. <i>Infection and Immunity</i> , 2023, 91, .	1.0	3
31835	Transcriptome Analysis Reveals Differentially Expressed Genes Involved in Cadmium and Arsenic Accumulation in Tea Plant ( <i>Camellia sinensis</i> ). <i>Plants</i> , 2023, 12, 1182.	1.6	2
31836	Phylogeny, Expression Profiling, and Coexpression Networks Reveals the Critical Roles of Nucleotide-BindingLeucine-Rich Repeats on Valsa Canker Resistance. <i>Horticulturae</i> , 2023, 9, 345.	1.2	0
31837	Apatinib Inhibits Bladder Cancer through Suppression of The VEGFR2-PI3K-AKT Signaling Pathway as revealed by Network Pharmacology and In Vitro Experimental Verification. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, .	0.6	0
31838	Data-Driven Radiogenomic Approach for Deciphering Molecular Mechanisms Underlying Imaging Phenotypes in Lung Adenocarcinoma: A Pilot Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4947.	1.8	0
31839	Development and Experimental Validation of a Novel Prognostic Signature for Gastric Cancer. <i>Cancers</i> , 2023, 15, 1610.	1.7	0
31840	Identification of Distinct Vaginal Microbiota Signatures Contributing Toward Preterm Birth Using an Integrative Computational Approach. <i>Microbiology and Biotechnology Letters</i> , 2023, 51, 109-123.	0.2	1
31841	Computational analysis of crosstalk between transcriptional regulators and RNA-binding proteins suggests mutual regulation of polycomb proteins and SRSF1 influencing adult hippocampal neurogenesis. <i>Discover Mental Health</i> , 2023, 3, .	1.0	0
31842	Genome-Wide Identification and Expression Analysis of the HSF Gene Family in Poplar. <i>Forests</i> , 2023, 14, 510.	0.9	4
31843	Transcriptomic analysis of the cerebral hippocampal tissue in spontaneously hypertensive rats exposed to acute hypobaric hypoxia: associations with inflammation and energy metabolism. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31845	Identification of a novel circRNAâ€™miRNAâ€™mRNA regulatory axis in hepatocellular carcinoma based on bioinformatics analysis. <i>Scientific Reports</i> , 2023, 13, .	1.6	2



#	ARTICLE	IF	CITATIONS
31846	Proteome Dynamics Analysis Reveals the Potential Mechanisms of Salinity and Drought Response during Seed Germination and Seedling Growth in <i>Tamarix hispida</i> . <i>Genes</i> , 2023, 14, 656.	1.0	2
31847	Detection and targeting of splicing deregulation in pediatric acute myeloid leukemia stem cells. <i>Cell Reports Medicine</i> , 2023, 4, 100962.	3.3	8
31848	The proteome and transcriptome of stress granules and P bodies during human T lymphocyte activation. <i>Cell Reports</i> , 2023, 42, 112211.	2.9	2
31850	The shared genetic architecture of suicidal behaviour and psychiatric disorders: A genomic structural equation modelling study. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31851	Differentially expressed discriminative genes and significant meta-hub genes based key genes identification for hepatocellular carcinoma using statistical machine learning. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
31852	Insights into the mechanisms of triptolide nephrotoxicity through network pharmacology-based analysis and RNA-seq. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
31854	Parental Preconception and Pre-Hatch Exposure to A Developmental Insult Alters Offspring's Gene Expression and Epigenetic Regulations: An Avian Model. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5047.	1.8	2
31855	Terpene synthases and pathways in animals: enzymology and structural evolution in the biosynthesis of volatile infochemicals. <i>Natural Product Reports</i> , 2023, 40, 766-793.	5.2	5
31857	A knowledge empowered explainable gene ontology fingerprint approach to improve gene functional explication and prediction. <i>IScience</i> , 2023, 26, 106356.	1.9	2
31858	Quantitative Proteomics of Nervous System Regeneration: From Sample Preparation to Functional Data Analyses. <i>Methods in Molecular Biology</i> , 2023, , 343-366.	0.4	0
31861	Development of an immune-related gene prognostic risk model and identification of an immune infiltration signature in the tumor microenvironment of colon cancer. <i>BMC Gastroenterology</i> , 2023, 23, .	0.8	2
31862	Integrated bioinformatics analysis identifies shared immune changes between ischemic stroke and COVID 19. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31863	Exploring the components and mechanism of <i>Solanum nigrum</i> L. for colon cancer treatment based on network pharmacology and molecular docking. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	2
31864	Brain injury accelerates the onset of a reversible age-related microglial phenotype associated with inflammatory neurodegeneration. <i>Science Advances</i> , 2023, 9, .	4.7	16
31865	Data-Independent Acquisition Proteomics Reveals the Effects of Red and Blue Light on the Growth and Development of Moso Bamboo ( <i>Phyllostachys edulis</i> ) Seedlings. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5103.	1.8	2
31866	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
31870	Evidence of polygenic regulation of the physiological presence of neurofilament light chain in human serum. <i>Frontiers in Neurology</i> , 0, 14, .	1.1	0
31871	Overexpression of Parkin in the Neuronal Progenitor Cells from a Patient with Parkinson's Disease Shifts the Transcriptome Towards the Normal State. <i>Molecular Neurobiology</i> , 0, , .	1.9	0

#	ARTICLE	IF	CITATIONS
31872	Tissue-embedded stretchable nanoelectronics reveal endothelial cell-mediated electrical maturation of human 3D cardiac microtissues. <i>Science Advances</i> , 2023, 9, .	4.7	8
31873	Genomic Analysis, Evolution and Characterization of E3 Ubiquitin Protein Ligase (TRIM) Gene Family in Common Carp ( <i>Cyprinus carpio</i> ). <i>Genes</i> , 2023, 14, 667.	1.0	0
31874	The use of data independent acquisition based proteomic analysis and machine learning to reveal potential biomarkers for autism spectrum disorder. <i>Journal of Proteomics</i> , 2023, 278, 104872.	1.2	3
31875	Integrated analysis of cell-specific gene expression in peripheral blood using ISG15 as a marker of rejection in kidney transplantation. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31878	Discovery of therapeutic targets of quercetin for endometrial carcinoma patients infected with COVID-19 through network pharmacology. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	0
31879	Genome-wide association studies for additive and dominance effects for body composition traits in commercial crossbred PiÅ©train pigs. <i>Journal of Animal Breeding and Genetics</i> , 2023, 140, 413-430.	0.8	6
31880	Comparative Analyses of Human Exosome Proteomes. <i>Protein Journal</i> , 2023, 42, 365-373.	0.7	4
31881	Phototrophic Biofilms Transform Soil-Dissolved Organic Matter Similarly Despite Compositional and Environmental Differences. <i>Environmental Science &amp; Technology</i> , 2023, 57, 4679-4689.	4.6	4
31882	Prioritization of Microorganisms Isolated from the Indian Ocean Sponge <i>Scopalina hapalia</i> Based on Metabolomic Diversity and Biological Activity for the Discovery of Natural Products. <i>Microorganisms</i> , 2023, 11, 697.	1.6	2
31883	Variation in synonymous evolutionary rates in the SARS-CoV-2 genome. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
31884	Novel Data Science Methodologies for Essential Genes Identification Based on Network Analysis. <i>Studies in Computational Intelligence</i> , 2023, , 117-145.	0.7	0
31886	Molecular mechanism and diagnostic marker investigation of endoplasmic reticulum stress on periodontitis. <i>BMC Oral Health</i> , 2023, 23, .	0.8	2
31887	Bulk and single-cell transcriptome analyses of islet tissue unravel gene signatures associated with pyroptosis and immune infiltration in type 2 diabetes. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	3
31888	Comparative transcriptome analysis identifies candidate genes related to seed coat color in rapeseed. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31889	Platelet-Derived MicroRNAs Regulate Cardiac Remodeling After Myocardial Ischemia. <i>Circulation Research</i> , 2023, 132, .	2.0	8
31890	Identification of immune-related genes in diagnosing atherosclerosis with rheumatoid arthritis through bioinformatics analysis and machine learning. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31891	Bioherbicidal Activity and Metabolic Profiling of Allelopathic Metabolites of Three <i>Cassia</i> species using UPLC-qTOF-MS/MS and Molecular Networking. <i>Metabolomics</i> , 2023, 19, .	1.4	5
31892	Larger cerebral cortex is genetically correlated with greater frontal area and dorsal thickness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	0

#	ARTICLE	IF	CITATIONS
31893	Analysis of <i>Corynebacterium silvaticum</i> genomes from Portugal reveals a single cluster and a clade suggested to produce diphtheria toxin. <i>PeerJ</i> , 0, 11, e14895.	0.9	1
31894	GWAS and genetic and phenotypic correlations of plasma metabolites with complete blood count traits in healthy young pigs reveal implications for pig immune response. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	2
31896	Proteomic and Bioinformatic Tools to Identify Potential Hub Proteins in the Audiogenic Seizure-Prone Hamster GASH/Sal. <i>Diagnostics</i> , 2023, 13, 1048.	1.3	1
31897	The human sperm proteome—Toward a panel for male fertility testing. <i>Andrology</i> , 2023, 11, 1418-1436.	1.9	1
31898	Computational Analysis to Predict Drug Targets for the Therapeutic Management of <i>Mycobacterium avium</i> sub. <i>Paratuberculosis</i> . <i>Current Drug Discovery Technologies</i> , 2023, 20, .	0.6	0
31900	Dissecting the effect of ethylene in the transcriptional regulation of chilling treatment in grapevine leaves. <i>Plant Physiology and Biochemistry</i> , 2023, 196, 1084-1097.	2.8	2
31901	Network pharmacology and experimental validation to reveal the target of matriline against PRRSV. <i>IScience</i> , 2023, 26, 106371.	1.9	1
31903	Bioinformatics analysis and verification of <i>m6A</i> related genes based on the construction of keloid diagnostic model. <i>International Wound Journal</i> , 2023, 20, 2700-2717.	1.3	1
31904	Development and validation of a genomic nomogram based on a ceRNA network for comprehensive analysis of obstructive sleep apnea. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31906	Transcriptome and Co-Expression Network Analysis Reveals the Molecular Mechanism of Rice Root Systems in Response to Low-Nitrogen Conditions. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5290.	1.8	1
31907	Assessment of lipid metabolism-disrupting effects of non-phthalate plasticizer diisobutyl adipate through in silico and in vitro approaches. <i>Environmental Toxicology</i> , 0, .	2.1	1
31908	Characteristics of plant trait network and its influencing factors in impounded lakes and channel rivers of South-to-North Water Transfer Project, China. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31909	An integrated approach of high-performance liquid chromatography-mass spectrometry-based chemical profiling, network pharmacology, and molecular docking to reveal the potential mechanisms of Qishen Gubiao granules for treating coronavirus disease 2019. <i>Journal of Separation Science</i> , 2023, 46, .	1.3	4
31910	Network Pharmacology Prediction and Experimental Verification for Anti-Ferroptosis of Edaravone After Experimental Intracerebral Hemorrhage. <i>Molecular Neurobiology</i> , 0, .	1.9	1
31911	Global expression and functional analysis of human piRNAs during HSV-1 infection. <i>Virus Research</i> , 2023, 328, 199087.	1.1	3
31912	The genetic overlap between Alzheimer's disease, amyotrophic lateral sclerosis, Lewy body dementia, and Parkinson's disease. <i>Neurobiology of Aging</i> , 2023, 127, 99-112.	1.5	3
31913	Systematic review of molecular pathways in burn wound healing. <i>Burns</i> , 2023, 49, 1525-1533.	1.1	4
31915	The temporal transcriptomic signature of cartilage formation. <i>Nucleic Acids Research</i> , 2023, 51, 3590-3617.	6.5	8

