

BiNGO: a Cytoscape plugin to assess overrepresentation Biological Networks

Bioinformatics

21, 3448-3449

DOI: [10.1093/bioinformatics/bti551](https://doi.org/10.1093/bioinformatics/bti551)

Citation Report

#	ARTICLE	IF	CITATIONS
2	DISCOVERING REGULATED NETWORKS DURING HIV-1 LATENCY AND REACTIVATION. , 2005, , .		4
3	Systematic screening of polyphosphate (poly P) levels in yeast mutant cells reveals strong interdependence with primary metabolism. <i>Genome Biology</i> , 2006, 7, R109.	13.9	68
4	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006, 7, R80.	13.9	598
5	Identification of 491 proteins in the tear fluid proteome reveals a large number of proteases and protease inhibitors. <i>Genome Biology</i> , 2006, 7, R72.	13.9	344
6	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. <i>Nucleic Acids Research</i> , 2006, 34, W645-W650.	6.5	487
7	Effects of prostratin on Cyclin T1/P-TEFb function and the gene expression profile in primary resting CD4+T cells. <i>Retrovirology</i> , 2006, 3, 66.	0.9	74
8	[22] Visualizing Networks. <i>Methods in Enzymology</i> , 2006, 411, 408-421.	0.4	20
9	Microarray analysis of gene expression: considerations in data mining and statistical treatment. <i>Physiological Genomics</i> , 2006, 25, 355-363.	1.0	67
10	Proteomic and transcriptomic analysis of Arabidopsis seeds: molecular evidence for successive processing of seed proteins and its implication in the stress response to sulfur nutrition. <i>Plant Journal</i> , 2006, 48, 557-571.	2.8	75
11	Aggregation of bioinformatics data using Semantic Web technology. <i>Web Semantics</i> , 2006, 4, 216-221.	2.2	30
12	The Arabidopsis leaf as a model system for investigating the role of cell cycle regulation in organ growth. <i>Journal of Plant Research</i> , 2006, 119, 43-50.	1.2	51
13	Genomics of TGF- β 1 signaling in stem cell commitment and dendritic cell development. <i>Cellular Immunology</i> , 2006, 244, 116-120.	1.4	7
14	GOFFA: Gene Ontology For Functional Analysis – A FDA Gene Ontology Tool for Analysis of Genomic and Proteomic Data. <i>BMC Bioinformatics</i> , 2006, 7, S23.	1.2	51
15	Global similarity and local divergence in human and mouse gene co-expression networks. <i>BMC Evolutionary Biology</i> , 2006, 6, 70.	3.2	75
16	Genomic Variation in Rice: Genesis of Highly Polymorphic Linkage Blocks during Domestication. <i>PLoS Genetics</i> , 2006, 2, e199.	1.5	57
17	Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30.	1.5	102
18	Mapping Determinants of Gene Expression Plasticity by Genetical Genomics in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2006, 2, e222.	1.5	269
19	Identification of regulatory modules by co-clustering latent variable models: stem cell differentiation. <i>Bioinformatics</i> , 2006, 22, 2005-2011.	1.8	25