#	ARTICLE	IF	CITATIONS
31917	Airway transcriptome networks identify susceptibility to frequent asthma exacerbations in children. <i>Journal of Allergy and Clinical Immunology</i> , 2023, 152, 73-83.	1.5	1
31918	Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. <i>Plant Communications</i> , 2023, , 100574.	3.6	1
31919	Genome-wide identification and characterization of tomato <i>SITFT6</i> genes and functional analysis of <i>SITFT6</i> under heat stress. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	4
31921	A learning experience elicits sex-dependent neurogenomic responses in <i>Bicyclus anynana</i> butterflies. <i>Molecular Ecology</i> , 2023, 32, 3220-3238.	2.0	2
31922	Combinatorial Network of Transcriptional and miRNA Regulation in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5356.	1.8	0
31923	Bioinformatics-Based Analysis of Key Genes in Steroid-Induced Osteonecrosis of the Femoral Head That Are Associated with Copper Metabolism. <i>Biomedicines</i> , 2023, 11, 873.	1.4	0
31924	Design and Computational Analysis of an MMP9 Inhibitor in Hypoxia-Induced Glioblastoma Multiforme. <i>ACS Omega</i> , 2023, 8, 10565-10590.	1.6	1
31925	Identification of CNGCs in <i>Glycine max</i> and Screening of Related Resistance Genes after <i>Fusarium solani</i> Infection. <i>Biology</i> , 2023, 12, 439.	1.3	1
31926	Network Pharmacology Combined with Experimental Validation Reveals the Anti-tumor Effect of <i>Duchesnea indica</i> against Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2023, 14, 505-518.	1.2	1
31927	Triap1 upregulation promotes escape from mitotic-slippage-induced G1 arrest. <i>Cell Reports</i> , 2023, 42, 112215.	2.9	0
31928	Single-cell analysis of lymphatic endothelial cell fate specification and differentiation during zebrafish development. <i>EMBO Journal</i> , 2023, 42, .	3.5	4
31929	Quantitative proteomic landscape of unstable atherosclerosis identifies molecular signatures and therapeutic targets for plaque stabilization. <i>Communications Biology</i> , 2023, 6, .	2.0	1
31930	Characteristic Analysis of Featured Genes Associated with Cholangiocarcinoma Progression. <i>Biomedicines</i> , 2023, 11, 847.	1.4	0
31931	Cholinesterase Inhibitors from an Endophytic Fungus <i>Aspergillus niveus</i> Fv-er401: Metabolomics, Isolation and Molecular Docking. <i>Molecules</i> , 2023, 28, 2559.	1.7	9
31932	Systematic identification of potential key microRNAs and circRNAs in the dorsal root ganglia of mice with sciatic nerve injury. <i>Frontiers in Molecular Neuroscience</i> , 0, 16, .	1.4	1
31933	Comprehensive analysis reveals the value of the expression of chromobox family members for bladder urothelial carcinoma prognosis. <i>Oncology Letters</i> , 2023, 25, .	0.8	2
31934	Plasma proteomics of SARS-CoV-2 infection and severity reveals impact on Alzheimer's and coronary disease pathways. <i>IScience</i> , 2023, 26, 106408.	1.9	4
31936	Honokiol, an inducer of sirtuin3, protects against nonsteroidal anti-inflammatory drug-induced gastric mucosal mitochondrial pathology, apoptosis and inflammatory tissue injury. <i>British Journal of Pharmacology</i> , 2023, 180, 2317-2340.	2.7	1

#	ARTICLE	IF	CITATIONS
31939	Network pharmacology and molecular modelling study of <i>Enhydra fluctuans</i> for the prediction of the molecular mechanisms involved in the amelioration of nephrolithiasis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 15400-15410.	2.0	5
31940	Genetic architecture of spatial electrical biomarkers for cardiac arrhythmia and relationship with cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	5.8	1
31941	Genome-wide analysis of genetic pleiotropy and causal genes across three age-related ocular disorders. <i>Human Genetics</i> , 2023, 142, 507-522.	1.8	3
31942	UV-induced mutagenesis of <i>Beauveria bassiana</i> ( <i>Hypocreales</i> ): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Management Science, 2023, 79, 2762-2779.	1.7	2
31943	Identification of long noncoding RNAs involved in plumule-vernalization of Chinese cabbage. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
31944	The potential value of cuproptosis in myocardial immune infiltration that occurs in pediatric congenital heart disease in response to surgery with cardiopulmonary bypass. <i>Immunity, Inflammation and Disease</i> , 2023, 11, .	1.3	0
31945	Engineered Mesenchymal Stem Cells Over-Expressing BDNF Protect the Brain from Traumatic Brain Injury-Induced Neuronal Death, Neurological Deficits, and Cognitive Impairments. <i>Pharmaceuticals</i> , 2023, 16, 436.	1.7	5
31946	RPflex: A Coarse-Grained Network Model for RNA Pocket Flexibility Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5497.	1.8	1
31951	MFGE8 links absorption of dietary fatty acids with catabolism of enterocyte lipid stores through HNF4 $\beta$ -dependent transcription of CES enzymes. <i>Cell Reports</i> , 2023, 42, 112249.	2.9	2
31952	Interactomics in plant defence: progress and opportunities. <i>Molecular Biology Reports</i> , 0, , .	1.0	1
31953	PDE3A and GSK3B as Atrial Fibrillation Susceptibility Genes in the Chinese Population via Bioinformatics and Genome-Wide Association Analysis. <i>Biomedicines</i> , 2023, 11, 908.	1.4	0
31954	Exploration of the Production of Three Thiodiketopiperazines by an Endophytic Fungal Strain of <i>Cophinforma mamane</i> . <i>Chemistry and Biodiversity</i> , 2023, 20, .	1.0	0
31955	Unraveling the Gene Regulatory Networks of the Global Regulators VeA and LaeA in <i>Aspergillus nidulans</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
31956	Estrogen receptor alpha deficiency in cardiomyocytes reprograms the heart-derived extracellular vesicle proteome and induces obesity in female mice. , 2023, 2, 268-289.		1
31958	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. <i>Nature Communications</i> , 2023, 14, .	5.8	12
31959	Human Polo-like Kinase Inhibitors as Antiplasmodials. <i>ACS Infectious Diseases</i> , 2023, 9, 1004-1021.	1.8	2
31960	Increasing lysergic acid levels for ergot alkaloid biosynthesis: Directing catalysis via the F-G loop of Clavine oxidases. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
31961	Dynamic changes in clinical biomarkers of cardiometabolic diseases by changes in exercise behavior, and network comparisons: a community-based prospective cohort study in Korea. <i>Epidemiology and Health</i> , 0, 45, e2023026.	0.8	0

#	ARTICLE	IF	CITATIONS
31962	Molecular mechanisms of Huanglian Jiedu decoction in treating Alzheimer's disease by regulating microbiome via network pharmacology and molecular docking analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
31963	Microbial network and composition changes according to tobacco varieties and interferes differently in black shank disease defense. <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	0
31964	Potential Toxic Mechanisms of Neonicotinoid Insecticides in Rice: Inhibiting Auxin-Mediated Signal Transduction. <i>Environmental Science &amp; Technology</i> , 2023, 57, 4852-4862.	4.6	10
31965	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
31966	The clusterin connectome: Emerging players in chondrocyte biology and putative exploratory biomarkers of osteoarthritis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
31967	Exploring Tabular Data Through Networks. <i>Lecture Notes in Computer Science</i> , 2023, , 195-200.	1.0	0
31968	The reciprocal changes in dominant species with complete metabolic functions explain the decoupling phenomenon of microbial taxonomic and functional composition in a grassland. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
31969	Moderate maternal nutrient reduction in pregnancy alters fatty acid oxidation and RNA splicing in the nonhuman primate fetal liver. <i>Journal of Developmental Origins of Health and Disease</i> , 2023, 14, 381-388.	0.7	2
31970	Proteomic and phosphoproteomic characteristics of the cortex, hippocampus, thalamus, lung, and kidney in COVID-19-infected female K18-hACE2 mice. <i>EBioMedicine</i> , 2023, 90, 104518.	2.7	1
31971	Integration of Human and Viral miRNAs in Epstein-Barr Virus-Associated Tumors and Implications for Drug Repurposing. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 93-108.	1.0	0
31972	An <i>in silico</i> approach to the identification of diagnostic and prognostic markers in low-grade gliomas. <i>PeerJ</i> , 0, 11, e15096.	0.9	1
31973	Identification of potential LncRNAs as papillary thyroid carcinoma biomarkers based on integrated bioinformatics analysis using TCGA and RNA sequencing data. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31974	MOPA: An integrative multi-omics pathway analysis method for measuring omics activity. <i>PLoS ONE</i> , 2023, 18, e0278272.	1.1	1
31975	Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. <i>Viruses</i> , 2023, 15, 758.	1.5	0
31976	Transcriptome analysis reveals defense-related genes and pathways during dodder ( <i>Cuscuta australis</i> ) parasitism on white clover ( <i>Trifolium repens</i> ). <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31977	Matured compost amendment improves compost nutrient content by changing the bacterial community during the composting of Chinese herb residues. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
31978	Genome-Wide Identification and Characterization of Bovine Fibroblast Growth Factor (FGF) Gene and Its Expression during Adipocyte Differentiation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5663.	1.8	2
31979	Network pharmacology predicts combinational effect of novel herbal pair consist of Ephedrae herba and Coicis semen on adipogenesis in 3T3-L1 cells. <i>PLoS ONE</i> , 2023, 18, e0282875.	1.1	3



#	ARTICLE	IF	CITATIONS
31980	In silico analysis to identify miR-1271-5p/PLCB4 (phospholipase C Beta 4) axis mediated oxaliplatin resistance in metastatic colorectal cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31981	Intratatumoral Bacteria Dysbiosis Is Associated with Human Papillary Thyroid Cancer and Correlated with Oncogenic Signaling Pathways. <i>Engineering</i> , 2023, , .	3.2	0
31982	Insights into the genomic evolution and the alkali tolerance mechanisms of <i>Agaricus sinodeliciosus</i> by comparative genomic and transcriptomic analyses. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
31983	Mining the potential therapeutic targets for <scp>COVID</scp> â€“19 infection in patients with severe burn injuries via bioinformatics analysis. <i>International Wound Journal</i> , 0, , .	1.3	0
31984	A central chaperone-like role for 14-3-3 proteins in human cells. <i>Molecular Cell</i> , 2023, 83, 974-993.e15.	4.5	16
31985	â€œIn the light of evolution:â€•keratins as exceptional tumor biomarkers. <i>PeerJ</i> , 0, 11, e15099.	0.9	5
31986	Comparison of gene expression between human and mouse iPSC-derived cardiomyocytes for stem cell therapies of cardiovascular defects via bioinformatic analysis. <i>Translational Medicine Communications</i> , 2023, 8, .	0.5	0
31987	Antiviral and antiâ€“inflammatory activity of natural compounds against Japanese encephalitis virus via inhibition of NS5 protein and regulation of key immune and inflammatory signaling pathways. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	2
31988	Demystifying the Role of Prognostic Biomarkers in Breast Cancer through Integrated Transcriptome and Pathway Enrichment Analyses. <i>Diagnostics</i> , 2023, 13, 1142.	1.3	1
31989	dupA+ <i>H. pylori</i> reduces diversity of gastric microbiome and increases risk of erosive gastritis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	3
31990	BZINB Model-Based Pathway Analysis and Module Identification Facilitates Integration of Microbiome and Metabolome Data. <i>Microorganisms</i> , 2023, 11, 766.	1.6	0
31991	State of the Art of the Molecular Biology of the Interaction between Cocoa and Witchesâ€™ Broom Disease: A Systematic Review. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5684.	1.8	5
31992	Rhizosphere Fungal Dynamics in Sugarcane during Different Growth Stages. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5701.	1.8	5
31993	Susceptibility and Permissivity of Zebrafish ( <i>Danio rerio</i> ) Larvae to Cypriniviruses. <i>Viruses</i> , 2023, 15, 768.	1.5	2
31994	NecroX Improves Polyhexamethylene Guanidineâ€“induced Lung Injury by Regulating Mitochondrial Oxidative Stress and Endoplasmic Reticulum Stress. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2023, 69, 57-72.	1.4	2
31995	Identification of predictors for neurological outcome after cardiac arrest in peripheral blood mononuclear cells through integrated bioinformatics analysis and machine learning. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	0
31996	A Comparative Study on Growth Performance, Body Composition, and Liver Tissue Metabolism Rearing on Soybean Lecithin-Enriched <i>Artemia Nauplii</i> and Microdiet in Rock Bream ( <i>Oplegnathus fasciatus</i> ) Larvae. <i>Aquaculture Nutrition</i> , 2023, 2023, 1-18.	1.1	2
31997	Identification of immune cells infiltrating in hippocampus and key genes associated with Alzheimerâ€™s disease. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	4

#	ARTICLE	IF	CITATIONS
31998	An integrated approach of network pharmacology, molecular docking, and experimental verification uncovers kaempferol as the effective modulator of HSD17B1 for treatment of endometrial cancer. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	7
31999	COL3A1, CXCL8, VCAN, THBS2, and COL1A2 are correlated with the onset of biliary atresia. <i>Medicine (United States)</i> , 2023, 102, e33299.	0.4	1
32000	Identification of a pediatric acute hypoxemic respiratory failure signature in peripheral blood leukocytes at 24 hours post-ICU admission with machine learning. <i>Frontiers in Pediatrics</i> , 0, 11, .	0.9	1
32001	FERMT1 Is a Prognostic Marker Involved in Immune Infiltration of Pancreatic Adenocarcinoma Correlating with m6A Modification and Necroptosis. <i>Genes</i> , 2023, 14, 734.	1.0	1
32002	Identification of new potential downstream transcriptional targets of the strigolactone pathway including glucosinolate biosynthesis. <i>Plant Direct</i> , 2023, 7, .	0.8	6
32004	Vacuolar protein sorting 35 (VPS35) acts as a tumor promoter via facilitating cell cycle progression in pancreatic ductal adenocarcinoma. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	0
32007	Xanthohumol improves cognitive impairment by regulating miRNA-532-3p/Mppd1 in ovariectomized mice. <i>Psychopharmacology</i> , 2023, 240, 1169-1178.	1.5	1
32008	SCL14 Inhibits the Functions of the NAC043â€œMYB61 Signaling Cascade to Reduce the Lignin Content in Autotetraploid <i>Populus hopeiensis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 5809.	1.8	6
32009	A multi-omic approach identifies an autism spectrum disorder (<scp>ASD</scp>) regulatory complex of functional epimutations in placentas from children born preterm. <i>Autism Research</i> , 2023, 16, 918-934.	2.1	0
32011	Differences in Whole-Blood Transcriptional Profiles in Inflammatory Bowel Disease Patients Responding to Vedolizumab Compared with Non-Responders. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5820.	1.8	2
32012	MicroRNAs in tear fluids predict underlying molecular changes associated with Alzheimerâ€™s disease. <i>Life Science Alliance</i> , 2023, 6, e202201757.	1.3	4
32013	Fire and Rhizosphere Effects on Bacterial Co-Occurrence Patterns. <i>Microorganisms</i> , 2023, 11, 790.	1.6	2
32014	Transcriptomic Modulation Reveals the Specific Cellular Response in Chinese Sea Bass ( <i>Lateolabrax</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Sciences</i> , 2023, 24, 5877.	1.8	5
32015	Exploration of the common genetic landscape of COVID-19 and male infertility. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
32016	Genome-wide characterization of ubiquitin-conjugating enzyme gene family explores its genetic effects on the oil content and yield of <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
32017	The Molecular Mechanism of the TEAD1 Gene and miR-410-5p Affect Embryonic Skeletal Muscle Development: A miRNA-Mediated ceRNA Network Analysis. <i>Cells</i> , 2023, 12, 943.	1.8	2
32022	Trends of therapy in the treatment of asthma. <i>Therapeutic Advances in Respiratory Disease</i> , 2023, 17, 175346662311557.	1.0	6
32023	Comparative transcriptome analysis of molecular mechanisms underlying adventitious root developments in Huangshan Bitter tea ( <i>Camellia gymnogyna</i> Chang) under red light quality. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2

#	ARTICLE	IF	CITATIONS
32024	LCN2 inhibits the BMP9-induced osteogenic differentiation through reducing Wnt/ $\beta$ -catenin signaling via interacting with LRP6 in mouse embryonic fibroblasts. <i>Current Stem Cell Research and Therapy</i> , 2023, 18, .	0.6	1
32025	Sexual behavior shapes male genitourinary microbiome composition. <i>Cell Reports Medicine</i> , 2023, 4, 100981.	3.3	4
32026	Lower respiratory tract microbiome composition and community interactions in smokers. <i>Access Microbiology</i> , 2023, 5, .	0.2	1
32027	The characteristics of soil microbial co-occurrence networks across a high-latitude forested wetland ecotone in China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
32028	Biosynthesis of 3,6-Dideoxy-heptoses for the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2023, 62, 1287-1297.	1.2	3
32029	Epigenetic dosage identifies two major and functionally distinct $\beta^2$ cell subtypes. <i>Cell Metabolism</i> , 2023, 35, 821-836.e7.	7.2	12
32030	Integrating network pharmacology approaches for the investigation of multi-target pharmacological mechanism of 6-shogaol against cervical cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 14135-14151.	2.0	6
32031	Identification of common molecular signatures of SARS-CoV-2 infection and its influence on acute kidney injury and chronic kidney disease. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
32034	Network-level analysis of ageing and its relationship with diseases and tissue regeneration in the mouse liver. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
32035	The eTM $\hat{c}$ miR858 $\hat{c}$ MYB62 $\hat{c}$ like module regulates anthocyanin biosynthesis under low $\hat{c}$ nitrogen conditions in <i>Malus spectabilis</i> . <i>New Phytologist</i> , 2023, 238, 2524-2544.	3.5	10
32036	Neutrophil Activation and Immune Thrombosis Profiles Persist in Convalescent COVID-19. <i>Journal of Clinical Immunology</i> , 2023, 43, 882-893.	2.0	1
32037	Longevity-Associated Transcription Factor <i>ATF7</i> Promotes Healthspan by Suppressing Cellular Senescence and Systemic Inflammation. , 2022, .		1
32038	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
32040	Bioinformatics-based investigation on the genetic influence between SARS-CoV-2 infections and idiopathic pulmonary fibrosis (IPF) diseases, and drug repurposing. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
32041	Accelerating network layouts using graph neural networks. <i>Nature Communications</i> , 2023, 14, .	5.8	3
32042	Downregulation of lncRNA <i>SNHG1</i> in hypoxia and stem cells is associated with poor disease prognosis in gliomas. <i>Cell Cycle</i> , 2023, 22, 1135-1153.	1.3	0
32044	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. <i>Microbiome</i> , 2023, 11, .	4.9	11
32045	Cellular proteomic profiling of esophageal epithelial cells cultured under physioxia or normoxia reveals high correlation of radiation response. <i>Radiation Medicine and Protection</i> , 2023, , .	0.4	0

#	ARTICLE	IF	CITATIONS
32046	Syntactic Network Analysis in Schizophrenia-Spectrum Disorders. <i>Schizophrenia Bulletin</i> , 2023, 49, S172-S182.	2.3	7
32048	Network Analysis Reveals the Molecular Bases of Statin Pleiotropy That Vary with Genetic Background. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
32049	Antileishmanial Activity of Cinnamic Acid Derivatives against <i>Leishmania infantum</i> . <i>Molecules</i> , 2023, 28, 2844.	1.7	2
32050	Construction and analysis of protein-protein interaction networks based on nuclear proteomics data of the desiccation-tolerant <i>Xerophyta schlechteri</i> leaves subjected to dehydration stress. <i>Communicative and Integrative Biology</i> , 2023, 16, .	0.6	1
32051	Positive and Relaxed Selective Pressures Have Both Strongly Influenced the Evolution of Cryonotothenioid Fishes during Their Radiation in the Freezing Southern Ocean. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	7
32052	Fungal Symbionts Generate Water-Saver and Water-Spender Plant Drought Strategies via Diverse Effects on Host Gene Expression. <i>Phytobiomes Journal</i> , 2023, 7, 172-183.	1.4	3
32053	Machine learning classifier approaches for predicting response to RTK-Type-III Inhibitors demonstrates high accuracy using transcriptomic signatures and ex vivo data. <i>Bioinformatics Advances</i> , 0, , .	0.9	0
32054	Full-length RNA sequencing reveals the mechanisms by which an TSWV-HCRV complex suppresses plant basal resistance. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
32055	Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in <i>Chrysanthemum</i> . <i>Genes</i> , 2023, 14, 766.	1.0	1
32056	Pneumolysin as a target for new therapies against pneumococcal infections: A systematic review. <i>PLoS ONE</i> , 2023, 18, e0282970.	1.1	5
32057	Identification and analysis of lignin biosynthesis genes related to fruit ripening and stress response in banana ( <i>Musa acuminata</i> L. AAA group, cv. Cavendish). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
32058	DDX58 expression promotes inflammation and growth arrest in Sertoli cells by stabilizing p65 mRNA in patients with Sertoli cell-only syndrome. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
32059	Integrative omics-analysis of lipid metabolism regulation by peroxisome proliferator-activated receptor $\alpha$ and $\beta$ agonists in male Atlantic cod. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	1
32060	Capture RIC-seq reveals positional rules of PTBP1-associated RNA loops in splicing regulation. <i>Molecular Cell</i> , 2023, 83, 1311-1327.e7.	4.5	11
32063	Systemic Anti-Inflammatory Therapy Aided by Curcumin-Laden Double-Headed Nanoparticles Combined with Injectable Long-Acting Insulin in a Rodent Model of Diabetes Eye Disease. <i>ACS Nano</i> , 2023, 17, 6857-6874.	7.3	6
32064	Centipeda minima active components and mechanisms in lung cancer. <i>BMC Complementary Medicine and Therapies</i> , 2023, 23, .	1.2	1
32065	Exploring the mechanism of action of herbal compounding in the treatment of myasthenia gravis based on network pharmacology. <i>Biotechnology and Genetic Engineering Reviews</i> , 0, , 1-16.	2.4	0
32066	Comparison of hepatic responses to glucose perturbation between healthy and obese mice based on the edge type of network structures. <i>Scientific Reports</i> , 2023, 13, .	1.6	1

#	ARTICLE	IF	CITATIONS
32067	Diel dynamics of multi-omics in elkhorn fern provide new insights into weak CAM photosynthesis. <i>Plant Communications</i> , 2023, 4, 100594.	3.6	0
32068	The m6A methylation landscape, molecular characterization and clinical relevance in prostate adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
32069	An Interaction Network Driven Approach for Identifying Cervical, Endometrial, Vulvar Carcinomic Biomarkers and Their Multi-targeted Inhibitory Agents from Few Widely Available Medicinal Plants. <i>Applied Biochemistry and Biotechnology</i> , 2023, 195, 6893-6912.	1.4	1
32070	Notch activation promotes bone metastasis via <sc>SPARC</sc> inhibition in adenoid cystic carcinoma. <i>Oral Diseases</i> , 0, , .	1.5	1
32071	Enterohemorrhagic <i>Escherichia coli</i> responds to gut microbiota metabolites by altering metabolism and activating stress responses. <i>Gut Microbes</i> , 2023, 15, .	4.3	1
32072	fRNC: Uncovering the dynamic and condition-specific RBP-ncRNA circuits from multi-omics data. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2276-2285.	1.9	0
32073	Identification of a stable major sucrose-related QTL and diagnostic marker for flavor improvement in peanut. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	3
32074	Mena regulates nesprin-2 to control actinâ€“nuclear lamina associations, trans-nuclear membrane signalling and gene expression. <i>Nature Communications</i> , 2023, 14, .	5.8	8
32077	NetDriller-V3: A Powerful Social Network Analysis Tool. , 2022, , .		0
32080	Urinary-derived extracellular vesicles reveal a distinct microRNA signature associated with the development and progression of Fabry nephropathy. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	0
32081	Immune and ionic mechanisms mediating the effect of dexamethasone in severe COVID-19. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
32082	DiaPASEF proteotype analysis indicates changes in cell growth and metabolic switch induced by caspaseâ€“9 inhibition in chondrogenic cells. <i>Proteomics</i> , 0, , .	1.3	1
32084	Integrated analysis of multiple transcriptomic data identifies ST8SIA6â€“AS1 and LINC01093 as potential biomarkers in HBVâ€“associated liver cancer. <i>Oncology Letters</i> , 2023, 25, .	0.8	0
32085	Integrated metabolomic and transcriptomic analysis reveals the mechanism underlying the accumulation of anthocyanins and other flavonoids in the flesh and skin of teinturier grapes. <i>Plant Physiology and Biochemistry</i> , 2023, 197, 107667.	2.8	3
32086	Upregulation of Biomarker Limd1 Was Correlated with Immune Infiltration in Doxorubicin-Related Cardiotoxicity. <i>Mediators of Inflammation</i> , 2023, 2023, 1-23.	1.4	0
32087	Stem cell-based modeling and single-cell multiomics reveal gene-regulatory mechanisms underlying human skeletal development. <i>Cell Reports</i> , 2023, 42, 112276.	2.9	4
32088	Photobiomodulation Reduces the Cytokine Storm Syndrome Associated with COVID-19 in the Zebrafish Model. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6104.	1.8	2
32089	Metabarcoding and Metabolomics Reveal the Effect of the Invasive Alien Tree <i>Miconia calvescens</i> DC. on Soil Diversity on the Tropical Island of Moâ€“orea (French Polynesia). <i>Microorganisms</i> , 2023, 11, 832.	1.6	4

#	ARTICLE	IF	CITATIONS
32090	Comprehensive Analysis of Sorafenib Druggable Targets on Differential Gene Expression and ceRNA Network in Hepatocellular Carcinoma. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2023, , .	0.6	0
32091	Ginsenoside Rk3 is a novel PI3K/AKT-targeting therapeutics agent that regulates autophagy and apoptosis in hepatocellular carcinoma. <i>Journal of Pharmaceutical Analysis</i> , 2023, 13, 463-482.	2.4	7
32092	Reductive Enzyme Cascades for Valorization of Polyethylene Terephthalate Deconstruction Products. <i>ACS Catalysis</i> , 2023, 13, 4778-4789.	5.5	11
32093	FZD7, Regulated by Non-CpG Methylation, Plays an Important Role in Immature Porcine Sertoli Cell Proliferation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6179.	1.8	2
32094	Risk stratification based on DNA damage-repair-related signature reflects the microenvironmental feature, metabolic status and therapeutic response of breast cancer. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
32095	Predictive investigation of idiopathic pulmonary fibrosis subtypes based on cellular senescence-related genes for disease treatment and management. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
32096	Proteomic Profiling of Colorectal Adenomas Identifies a Predictive Risk Signature for Development of Metachronous Advanced Colorectal Neoplasia. <i>Gastroenterology</i> , 2023, 165, 121-132.e5.	0.6	4
32098	Identification of Genomic Signatures in Bullmastiff Dogs Using Composite Selection Signals Analysis of 23 Purebred Clades. <i>Animals</i> , 2023, 13, 1149.	1.0	1
32099	The Related Mechanisms Predicted through Network-Based Pharmacological Analysis and the Anti-Inflammatory Effects of <i>Fraxinus rhynchophylla</i> Hance Bark on Contact Dermatitis in Mice. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6091.	1.8	1
32100	Proteome-wide lysine acetylation profiling to investigate the involvement of histone deacetylase <sc>HDA5</sc> in the salt stress response of <i>Arabidopsis</i> leaves. <i>Plant Journal</i> , 2023, 115, 275-292.	2.8	7
32101	Comparative Study of Transcriptome Profile and Immune-related Genes Network Associated with Intestinal Epithelial Tissue based on Microarray Data in Poultry with Coccidiosis. <i>Research on Animal Production</i> , 2022, 13, 154-162.	0.2	0
32102	Comparative transcriptome analysis reveals the phosphate starvation alleviation mechanism of phosphate accumulating <i>Pseudomonas putida</i> in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	4
32103	A novel feedback regulated loop of circRRM2-IGF2BP1-MYC promotes breast cancer metastasis. <i>Cancer Cell International</i> , 2023, 23, .	1.8	2
32104	Weighted gene co-expression network analysis revealed T cell differentiation associated with the age-related phenotypes in COVID-19 patients. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	2
32105	The genomic landscape of reference genomes of cultivated human gut bacteria. <i>Nature Communications</i> , 2023, 14, .	5.8	12
32106	Rieske Oxygenases and Other Ferredoxin-Dependent Enzymes: Electron Transfer Principles and Catalytic Capabilities. <i>ChemBioChem</i> , 2023, 24, .	1.3	2
32107	Combining quantitative trait locus mapping with multiomics profiling reveals genetic control of corn leaf aphid (<i>Rhopalosiphum maidis</i>) resistance in maize. <i>Journal of Experimental Botany</i> , 0, , .	2.4	1
32109	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	8



#	ARTICLE	IF	CITATIONS
32110	Physiological, transcriptome and co-expression network analysis of chlorophyll-deficient mutants in flue-cured tobacco. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
32111	Investigation of targets and anticancer mechanisms of covalently acting natural products by functional proteomics. <i>Acta Pharmacologica Sinica</i> , 2023, 44, 1701-1711.	2.8	2
32112	<i>Tweedle</i> gene family of <i>Drosophila suzukii</i> (Matsumura) larva enhances the basal tolerance to cold and hypoxia. <i>Pest Management Science</i> , 2023, 79, 3012-3021.	1.7	1
32113	Proteome integral solubility alteration high-throughput proteomics assay identifies Collectin-12 as a non-apoptotic microglial caspase-3 substrate. <i>Cell Death and Disease</i> , 2023, 14, .	2.7	1
32114	Lipid metabolism-related miRNAs with potential diagnostic roles in prostate cancer. <i>Lipids in Health and Disease</i> , 2023, 22, .	1.2	3
32115	Deciphering molecular mechanisms of SARS-CoV-2 pathogenesis and drug repurposing through GRN motifs: a comprehensive systems biology study. <i>3 Biotech</i> , 2023, 13, .	1.1	1
32116	Identification of FCN1 as a novel macrophage infiltration-associated biomarker for diagnosis of pediatric inflammatory bowel diseases. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	4
32117	Identification of Diagnostic Markers in Synovial Tissue of Osteoarthritis by Weighted Gene Coexpression Network. <i>Biochemical Genetics</i> , 2023, 61, 2056-2075.	0.8	1
32118	Proteomic analysis of sialoliths from calcified, lipid and mixed groups as a source of potential biomarkers of deposit formation in the salivary glands. <i>Clinical Proteomics</i> , 2023, 20, .	1.1	0
32119	Identification of potential ferroptosis hub genes in acute-on-chronic liver failure based on bioinformatics analysis and experimental verification. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	0
32120	Genome-wide identification of the TIFY family reveals JAZ subfamily function in response to hormone treatment in <i>Betula platyphylla</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
32123	Identification and validation of ferroptosis-related genes in patients infected with dengue virus: implication in the pathogenesis of DENV. <i>Virus Genes</i> , 2023, 59, 377-390.	0.7	4
32124	Anti-CHAC1 exosomes for nose-to-brain delivery of miR-760-3p in cerebral ischemia/reperfusion injury mice inhibiting neuron ferroptosis. <i>Journal of Nanobiotechnology</i> , 2023, 21, .	4.2	19
32125	Meta-analyses of host metagenomes from colorectal cancer patients reveal strong relationship between colorectal cancer-associated species. <i>Molecular Omics</i> , 2023, 19, 429-444.	1.4	1
32126	Circulating Metabolomic and Lipidomic Signatures Identify a Type 2 Diabetes Risk Profile in Low-Birth-Weight Men with Non-Alcoholic Fatty Liver Disease. <i>Nutrients</i> , 2023, 15, 1590.	1.7	2
32127	Interferon-inducible phospholipids govern IFITM3-dependent endosomal antiviral immunity. <i>EMBO Journal</i> , 2023, 42, .	3.5	4
32128	Transcriptome differential display of a drought-tolerant early flowering spineless mutant of safflower ( <i>Carthamus tinctorius</i> ) and identification of candidate genes. <i>Crop Science</i> , 0, , .	0.8	0
32129	Uncovering biomarkers for potential therapeutic targeting for COVID-19-related acute kidney injury: A bioinformatic approach. <i>Journal of Translational Critical Care Medicine</i> , 2023, 5, .	0.0	0

#	ARTICLE	IF	CITATIONS
32130	Deciphering the complete human-monkeypox virus interactome: Identifying immune responses and potential drug targets. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	5
32131	Bone Marrow Mesenchymal Stem Cells Expanded Inside the Nichoid Micro-Scaffold: a Focus on Anti-Inflammatory Response. <i>Regenerative Engineering and Translational Medicine</i> , 0, , .	1.6	0
32132	Clinical features and shared mechanisms of chronic gastritis and osteoporosis. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
32134	Integrated analysis of transcriptomics and metabolomics of peach under cold stress. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
32135	Integrated Analysis of lncRNA-mRNA Regulatory Networks Related to Lipid Metabolism in High-Oleic-Acid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6277.	1.8	1
32136	Systemic Alterations of Cancer Cells and Their Boost by Polyploidization: Unicellular Attractor (UCA) Model. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6196.	1.8	4
32137	Highlighting In Vitro the Role of Brain-like Endothelial Cells on the Maturation and Metabolism of Brain Pericytes by SWATH Proteomics. <i>Cells</i> , 2023, 12, 1010.	1.8	0
32138	Microporous membrane and culture medium affect in vitro seedling development of <i>Dalbergia nigra</i> (Vell.) Ex Benth. (Fabaceae) by modulation of the protein profile and accumulation of ethylene and CO <sub>2</sub> . <i>Plant Cell, Tissue and Organ Culture</i> , 2023, 153, 559-576.	1.2	1
32140	Genome-Scale Analysis of Cellular Restriction Factors That Inhibit Transgene Expression from Adeno-Associated Virus Vectors. <i>Journal of Virology</i> , 2023, 97, .	1.5	2
32141	Phylogenetic Analyses and Transcriptional Survey Reveal the Characteristics, Evolution, and Expression Profile of NBS-Type Resistance Genes in Papaya. <i>Agronomy</i> , 2023, 13, 970.	1.3	0
32142	Anticancer Effect of Active Component of <i>Astragalus Membranaceus</i> Combined with Olaparib on Ovarian Cancer Predicted by Network-Based Pharmacology. <i>Applied Biochemistry and Biotechnology</i> , 0, , .	1.4	1
32143	Identifying potential biomarkers for the diagnosis and treatment of IgA nephropathy based on bioinformatics analysis. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	0
32144	The 2020 derecho revealed limited overlap between maize genes associated with root lodging and root system architecture. <i>Plant Physiology</i> , 2023, 192, 2394-2403.	2.3	2
32145	Loss of the Maternal Effect Gene <i>Nlrp2</i> Alters the Transcriptome of Ovulated Mouse Oocytes and Impacts Expression of Histone Demethylase <i>KDM1B</i> . <i>Reproductive Sciences</i> , 0, , .	1.1	1
32146	Potential Targets and Mechanisms of Jiedu Quyu Ziyin Decoction for Treating SLE-GIOP: Based on Network Pharmacology and Molecular Docking. <i>Journal of Immunology Research</i> , 2023, 2023, 1-15.	0.9	1
32147	Pharmacological Mechanism of <i>Aucklandia Radix</i> against Gastric Ulcer Based on Network Pharmacology and In Vivo Experiment. <i>Medicina (Lithuania)</i> , 2023, 59, 666.	0.8	1
32148	Bioactive Compounds and Signaling Pathways of <i>Wolfiporia extensa</i> in Suppressing Inflammatory Response by Network Pharmacology. <i>Life</i> , 2023, 13, 893.	1.1	1
32149	PDGF-D-induced immunoproteasome activation and cell-cell interactions. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2405-2418.	1.9	1

#	ARTICLE	IF	CITATIONS
32150	Combining bioinformatics and machine learning to identify common mechanisms and biomarkers of chronic obstructive pulmonary disease and atrial fibrillation. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	3
32152	Distinct gene dysregulation patterns herald precision medicine potentiality in systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2023, 136, 103025.	3.0	8
32153	Collagen Hydrogel Containing Polyethylenimineâ€“Gold Nanoparticles for Drug Release and Enhanced Beating Properties of Engineered Cardiac Tissues. <i>Advanced Healthcare Materials</i> , 2023, 12, .	3.9	14
32154	Urinary Metabolomics Identified Metabolic Perturbations Associated with Gutka, a Smokeless Form of Tobacco. <i>Chemical Research in Toxicology</i> , 2023, 36, 669-684.	1.7	0
32156	The Identification of Potential Drugs for Dengue Hemorrhagic Fever: Network-Based Drug Reprofilng Study. <i>JMIR Bioinformatics and Biotechnology</i> , 0, 4, e37306.	0.4	0
32158	Molecular mechanism study and tumor heterogeneity of Chinese angelica and Fructus aurantii in the treatment of colorectal cancer through computational and molecular dynamics. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	2
32159	Downregulated annexin A1 expression correlates with poor prognosis, metastasis, and immunosuppressive microenvironment in Ewingâ€™s sarcoma. <i>Aging</i> , 2023, 15, 2321-2346.	1.4	0
32160	Soil conditions and the plant microbiome boost the accumulation of monoterpenes in the fruit of <i>Citrus reticulata</i> â€“Chachiâ€™. <i>Microbiome</i> , 2023, 11, .	4.9	14
32161	Identification of transcription factors related to diabetic tubulointerstitial injury. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	4
32162	The genome of <i>Lactuca saligna</i> , a wild relative of lettuce, provides insight into nonâ€“host resistance to the downy mildew <i>Bremia lactucae</i> . <i>Plant Journal</i> , 2023, 115, 108-126.	2.8	2
32164	The inhibitory role of microRNA-141-3p in human cutaneous melanoma growth and metastasis through the fibroblast growth factor 13-mediated mitogen-activated protein kinase axis. <i>Melanoma Research</i> , 0, Publish Ahead of Print, .	0.6	0
32165	Transcriptomic analysis reveals shared gene signatures and molecular mechanisms between obesity and periodontitis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
32166	Comprehensive analysis of the expression and prognosis for RAI2: A promising biomarker in breast cancer. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
32167	Use of pain-related gene features to predict depression by support vector machine model in patients with fibromyalgia. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
32168	Molecular targets of metformin against ovarian cancer based on network pharmacology. <i>Chemical Biology and Drug Design</i> , 0, , .	1.5	0
32169	Bioinformatics screening of colorectal-cancer causing molecular signatures through gene expression profiles to discover therapeutic targets and candidate agents. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	5
32172	Generating Functional and Highly Proliferative Melanocytes Derived from Human Pluripotent Stem Cells: A Promising Tool for Biotherapeutic Approaches to Treat Skin Pigmentation Disorders. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6398.	1.8	0
32173	Gene enrichment and co-expression analysis shed light on transcriptional responses to <i>Ralstonia solanacearum</i> in tomato. <i>BMC Genomics</i> , 2023, 24, .	1.2	2

#	ARTICLE	IF	CITATIONS
32176	Transcriptome Analysis Reveals the Profile of Long Non-Coding RNAs during Myogenic Differentiation in Goats. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6370.	1.8	0
32177	Tobacco Alkaloid Assessment in a DSS-Induced Colitis Mouse Model with a Fully Humanized Immune System. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6419.	1.8	0
32178	Development and validation of a novel defined mutation classifier based on Lasso logistic regression for predicting the overall survival of immune checkpoint inhibitor therapy in renal cell carcinoma. <i>Translational Andrology and Urology</i> , 2023, 12, 406-424.	0.6	0
32179	Infection strategies of different chytrids in a diatom spring bloom. <i>Freshwater Biology</i> , 2023, 68, 972-986.	1.2	2
32180	Identifying diseases associated with Post-COVID syndrome through an integrated network biology approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2024, 42, 652-671.	2.0	2
32181	NGS-based profiling identifies miRNAs and pathways dysregulated in cisplatin-resistant esophageal cancer cells. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
32182	Regulatory Networks of lncRNAs, miRNAs, and mRNAs in Response to Heat Stress in Wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	1
32183	p21 facilitates chronic lung inflammation via epithelial and endothelial cells. <i>Aging</i> , 2023, 15, 2395-2417.	1.4	0
32184	Potential molecular mechanisms of Erlongjiaonang action in idiopathic sudden hearing loss: A network pharmacology and molecular docking analyses. <i>Frontiers in Neurology</i> , 0, 14, .	1.1	1
32185	Spermiogenesis alterations in the absence of CTCF revealed by single cell RNA sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
32186	The Secretome of Parental and Bone Metastatic Breast Cancer Elicits Distinct Effects in Human Osteoclast Activity after Activation of $\beta_2$ Adrenergic Signaling. <i>Biomolecules</i> , 2023, 13, 622.	1.8	1
32187	Linking trait network parameters with plant growth across light gradients and seasons. <i>Functional Ecology</i> , 2023, 37, 1732-1746.	1.7	9
32188	Human thymopoiesis produces polyspecific CD8+ $\beta_2$ T cells responding to multiple viral antigens. <i>ELife</i> , 0, 12, .	2.8	6
32189	Inferring Gene Regulatory Networks from RNA-seq Data Using Kernel Classification. <i>Biology</i> , 2023, 12, 518.	1.3	1
32190	Comprehensive chemical profiling and quantitative analysis of ethnic Yi medicine Miao-Fu-Zhi-Tong granules using UHPLC-MS/MS. <i>Chinese Journal of Natural Medicines</i> , 2023, 21, 214-225.	0.7	2
32191	Novel Transcriptomic Interactomes of Noncoding RNAs in the Heart under Altered Thyroid Hormonal States. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6560.	1.8	1
32192	The Bacterial Microbiome of the Coral Skeleton Algal Symbiont <i>Ostreobium</i> Shows Preferential Associations and Signatures of Phyllosymbiosis. <i>Microbial Ecology</i> , 0, , .	1.4	3
32193	Prognostic biomarkers and molecular pathways mediating <i>Helicobacter pylori</i> induced gastric cancer: a network-biology approach. <i>Genomics and Informatics</i> , 2023, 21, e8.	0.4	1

#	ARTICLE	IF	CITATIONS
32194	Global Transcriptomic Analyses Provide New Insight into the Molecular Mechanisms of Endocarp Formation and Development in Iron Walnut ( <i>Juglans sigillata</i> Dode). <i>International Journal of Molecular Sciences</i> , 2023, 24, 6543.	1.8	2
32195	Identification of the NAC Transcription Factor Family during Early Seed Development in <i>Akebia trifoliata</i> (Thunb.) Koidz. <i>Plants</i> , 2023, 12, 1518.	1.6	5
32196	Network Pharmacological Analysis and Experimental Validation of the Effect of <i>Smilacis Glabrae</i> Rhizoma on Gastrointestinal Motility Disorder. <i>Plants</i> , 2023, 12, 1509.	1.6	1
32197	Mechanism and Molecular Targets of a Water-Soluble Extract of <i>Artemisia annua</i> on the Treatment of Alzheimer's Disease Based on Network Pharmacology and Experimental Validation. <i>The American Journal of Chinese Medicine</i> , 2023, 51, 595-622.	1.5	1
32199	Mechanism of skin whitening through San-Bai decoction-induced tyrosinase inhibition and discovery of natural products targeting tyrosinase. <i>Medicine (United States)</i> , 2023, 102, e33420.	0.4	1
32200	A network pharmacology and molecular docking approach in the exploratory investigation of the biological mechanisms of lagundi ( <i>Vitex negundo</i> L.) compounds against COVID-19. <i>Genomics and Informatics</i> , 2023, 21, e4.	0.4	0
32201	Transcriptome profiling reveals transcriptional regulation of VISTA in T cell activation. <i>Molecular Immunology</i> , 2023, 157, 101-111.	1.0	2
32202	Runs of homozygosity and signatures of selection for number of oocytes and embryos in the Gir Indicine cattle. <i>Mammalian Genome</i> , 2023, 34, 482-496.	1.0	2
32203	Insight into the mechanism of DNA methylation and miRNA-mRNA regulatory network in ischemic stroke. <i>Mathematical Biosciences and Engineering</i> , 2023, 20, 10264-10283.	1.0	2
32204	Executable Network Models of Integrated Multiomics Data. <i>Journal of Proteome Research</i> , 2023, 22, 1546-1556.	1.8	4
32207	Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2023, 32, 3524-3540.	2.0	3
32209	V-Mapper: topological data analysis for high-dimensional data with velocity. <i>Nonlinear Theory and Its Applications IEICE</i> , 2023, 14, 92-105.	0.4	0
32210	The m6A-regulation and single cell effect pattern in sunitinib resistance on clear cell renal cell carcinoma: Identification and validation of targets. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	0
32211	Integration of proteomic data obtained from the saliva of children with caries through bioinformatic analysis. <i>Current Proteomics</i> , 2023, 20, .	0.1	0
32212	Molecules interact. But how strong and how much?. <i>BioEssays</i> , 2023, 45, .	1.2	4
32213	Pasture-finishing of bison improves animal metabolic health and potential health-promoting compounds in meat. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	2
32214	Extracellular Matrix and Protein Phosphorylation Dysregulation Related to Diabetes-Induced Erectile Dysfunction. <i>Andrologia</i> , 2023, 2023, 1-13.	1.0	0
32215	Glycosylation increases active site rigidity leading to improved enzyme stability and turnover. <i>FEBS Journal</i> , 2023, 290, 3812-3827.	2.2	5

#	ARTICLE	IF	CITATIONS
32216	Establishment of killer whale ( <i>Orcinus orca</i> ) primary fibroblast cell cultures and their transcriptomic responses to pollutant exposure. <i>Environment International</i> , 2023, 174, 107915.	4.8	2
32219	Analysis of exome data in a UK cohort of 603 patients with syndromic orofacial clefting identifies causal molecular pathways. <i>Human Molecular Genetics</i> , 0, , .	1.4	2
32220	Dynamics of inflammatory cytokine expression in bovine endometrial cells exposed to cow blood plasma small extracellular vesicles (sEV) may reflect high fertility. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
32221	Genome-wide DNA methylation profiling after Ayurveda intervention to bronchial asthmatics identifies differential methylation in several transcription factors with immune process related function. <i>Journal of Ayurveda and Integrative Medicine</i> , 2023, 14, 100692.	0.9	0
32222	GWAS across multiple environments and WGCNA suggest the involvement of <i>ZmARF23</i> in embryonic callus induction from immature maize embryos. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	7
32223	The Unusual Dominance of the Yeast Genus <i>Glaciozyma</i> in the Deeper Layer in an Antarctic Permafrost Core (Ad�lie Cove, Northern Victoria Land) Is Driven by Elemental Composition. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 435.	1.5	1
32224	Transcriptomic data meta-analysis reveals common and injury model specific gene expression changes in the regenerating zebrafish heart. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
32225	Altered Expression of <i>CYSLTR1</i> is Associated With Adverse Clinical Outcome in Triple Negative Breast Tumors: An <i>In Silico</i> Approach. <i>The Journal of Breast Health</i> , 2023, 19, 148-158.	0.4	0
32226	Identification of Bone Metastatic and Prognostic Alternative Splicing Signatures in Prostate Adenocarcinoma. <i>Biochemical Genetics</i> , 2023, 61, 2242-2259.	0.8	0
32227	Skeletal muscle gene expression dysregulation in long-term spaceflights and aging is clock-dependent. <i>Npj Microgravity</i> , 2023, 9, .	1.9	2
32228	Serum soluble mediators as prognostic biomarkers for morbidity, disease outcome, and late-relapsing hepatitis in yellow fever patients. <i>Clinical Immunology</i> , 2023, , 109321.	1.4	1
32229	Inter- and intraspecific phytochemical variation correlate with epiphytic flower and leaf bacterial communities. <i>Environmental Microbiology</i> , 2023, 25, 1624-1643.	1.8	3
32230	Network Pharmacologic Study of <i>Radix Pae-oniae Rubra</i> in the Treatment of Diabetes Retinopathy. <i>Advances in Clinical Medicine</i> , 2023, 13, 5002-5016.	0.0	0
32231	mIR-99a-5p and mIR-148a-3p as Candidate Molecular Biomarkers for the Survival of Lung Cancer Patients. , 2023, 52, 87-100.		0
32233	Smoking-related epigenetic modifications are associated with the prognosis and chemotherapeutics of patients with bladder cancer. <i>International Journal of Immunopathology and Pharmacology</i> , 2023, 37, 039463202311667.	1.0	1
32234	CircPVT1 promotes ER�positive breast tumorigenesis and drug resistance by targeting <i>ESR1</i> and MAVS. <i>EMBO Journal</i> , 2023, 42, .	3.5	17
32235	Allelic phenotype prediction of phenylketonuria based on the machine learning method. <i>Human Genomics</i> , 2023, 17, .	1.4	0
32236	Quantitative Proteomic Analysis Reveals apoE4-Dependent Phosphorylation of the Actin-Regulating Protein VASP. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100541.	2.5	3



#	ARTICLE	IF	CITATIONS
32237	Shared molecular signatures between coronavirus infection and neurodegenerative diseases provide targets for broad-spectrum drug development. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
32238	Dysregulation of murine long non-coding single cell transcriptome in non-alcoholic steatohepatitis and liver fibrosis. <i>Rna</i> , 0, , rna.079580.123.	1.6	2
32239	Anti-inflammatory potential of selective small compounds by targeting TNF- $\hat{\pm}$ & NF- $\kappa$ B signaling: a comprehensive molecular docking and simulation study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 13815-13828.	2.0	4
32245	A Systematic Review of Molecular Pathway Analysis of Drugs for Potential Use in Liver Cancer Treatment. , 2023, 2, 210-231.		0
32247	Investigation of shared genes and regulatory mechanisms associated with coronavirus disease 2019 and ischemic stroke. <i>Frontiers in Neurology</i> , 0, 14, .	1.1	1
32248	Hypoxia-inducible factor stabilisation-related lncRNAs in retinopathy of prematurity. <i>Journal of Obstetrics and Gynaecology</i> , 2023, 43, .	0.4	0
32249	Small RNA sequencing of circulating small extracellular vesicles microRNAs in patients with amyotrophic lateral sclerosis. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
32250	Vertically stratified methane, nitrogen and sulphur cycling and coupling mechanisms in mangrove sediment microbiomes. <i>Microbiome</i> , 2023, 11, .	4.9	7
32251	clusterMaker2: a major update to clusterMaker, a multi-algorithm clustering app for Cytoscape. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	3
32254	Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome. <i>Plant Cell Reports</i> , 0, , .	2.8	1
32255	Rewiring of miRNA-mRNA bipartite co-expression network as a novel way to understand the prostate cancer related players. <i>Systems Biology in Reproductive Medicine</i> , 0, , 1-12.	1.0	0
32256	lncRNA expression analysis by comparative transcriptomics among closely related poplars and their regulatory roles in response to salt stress. <i>Tree Physiology</i> , 2023, 43, 1233-1249.	1.4	2
32257	TnpB structure reveals minimal functional core of Cas12 nuclease family. <i>Nature</i> , 2023, 616, 384-389.	13.7	27
32258	Identification of Potential Drug Targets in Erythrocyte Invasion Pathway of <i>Plasmodium falciparum</i> . <i>Current Microbiology</i> , 2023, 80, .	1.0	1
32259	Graph Visualization: Alternative Models Inspired by Bioinformatics. <i>Sensors</i> , 2023, 23, 3747.	2.1	1
32260	Advanced Electronic and Optoelectronic Sensors, Applications, Modelling and Industry 5.0 Perspectives. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 4582.	1.3	7
32261	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats. <i>Nature Microbiology</i> , 2023, 8, 946-957.	5.9	15
32264	Nervous system-related gene regulatory networks and functional evolution of ETS proteins across species. <i>BioSystems</i> , 2023, 227-228, 104891.	0.9	1

#	ARTICLE	IF	CITATIONS
32267	Metabolite Analysis of Alternaria Mycotoxins by LC-MS/MS and Multiple Tools. <i>Molecules</i> , 2023, 28, 3258.	1.7	2
32268	Genome-wide association and transcriptome analysis provide the SNPs and molecular insights into the hypoxia tolerance in large yellow croaker ( <i>Larimichthys crocea</i> ). <i>Aquaculture</i> , 2023, 573, 739547.	1.7	2
32269	Soil organic carbon fraction accumulation and bacterial characteristics in curtilage soil: Effects of land conversion and land use. <i>PLoS ONE</i> , 2023, 18, e0283802.	1.1	0
32270	Nuclear translocation of cGAS orchestrates VEGF-A-mediated angiogenesis. <i>Cell Reports</i> , 2023, 42, 112328.	2.9	4
32271	Esearch3D: propagating gene expression in chromatin networks to illuminate active enhancers. <i>Nucleic Acids Research</i> , 0, , .	6.5	1
32272	Application of TraDIS to define the core essential genome of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>BMC Microbiology</i> , 2023, 23, .	1.3	1
32274	Ferroptosis Signature Shapes the Immune Profiles to Enhance the Response to Immune Checkpoint Inhibitors in Head and Neck Cancer. <i>Advanced Science</i> , 2023, 10, .	5.6	7
32275	Investigation on the mechanism of Ginkgo Folium in the treatment of Non-alcoholic Fatty Liver Disease by strategy of network pharmacology and molecular docking. <i>Technology and Health Care</i> , 2023, 31, 209-221.	0.5	2
32276	Study on mechanism of hepatoprotective effect of <i>Chrysanthemum morifolium</i> Ramat. based on metabolomics with network analysis and network pharmacology. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2023, 1222, 123711.	1.2	0
32277	Distinct maternal metabolites are associated with obesity and glucose-insulin axis in the first trimester of pregnancy. <i>International Journal of Obesity</i> , 0, , .	1.6	1
32278	Widespread RNA hypoediting in schizophrenia and its relevance to mitochondrial function. <i>Science Advances</i> , 2023, 9, .	4.7	5
32279	Identification of key genes and immune infiltration based on weighted gene co-expression network analysis in vestibular schwannoma. <i>Medicine (United States)</i> , 2023, 102, e33470.	0.4	0
32280	Transcriptome and Anatomical Comparisons Reveal the Effects of Methyl Jasmonate on the Seed Development of <i>Camellia oleifera</i> . <i>Journal of Agricultural and Food Chemistry</i> , 0, , .	2.4	1
32281	Amplification of protease-activated receptors signaling in sporadic cerebral cavernous malformation endothelial cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2023, 1870, 119474.	1.9	0
32282	Standardization and Interpretation of RNA-sequencing for Transplantation. <i>Transplantation</i> , 2023, 107, 2155-2167.	0.5	3
32283	Structure-based molecular networking, molecular docking, dynamics simulation and pharmacokinetic studies of <i>Oloxololone</i> for identification of potential inhibitors against selected cancer targets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2024, 42, 1110-1125.	2.0	0
32285	Tear film microbiome in Sjogren's and non-Sjogren's aqueous deficiency dry eye. <i>Indian Journal of Ophthalmology</i> , 2023, 71, 1566-1573.	0.5	1
32288	Identification and tracking of HTLV-1-infected T cell clones in virus-associated neurologic disease. <i>JCI Insight</i> , 2023, 8, .	2.3	2

#	ARTICLE	IF	CITATIONS
32289	Genome-Wide Meta-Analysis Identifies Multiple Novel Rare Variants to Predict Common Human Infectious Diseases Risk. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7006.	1.8	1
32290	Identification of RPD3/HDA1 Family Genes in Sugar Beet and Response to Abiotic Stresses. <i>Sugar Tech</i> , 2023, 25, 834-845.	0.9	2
32291	Identification of Long Intergenic Noncoding RNAs in <i>Rhizoctonia cerealis</i> following Inoculation of Wheat. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
32293	Bioinformatics and network pharmacology-based study to elucidate the multi-target pharmacological mechanism of the indigenous plants of Medina valley in treating HCV-related hepatocellular carcinoma. <i>Saudi Pharmaceutical Journal</i> , 2023, , .	1.2	3
32294	Mori fructus aqueous extracts attenuates liver injury by inhibiting ferroptosis via the Nrf2 pathway. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	5
32295	Sensory plastid-associated <i>PsBP DOMAIN-CONTAINING 3</i> triggers plant growth and defense-related epigenetic responses. <i>Plant Journal</i> , 0, , .	2.8	0
32296	Insights into microRNA regulation of flower coloration in a lily cultivar Vivian petal. <i>Ornamental Plant Research</i> , 2023, 3, 0-0.	0.2	0
32297	The effect of temperature and invasive alien predator on genetic and phenotypic variation in the damselfly <i>Ischnura elegans</i> : cross-latitude comparison. <i>Frontiers in Zoology</i> , 2023, 20, .	0.9	1
32298	Multi-omic characterization of the maize GPI synthesis mutant <i>gwt1</i> with defects in kernel development. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
32299	Population genomics reveals demographic history and selection signatures of hazelnut ( <i>Corylus</i> ). <i>Horticulture Research</i> , 0, , .	2.9	0
32300	Unrevealing of dysregulated hub genes linked with immune system and inflammatory signaling pathways in the pathogenesis of irritable bowel syndrome by system biology approaches. <i>Informatics in Medicine Unlocked</i> , 2023, 39, 101241.	1.9	1
32302	Identification of CLIC5 as a Prognostic Biomarker and Correlated Immunomodulator for Lung Adenocarcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, .	0.6	1
32303	The mature phyllosphere microbiome of grapevine is associated with resistance against <i>Plasmopara viticola</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
32305	A prognostic and immunological analysis of 7B-containing Kelch structural domain (KLHDC7B) in pan-cancer: a potential target for immunotherapy and survival. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 7857-7876.	1.2	1
32306	MicroRNAs-mediated regulation of the differentiation of dental pulp-derived mesenchymal stem cells: a systematic review and bioinformatic analysis. <i>Stem Cell Research and Therapy</i> , 2023, 14, .	2.4	1
32307	Targeting Essential Hypothetical Proteins of <i>Pseudomonas aeruginosa</i> PAO1 for Mining of Novel Therapeutics: An In Silico Approach. <i>BioMed Research International</i> , 2023, 2023, 1-28.	0.9	2
32308	VisWaterNet: A Python package for visualization of water distribution networks. <i>Journal of Open Source Software</i> , 2023, 8, 5139.	2.0	2
32309	SIR telomere silencing depends on nuclear envelope lipids and modulates sensitivity to a lysolipid. <i>Journal of Cell Biology</i> , 2023, 222, .	2.3	1

#	ARTICLE	IF	CITATIONS
32310	Activation of AMPK promotes cardiac differentiation by stimulating the autophagy pathway. <i>Journal of Cell Communication and Signaling</i> , 2023, 17, 939-955.	1.8	2
32311	Monkeypox virus: phylogenomics, host-pathogen interactome and mutational cascade. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
32314	Transcriptomics reveals the effects of NTRK1 on endoplasmic reticulum stress response-associated genes in human neuronal cell lines. <i>PeerJ</i> , 0, 11, e15219.	0.9	1
32315	Large-scale phage cultivation for commensal human gut bacteria. <i>Cell Host and Microbe</i> , 2023, 31, 665-677.e7.	5.1	10
32316	De novo full length transcriptome analysis of a naturally caffeine-free tea plant reveals specificity in secondary metabolic regulation. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
32317	Integrative analysis of HASMCs gene expression profile revealed the role of thrombin in the pathogenesis of atherosclerosis. <i>BMC Cardiovascular Disorders</i> , 2023, 23, .	0.7	2
32318	Plasma Exosomal Non-Coding RNA Profile Associated with Renal Damage Reveals Potential Therapeutic Targets in Lupus Nephritis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7088.	1.8	4
32320	Integrated LC-MS/MS and network pharmacology approach for predicting active ingredients and pharmacological mechanisms of <i>Tribulus terrestris</i> L. against cardiac diseases. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-16.	2.0	1
32321	Multimomics and spatial mapping characterizes human CD8 <sup>+</sup> T cell states in cancer. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	16
32322	Identifying a dynamic transcriptomic landscape of the cynomolgus macaque placenta during pregnancy at single-cell resolution. <i>Developmental Cell</i> , 2023, 58, 806-821.e7.	3.1	3
32323	Long-Term Transcriptomic Changes and Cardiomyocyte Hyperpolyploidy after Lactose Intolerance in Neonatal Rats. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7063.	1.8	2
32324	In-depth proteomic analysis of juvenile dermatomyositis serum reveals protein expression associated with muscle-specific autoantibodies. <i>Rheumatology</i> , 0, , .	0.9	0
32325	Coliphages of the human urinary microbiota. <i>PLoS ONE</i> , 2023, 18, e0283930.	1.1	1
32326	Identification of diagnostic biomarks and immune cell infiltration in ulcerative colitis. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
32327	Exercise training remodels inguinal white adipose tissue through adaptations in innervation, vascularization, and the extracellular matrix. <i>Cell Reports</i> , 2023, 42, 112392.	2.9	9
32328	Transcriptomic analysis identified SLC40A1 as a key iron metabolism-related gene in airway macrophages in childhood allergic asthma. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
32329	Connecting islet-specific hub genes and pathways in type 2 diabetes mellitus through the bioinformatics lens. , 2023, 36, 201177.		0
32330	Serum metabolic alterations in peritoneal dialysis patients with excessive daytime sleepiness. <i>Renal Failure</i> , 2023, 45, .	0.8	0

#	ARTICLE	IF	CITATIONS
32332	Graphene oxide exposure alters gut microbial community composition and metabolism in an in vitro human model. <i>NanoImpact</i> , 2023, 30, 100463.	2.4	4
32333	Mapping CircRNAâ€“miRNAâ€“mRNA regulatory axis identifies hsa_circ_0080942 and hsa_circ_0080135 as a potential theranostic agents for SARS-CoV-2 infection. <i>PLoS ONE</i> , 2023, 18, e0283589.	1.1	3
32334	Genomic and transcriptomic analyses support a silk gland origin of spider venom glands. <i>BMC Biology</i> , 2023, 21, .	1.7	5
32335	Identification of common candidate genes and pathways for Spina Bifida and Wilmâ€™s Tumor using an integrative bioinformatics analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2024, 42, 977-992.	2.0	0
32337	BABA-induced pathogen resistance: a multi-omics analysis of the tomato response reveals a hyper-receptive status involving ethylene. <i>Horticulture Research</i> , 2023, 10, .	2.9	1
32338	Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	4
32339	Genomic and metabolic analyses reveal antagonistic lanthipeptides in archaea. <i>Microbiome</i> , 2023, 11, .	4.9	4
32340	Sequence-Based Platforms for Discovering Biomarkers in Liquid Biopsy of Non-Small-Cell Lung Cancer. <i>Cancers</i> , 2023, 15, 2275.	1.7	3
32341	Molecular Docking and Network Pharmacology Interaction Analysis of Gingko Biloba (EGB761) Extract with Dual Target Inhibitory Mechanism in Alzheimerâ€™s Disease. <i>Journal of Alzheimer's Disease</i> , 2023, 93, 705-726.	1.2	3
32342	Macrophage-Induced Exacerbation of Nasopharyngeal Inflammatory Lymphocytes in COVID-19 Disease. <i>Covid</i> , 2023, 3, 567-591.	0.7	0
32343	Construction of an m6A-related lncRNA model for predicting prognosis and immunotherapy in patients with lung adenocarcinoma. <i>Medicine (United States)</i> , 2023, 102, e33530.	0.4	0
32344	Specific pupylation as IDentity reporter (SPIDER) for the identification of protein-biomolecule interactions. <i>Science China Life Sciences</i> , 0, , .	2.3	0
32345	Antidepressants amitriptyline, fluoxetine, and traditional Chinese medicine Xiaoyaosan caused alterations in gut DNA virome composition and function in rats exposed chronic unpredictable mild stress. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
32346	Identification and validation of chemokine system-related genes in idiopathic pulmonary fibrosis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
32347	Investigation of changes in DNA methylation associated with alterations in gene expression resulting in differences between lean and obese adipogenesis. <i>Genomics</i> , 2023, 115, 110623.	1.3	1
32348	Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Airâ€“Liquid Interface. <i>Viruses</i> , 2023, 15, 961.	1.5	0
32349	Identification of Differentially Expressed Genes and Molecular Pathways Involved in Osteoclastogenesis Using RNA-seq. <i>Genes</i> , 2023, 14, 916.	1.0	5
32350	From observational to actionable: rethinking omics in biologics production. <i>Trends in Biotechnology</i> , 2023, , .	4.9	0

#	ARTICLE	IF	CITATIONS
32351	Multi-omics analysis reveals a macrophage-related marker gene signature for prognostic prediction, immune landscape, genomic heterogeneity, and drug choices in prostate cancer. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
32352	Identification of Critical Modules and Biomarkers of Ulcerative Colitis by Using WGCNA. <i>Journal of Inflammation Research</i> , 0, Volume 16, 1611-1628.	1.6	2
32353	Identification of Common Dysregulated Genes in COVID-19 and Hypersensitivity Pneumonitis: A Systems Biology and Machine Learning Approach. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 205-214.	1.0	2
32354	Clinical features and molecular genetics associated with brain metastasis in suspected early-stage non-small cell lung cancer. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	1
32356	Drug Discovery in Canine Pyometra Disease Identified by Text Mining and Microarray Data Analysis. <i>BioMed Research International</i> , 2023, 2023, 1-11.	0.9	0
32358	Network Biology Analyses and Dynamic Modeling of Gene Regulatory Networks under Drought Stress Reveal Major Transcriptional Regulators in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7349.	1.8	4
32360	Secretome Screening of BRAFV600E-Mutated Colon Cancer Cells Resistant to Vemurafenib. <i>Biology</i> , 2023, 12, 608.	1.3	1
32361	Phosphorylation and stabilization of EZH2 by DCAF1/MprBP trigger aberrant gene silencing in colon cancer. <i>Nature Communications</i> , 2023, 14, .	5.8	6
32362	The diagnostic combination of serum circulating miR-488 and lncRNA AC018761 as biomarkers for hypopharyngeal squamous cell carcinoma (HPSCC). <i>Arabian Journal of Chemistry</i> , 2023, 16, 104909.	2.3	0
32364	Unexplored diversity and ecological functions of transposable phages. <i>ISME Journal</i> , 2023, 17, 1015-1028.	4.4	2
32365	A new window into fish welfare: A proteomic discovery study of stress biomarkers in the skin mucus of gilthead seabream ( <i>Sparus aurata</i> ). <i>Journal of Proteomics</i> , 2023, 281, 104904.	1.2	2
32366	Evolutionary analysis of the OSCA gene family in sunflower ( <i>Helianthus annuus</i> L.) and expression analysis under NaCl stress. <i>PeerJ</i> , 0, 11, e15089.	0.9	2
32367	MicroRNA Signatures in Cartilage Ageing and Osteoarthritis. <i>Biomedicines</i> , 2023, 11, 1189.	1.4	3
32368	m7Gâ€related genesâ€” <i>NCBP2</i> and <i>EIF4E3</i> determine immune contexture in head and neck squamous cell carcinoma by regulating <i>CCL4</i> / <i>CCL5</i> expression. <i>Molecular Carcinogenesis</i> , 2023, 62, 1091-1106.	1.3	4
32370	Integrated analysis of endoplasmic reticulum stress regulatorsâ€™™ expression identifies distinct subtypes of autism spectrum disorder. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	0
32371	Elucidating the Corneal Endothelial Cell Proliferation Capacity through an Interspecies Transcriptome Comparison. <i>Advanced Biology</i> , 0, , .	1.4	0
32372	The Î±-Synuclein Monomer May Have Different Misfolding Mechanisms in the Induction of Î±-Synuclein Fibrils with Different Polymorphs. <i>Biomolecules</i> , 2023, 13, 682.	1.8	0
32373	Proanthocyanidins Inhibit Osteoblast Apoptosis via the PI3K/AKT/Bcl-xL Pathway in the Treatment of Steroid-Induced Osteonecrosis of the Femoral Head in Rats. <i>Nutrients</i> , 2023, 15, 1936.	1.7	0



#	ARTICLE	IF	CITATIONS
32374	A systematic anti-diarrhoeal evaluation of a vegetable root <i>Begonia roxburghii</i> and its marker flavonoids against nonpathogenic and pathogenic diarrhoea. <i>Food Bioscience</i> , 2023, 53, 102672.	2.0	2
32375	Integrative analysis of TP53 mutations in lung adenocarcinoma for immunotherapies and prognosis. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
32376	Preserved correlation matrices pinpoint extracellular matrix organization as a critical factor in pancreatic ductal adenocarcinoma. <i>F1000Research</i> , 0, 12, 418.	0.8	0
32377	Dysregulation of hypoxia-inducible factor 1 $\alpha$ in the sympathetic nervous system accelerates diabetic cardiomyopathy. <i>Cardiovascular Diabetology</i> , 2023, 22, .	2.7	4
32378	FARSB serves as a novel hypomethylated and immune cell infiltration related prognostic biomarker in hepatocellular carcinoma. <i>Aging</i> , 0, , .	1.4	0
32379	microRNA-96 targets the INS/AKT/GLUT4 signaling axis: Association with and effect on diabetic retinopathy. <i>Heliyon</i> , 2023, 9, e15539.	1.4	3
32381	Serum proteome and metabolome uncover novel biomarkers for the assessment of disease activity and diagnosing of systemic lupus erythematosus. <i>Clinical Immunology</i> , 2023, 251, 109330.	1.4	3
32382	Dosage sensitivity to <i>Pumilio1</i> variants in the mouse brain reflects distinct molecular mechanisms. <i>EMBO Journal</i> , 2023, 42, .	3.5	1
32385	Comprehensive Interactome Mapping of the DNA Repair Scaffold SLX4 Using Proximity Labeling and Affinity Purification. <i>Journal of Proteome Research</i> , 2023, 22, 1660-1681.	1.8	1
32388	Metabolic alterations of the gut-liver axis induced by cholic acid contribute to hepatic steatosis in rats. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2023, 1868, 159319.	1.2	2
32389	Systematic Review of Nonsyndromic Craniosynostosis: Genomic Alterations and Impacted Signaling Pathways. <i>Plastic and Reconstructive Surgery</i> , 2024, 153, 383e-396e.	0.7	0
32390	Obesity-induced inflammation exacerbates clonal hematopoiesis. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	16
32391	Metabolic switch in the aging astrocyte supported via integrative approach comprising network and transcriptome analyses. <i>Aging</i> , 2023, 15, 9896-9912.	1.4	2
32392	Bioinformatics analysis of the pathogenic link between Epstein-Barr virus infection, systemic lupus erythematosus and diffuse large B cell lymphoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
32396	Integrated glycoproteomic characterization of clear cell renal cell carcinoma. <i>Cell Reports</i> , 2023, 42, 112409.	2.9	1
32397	Neuroprotective effects of photobiomodulation by hormesis on scopolamine induced neurodegenerative diseases of memory disorders in rats a paradigm shift. <i>Journal of Biophotonics</i> , 2023, 16, .	1.1	3
32399	Influence of plant domestication on plant-pollinator interactions: Floral attributes and floral visitor communities in wild and cultivated squash plants. <i>American Journal of Botany</i> , 2023, 110, .	0.8	1
32400	Meta-analysis of expression and the targeting of cell adhesion associated genes in nine cancer types – A one research lab re-evaluation. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2824-2836.	1.9	2

#	ARTICLE	IF	CITATIONS
32401	Integrated analysis of coexpression and a tumor-specific ceRNA network revealed a potential prognostic biomarker in breast cancer. <i>Translational Cancer Research</i> , 2023, .	0.4	0
32402	Attractor dynamics drives self-reproduction in protobiological catalytic networks. <i>Cell Reports Physical Science</i> , 2023, 4, 101384.	2.8	4
32403	Regulatory networks of hormone-involved transcription factors and their downstream pathways during somatic embryogenesis of <i>Arabidopsis thaliana</i> . <i>3 Biotech</i> , 2023, 13, .	1.1	0
32404	Identification of Hub Genes and Immune Infiltration in Non-alcoholic Fatty Liver Disease -Related Hepatocellular Carcinoma by Bioinformatics Analysis. , 2023, 34, 383-393.		0
32405	Meta-analysis of commonly mutated genes in leptomeningeal carcinomatosis. <i>PeerJ</i> , 0, 11, e15250.	0.9	1
32406	Whole transcriptome analysis of trifoliolate orange ( <i>Poncirus trifoliata</i> (L.) Raf.) under osmotic stress. <i>Scientia Horticulturae</i> , 2023, 317, 112045.	1.7	0
32407	Metagenomic and metatranscriptomic exploration of the Egyptian Red Sea sponge <i>Theonella</i> sp. associated microbial community. <i>Marine Genomics</i> , 2023, 70, 101032.	0.4	1
32409	The impact of metabolic endotoxaemia on the browning process in human adipocytes. <i>BMC Medicine</i> , 2023, 21, .	2.3	3
32410	Applying network and genetic analysis to the potato metabolome. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
32411	RWP-RK Domain 3 ( <i>OsRKD3</i> ) induces somatic embryogenesis in black rice. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
32412	De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar ( <i>Cedrus atlantica</i> ). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
32414	Mitochondrial DNA Supplementation of Oocytes Has Downstream Effects on the Transcriptional Profiles of <i>Sus scrofa</i> Adult Tissues with High mtDNA Copy Number. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7545.	1.8	1
32416	Effects of Atherogenic Factors on Endothelial Cells: Bioinformatics Analysis of Differentially Expressed Genes and Signaling Pathways. <i>Biomedicines</i> , 2023, 11, 1216.	1.4	0
32418	Combination of single-nucleus and bulk RNA-seq reveals the molecular mechanism of thalamus haemorrhage-induced central poststroke pain. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
32419	Mechanisms of action of Fu Fang Gang Liu liquid in treating condyloma acuminatum by network pharmacology and experimental validation. <i>BMC Complementary Medicine and Therapies</i> , 2023, 23, .	1.2	0
32420	A comparison of anatomic and cellular transcriptome structures across 40 human brain diseases. <i>PLoS Biology</i> , 2023, 21, e3002058.	2.6	11
32421	Genome-wide analyses of LATERAL ORGAN BOUNDARIES in cassava reveal the role of LBD47 in defence against bacterial blight. <i>PLoS ONE</i> , 2023, 18, e0282100.	1.1	2
32422	Co-expression network analysis of diverse wheat landraces reveals markers of early thermotolerance and a candidate master regulator of thermotolerance genes. <i>Plant Journal</i> , 2023, 115, 614-626.	2.8	2

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32423	Discovery of New Siderophores from a Marine <i>Streptomyces</i> sp. via Combined Metabolomics and Analysis of Iron-Chelating Activity. <i>Journal of Agricultural and Food Chemistry</i> , 0, , .	2.4	2
32424	An Operational Burden Issue: Deciding on a Corneal Recipient From the Corneal Transplant Wait List for Elective Corneal Transplant. <i>Experimental and Clinical Transplantation</i> , 0, , .	0.2	0
32425	Distribution and molecular evolution of the anti-CRISPR family AcrIF7. <i>PLoS Biology</i> , 2023, 21, e3002072.	2.6	0
32426	Common factors among three types of cells aged in mice. <i>Biogerontology</i> , 0, , .	2.0	0
32427	Bioinformatics analysis combined with molecular dynamics simulation validation to elucidate the potential molecular mechanisms of Jianshen Decoction for treatment of osteoporotic fracture. <i>Medicine (United States)</i> , 2023, 102, e33610.	0.4	0
32428	Screening of feature genes related to immune and inflammatory responses in periodontitis. <i>BMC Oral Health</i> , 2023, 23, .	0.8	1
32429	Systems biology of autophagy in leishmanial infection and its diverse role in precision medicine. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	4
32430	Prognostic and Immunological Significance of the Molecular Subtypes and Risk Signatures Based on Cuproptosis in Hepatocellular Carcinoma. <i>Mediators of Inflammation</i> , 2023, 2023, 1-23.	1.4	3
32431	Serum amyloid A proteins reduce bone mass during mycobacterial infections. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
32433	Systems biology tools for the identification of potential drug targets and biological markers effective for cancer therapeutics. , 2023, , 259-292.		0
32434	Oscillation of Autophagy Induction under Cellular Stress and What Lies behind It, a Systems Biology Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7671.	1.8	2
32435	MyBrain-Seq: A Pipeline for MiRNA-Seq Data Analysis in Neuropsychiatric Disorders. <i>Biomedicines</i> , 2023, 11, 1230.	1.4	2
32436	Identification and validation of autophagy-related genes in Kawasaki disease. <i>Hereditas</i> , 2023, 160, .	0.5	1
32437	Comprehensive Analysis of NABP2 as a Prognostic Biomarker and Its Correlation with Immune Infiltration in Hepatocellular Carcinoma. <i>Journal of Inflammation Research</i> , 0, Volume 16, 1783-1804.	1.6	0
32438	Comparative Physiological and Transcriptomic Mechanisms of Defoliation in Cotton in Response to Thidiazuron versus Ethephon. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7590.	1.8	1
32439	A Pseudomonas Lysogenic Bacteriophage Crossing the Antarctic and Arctic, Representing a New Genus of Autographiviridae. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7662.	1.8	3
32440	Comprehensive analysis of circular RNAs in porcine small intestine epithelial cells associated with susceptibility to Escherichia coli F4ac diarrhea. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
32441	Screening and introduction of key cell cycle <i>microRNAs</i> deregulated in colorectal cancer by integrated bioinformatics analysis. <i>Chemical Biology and Drug Design</i> , 2023, 102, 137-152.	1.5	2

#	ARTICLE	IF	CITATIONS
32442	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
32444	Rhinovirus-induced epithelial RIG-I inflammasome suppresses antiviral immunity and promotes inflammation in asthma and COVID-19. <i>Nature Communications</i> , 2023, 14, .	5.8	8
32446	Single-Cell RNA Sequencing of <i>Sox17</i> -Expressing Lineages Reveals Distinct Gene Regulatory Networks and Dynamic Developmental Trajectories. <i>Stem Cells</i> , 2023, 41, 643-657.	1.4	1
32447	The hindgut microbiome contributes to host oxidative stress in postpartum dairy cows by affecting glutathione synthesis process. <i>Microbiome</i> , 2023, 11, .	4.9	9
32448	Elucidation of a Dearomatization Route in the Biosynthesis of Oxysporidinone Involving a TenA-like Cytochrome P450 Enzyme. <i>Angewandte Chemie</i> , 0, , .	1.6	1
32449	Elucidation of a Dearomatization Route in the Biosynthesis of Oxysporidinone Involving a TenA-like Cytochrome P450 Enzyme. <i>Angewandte Chemie - International Edition</i> , 2023, 62, .	7.2	2
32450	RRM2 as a novel prognostic and therapeutic target of NF1-associated MPNST. <i>Cellular Oncology (Dordrecht)</i> , 2023, 46, 1399-1413.	2.1	2
32451	In Silico Interactions of Natural and Synthetic Compounds with Key Proteins Involved in Alzheimer's Disease: Prospects for Designing New Therapeutics Compound. <i>Neurotoxicity Research</i> , 2023, 41, 408-430.	1.3	3
32452	<i>Populus</i> D-type cyclin gene <i>PsnCYCD1;1</i> accelerates cell division and participates in secondary growth of vascular bundles. <i>Journal of Experimental Botany</i> , 2023, 74, 4077-4092.	2.4	1
32454	Cardiac performance and heart gene network provide dynamic responses of bay scallop <i>Argopecten irradians</i> exposure to marine heatwaves. <i>Science of the Total Environment</i> , 2023, 882, 163594.	3.9	2
32455	Deciphering the protective effect of Buzhong Yiqi Decoction on osteoporotic fracture through network pharmacology and experimental validation. <i>Journal of Orthopaedic Surgery and Research</i> , 2023, 18, .	0.9	2
32456	Comparative Transcriptome Analysis Reveals the Mechanism Associated With Dynamic Changes in Meat Quality of the <i>Longissimus Thoracis</i> Muscle in Tibetan Sheep at Different Growth Stages. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
32637	Systems and network biology. , 2023, , 225-246.		0
32710	VisWaterNet: Visualization of Water Distribution Networks. , 2023, , .		0
32776	Unraveling Plant-Pathogen Interactions in Cereals Using RNA-seq. <i>Methods in Molecular Biology</i> , 2023, , 103-118.	0.4	0
32799	Metabolic Networks: Weighted Gene Correlation Network Analysis. <i>Methods in Molecular Biology</i> , 2023, , 317-325.	0.4	0
32831	Structure-based virtual screening. , 2023, , 239-262.		0
32834	Computational methods in the analysis of viral-host interactions. , 2023, , 285-302.		0

#	ARTICLE	IF	CITATIONS
32850	Dominating Sets in Protein-Protein Interaction Networks. , 2023, , 5-14.		0
32974	Visualizing Interaction Networks and Evidence in Biomedical Corpora. , 2023, , .		0
33111	A System Biology and Bioinformatics Approach to Determine the Molecular Signature, Core Ontologies, Functional Pathways, Drug Compounds in Between Stress and Type 2 Diabetes. Lecture Notes in Computer Science, 2023, , 320-331.	1.0	1
33113	Systematic Comparison of Advanced Network Analysis and Visualization of Lipidomics Data. Lecture Notes in Computer Science, 2023, , 378-389.	1.0	0
33288	Isolation of Chromatin Proteins by Genome Capture. Methods in Molecular Biology, 2023, , 91-99.	0.4	0
33317	éžâ-æ³Ĉä½"/â-æ³Ĉä½“éžç¼-çRNAsâœ”â;ăŽâ¿fè,ĈæĈ-æ»è°fèš,ăšă½œă,°è Šæ-æĈšç”Ÿç%œæ†â¿-ç%œæ-1éççš,ă½œç”		
33346	Proteomic analysis of cannabinoids in human oligodendrocyte cells. , 2023, , 407-416.		0
33356	Methodological Approaches to the Digital Analysis of Educational Media: Exploring Concepts of Europe and the Nation. Palgrave Studies in Educational Media, 2023, , 143-186.	0.3	0
33377	Functional analysis of a common BAG3 allele associated with protection from heart failure. , 2023, 2, 615-628.		2
33420	Network Pharmacology for Drug Repositioning in Anti-Alzheimerâ€™s Drug Development. Neuromethods, 2023, , 433-463.	0.2	0
33597	Network pharmacology, molecular docking, and molecular dynamics simulation to elucidate the mechanism of anti-aging action of Tinospora cordifolia. Molecular Diversity, 0, , .	2.1	4
33608	Proteinâ€™Protein Interaction Network Analysis Using NetworkX. Methods in Molecular Biology, 2023, , 457-467.	0.4	0
33611	Netzwerkanalyse. , 2023, , 389-422.		0
33615	Building Proteinâ€™Protein Interaction Graph Database Using Neo4j. Methods in Molecular Biology, 2023, , 469-479.	0.4	1
33617	Proteinâ€™Protein Interaction Network Exploration Using Cytoscape. Methods in Molecular Biology, 2023, , 419-427.	0.4	6
33620	Editorial: Computational and integrative approaches for developmental biology and molecular evolution. Frontiers in Genetics, 0, 14, .	1.1	0
33821	Finding Network Motifs: A comparative study between ILP and Symmetric Rank-One NMF. , 2023, , .		0
33940	Identification of potential inhibitor(s) against phospholipase A2 using a network pharmacology-based approach. , 2023, , 15-38.		0

#	ARTICLE	IF	CITATIONS
33965	Clinical application and pharmacological mechanism of polyherbal phytoformulations in breast cancer and depression treatment: review and network pharmacological analysis. Proceedings of the Indian National Science Academy, 2023, 89, 560-583.	0.5	0
33972	Host Transcriptome Analysis of Ferret Tissues Following Henipavirus Infection. Methods in Molecular Biology, 2023, , 281-299.	0.4	0
34009	Software for Drug Discovery and Protein Engineering: A Comparison Between the Alternatives and Recent Advancements in Computational Biology. , 2023, , 241-269.		0
34064	Machine Learning and Systems Level Insights into the Host-Pathogen Interactions of Post-infectious Reactive Arthritis. Algorithms for Intelligent Systems, 2023, , 729-744.	0.5	0
34524	A Robust and Clinically Applicable Sample Preparation Protocol for Urinary Extracellular Vesicle Isolation Suitable for Mass Spectrometry-Based Proteomics. Methods in Molecular Biology, 2023, , 235-251.	0.4	0
34542	A Practical Guide to Inferring Multi-Omics Networks in Plant Systems. Methods in Molecular Biology, 2023, , 233-257.	0.4	1
34578	Proposal of Knowledge Network Model Education for STEM/STEAM Education. Lecture Notes in Networks and Systems, 2024, , 571-579.	0.5	0
34613	Analysis of Differentially Expressed circRNAs and mRNAs and Their Correlation Network in Peripheral Blood of COVID-19 Patients. , 2023, , .		0
34683	Computational Genomics Approaches for Livestock Improvement and Management. Livestock Diseases and Management, 2023, , 351-376.	0.5	0
34704	Metabolomics and Transcriptomic Approach to Understand the Pathophysiology of Interstitial Lung Disease. , 2023, , 301-326.		0
34759	New Insights into Clinical Management for Sickle Cell Disease: Uncovering the Significant Pathways Affected by the Involvement of Sickle Cell Disease. Methods in Molecular Biology, 2024, , 121-132.	0.4	0
34763	Hubs and Bottlenecks in Protein-Protein Interaction Networks. Methods in Molecular Biology, 2024, , 227-248.	0.4	0
34765	Systems Biology Approach to Analyze Microarray Datasets for Identification of Disease-Causing Genes: Case Study of Oral Squamous Cell Carcinoma. Methods in Molecular Biology, 2024, , 13-31.	0.4	0
34769	Inference of Dynamic Growth Regulatory Network in Cancer Using High-Throughput Transcriptomic Data. Methods in Molecular Biology, 2024, , 51-77.	0.4	0
34776	Identification and Functional Annotation of circRNAs in Neuroblastoma Based on Bioinformatics. Lecture Notes in Computer Science, 2023, , 351-363.	1.0	0
34801	Genetic screening for pathogenic variants in type 2 diabetes of the Arab Gulf population: A systematic review and meta-analysis. International Journal of Diabetes in Developing Countries, 0, , .	0.3	0
34939	VegaProf: Profiling Vega Visualizations. , 2023, , .		1
35025	Actionable Environmental Science Through Social Media Platforms. , 2023, , 355-371.		0



#	ARTICLE	IF	CITATIONS
35105	How is Big Data reshaping preclinical aging research?. Lab Animal, 2023, 52, 289-314.	0.2	0
35191	Exploring the Archaeal Virosphere by Metagenomics. Methods in Molecular Biology, 2024, , 1-22.	0.4	0
35258	MOLECULAR GENETIC ANALYSIS OF THE B.AFZELLI, STRAIN ISOLATED IN THE DPR TERRITORY IN 2023. , 0, , .		0
35312	Applications and Future Perspectives of Computational Approaches in Livestock Animals. , 2023, , 279-309.		0
35313	AI-ML and System Biology for Drug Discovery in Livestock. , 2023, , 243-259.		0
35416	Prediction of COVID-19 Drug Targets Based on Protein Sequence and Network Properties Using Machine Learning Algorithm. Algorithms for Intelligent Systems, 2023, , 259-267.	0.5	0
35687	Atomistic Simulations of Sarcomere Proteins. Methods in Molecular Biology, 2024, , 27-41.	0.4	0
35780	ProtoGraph: A Non-Expert Toolkit for Creating Animated Graphs. , 2023, , .		0
35784	In-Silico Analysis for Differentially Expressed Genes in Multiple Sclerosis: Exploring Promising Biomarkers. , 2023, , .		0
35867	Bioinformatic and molecular docking studies of Zerumbone targets in breast cancer cells. AIP Conference Proceedings, 2023, , .	0.3	0
35964	Computational analysis in epithelial tissue regeneration. , 2024, , 443-459.		0
35992	Deciphering Stem Cell Pluripotency Using a Machine Learning Clustering Approach. Lecture Notes in Networks and Systems, 2024, , 375-388.	0.5	0
36098	Long COVID manifests with T cell dysregulation, inflammation and an uncoordinated adaptive immune response to SARS-CoV-2. Nature Immunology, 2024, 25, 218-225.	7.0	3
36162	Mechanism of Xuefu Zhuyu Tang in Myocardial Infarction Treatment Based on Network Pharmacology. , 2023, , .		0
36171	A network-based bioinformatic analysis for identifying potential repurposable active molecules in different types of human cancers. , 2023, , .		0
36204	Deciphering the complexities of stem cells through network biology approaches for their application in regenerative medicine. , 2024, , 289-302.		0
36207	Exploring imaging technologies and computational resources in stem cell research for regenerative medicine. , 2024, , 51-64.		0
36307	Deep Feature Selection Algorithm for Classification of Gastric Cancer Subtypes. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
36326	Genetics of Lipid Disorders. , 2023, , 163-195.		0
36392	Bioinformatics in Gene and Genome Analysis. , 2024, , 97-111.		0
36466	Visualizing Comparisons of Bill of Materials. , 2023, , .		0
36515	Protein-protein interaction network analysis for the identification of novel multi-target inhibitors and target miRNAs against Alzheimer's disease. <i>Advances in Protein Chemistry and Structural Biology</i> , 2024, , 405-467.	1.0	0
36604	Dual transcriptomics data and detection of host-pathogen interactions. , 2024, , 145-170.		0
36613	Biological interaction networks and their application for microbial pathogenesis. , 2024, , 131-143.		0
36657	Multi-omics Investigations in Endocrine Systems and Their Clinical Implications. <i>Advances in Experimental Medicine and Biology</i> , 2024, , 187-209.	0.8	0
36711	Integrated Multi-Omics Analysis and Validation in Yeast Model of Amyotrophic Lateral Sclerosis. <i>Methods in Molecular Biology</i> , 2024, , 397-419.	0.4	0
36712	In Silico Models to Validate Novel Blood-Based Biomarkers. <i>Methods in Molecular Biology</i> , 2024, , 321-344.	0.4	0
36716	Role of Network Pharmacology in Prediction of Mechanism of Neuroprotective Compounds. <i>Methods in Molecular Biology</i> , 2024, , 159-179.	0.4	0
36813	Computational aids for assessing bioactivities in phytochemical and natural products research. , 2024, , 357-393.		0
36837	Perspective Chapter: Integrated Network Pharmacology and Multiomics Approach to Elucidate the Repositioning of Fatal Food Toxins to Lifesaving Anticancer Drug. , 0, , .		0
36894	Librarians and Bioinformatics Communities Working Together to Advance Research and Instruction. , 2023, , 1070-1089.		0
36959	Glutathione Transferases. , 2024, , .		0