#	ARTICLE	IF	CITATIONS
20	A Network-based Analysis of Polyanion-binding Proteins Utilizing Yeast Protein Arrays. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2263-2278.	2.5	15
21	DAVID Bioinformatics Resources: expanded annotation database and novel algorithms to better extract biology from large gene lists. <i>Nucleic Acids Research</i> , 2007, 35, W169-W175.	6.5	1,934
22	Silencing of poly(ADP-ribose) polymerase in plants alters abiotic stress signal transduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15150-15155.	3.3	153
23	GeneTrail-advanced gene set enrichment analysis. <i>Nucleic Acids Research</i> , 2007, 35, W186-W192.	6.5	321
24	A genome-scale map of expression for a mouse brain section obtained using voxelation. <i>Physiological Genomics</i> , 2007, 30, 313-321.	1.0	27
25	Identification of Putative Androgen Receptor Interaction Protein Modules. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 252-271.	2.5	51
26	Enrichment or depletion of a GO category within a class of genes: which test?. <i>Bioinformatics</i> , 2007, 23, 401-407.	1.8	630
27	The Arabidopsis thaliana Homolog of Yeast BRE1 Has a Function in Cell Cycle Regulation during Early Leaf and Root Growth. <i>Plant Cell</i> , 2007, 19, 417-432.	3.1	168
28	Merging microarray cell synchronization experiments through curve alignment. <i>Bioinformatics</i> , 2007, 23, e64-e70.	1.8	33
29	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
30	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	2.5	359
31	GOLORize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. <i>Bioinformatics</i> , 2007, 23, 394-396.	1.8	105
32	Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data. , 2007, , 146-157.		6
33	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
34	PPAR β regulates the function of human dendritic cells primarily by altering lipid metabolism. <i>Blood</i> , 2007, 110, 3271-3280.	0.6	122
35	Gene Module Identification from Microarray Data Using Nonnegative Independent Component Analysis. <i>Gene Regulation and Systems Biology</i> , 2007, 1, 117762500700100.	2.3	6
36	Computational prediction of cancer-gene function. <i>Nature Reviews Cancer</i> , 2007, 7, 23-34.	12.8	81
38	The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists. <i>Genome Biology</i> , 2007, 8, R183.	13.9	2,105

#	ARTICLE	IF	CITATIONS
39	Decline of nucleotide excision repair capacity in aging <i>Caenorhabditis elegans</i> . <i>Genome Biology</i> , 2007, 8, R70.	13.9	93
40	Modular organization in the reductive evolution of protein-protein interaction networks. <i>Genome Biology</i> , 2007, 8, R94.	13.9	29
41	Genome mapping and expression analyses of human intronic noncoding RNAs reveal tissue-specific patterns and enrichment in genes related to regulation of transcription. <i>Genome Biology</i> , 2007, 8, R43.	13.9	209
42	Network visualization and network analysis. , 2007, 97, 245-275.		22
43	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2963-2972.	1.8	83
44	Genomic Organization and Evolutionary Conservation of Plant D-Type Cyclins. <i>Plant Physiology</i> , 2007, 145, 1558-1576.	2.3	52
45	Comparative proteome analysis of human epithelial ovarian cancer. <i>Proteome Science</i> , 2007, 5, 16.	0.7	47
46	Searching for master regulators of transcription in a human gene expression data set. <i>BMC Proceedings</i> , 2007, 1, S81.	1.8	3
47	Genes2Networks: Connecting Lists of Proteins by Using Background Literature-based Mammalian Networks. <i>Nature Precedings</i> , 2007, , .	0.1	0
48	Genes2Networks: Connecting Lists of Proteins by Using Background Literature-based Mammalian Networks. <i>Nature Precedings</i> , 2007, , .	0.1	0
49	ProbCD: enrichment analysis accounting for categorization uncertainty. <i>Nature Precedings</i> , 2007, , .	0.1	0
50	Androgen responsive intronic non-coding RNAs. <i>BMC Biology</i> , 2007, 5, 4.	1.7	73
51	Time-course study of histological and genetic patterns of differentiation in human engineered oral mucosa. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2007, 1, 350-359.	1.3	34
52	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
53	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	5.5	2,275
54	Genes2Networks: connecting lists of gene symbols using mammalian protein interactions databases. <i>BMC Bioinformatics</i> , 2007, 8, 372.	1.2	130
55	ProbCD: enrichment analysis accounting for categorization uncertainty. <i>BMC Bioinformatics</i> , 2007, 8, 383.	1.2	18
56	Inferring biological networks with output kernel trees. <i>BMC Bioinformatics</i> , 2007, 8, S4.	1.2	20

#	ARTICLE	IF	CITATIONS
57	Validating module network learning algorithms using simulated data. BMC Bioinformatics, 2007, 8, S5.	1.2	34
58	Genes involved in TGF β 1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. BMC Genomics, 2007, 8, 383.	1.2	20
59	A systems biology analysis of protein-protein interactions between yeast superoxide dismutases and DNA repair pathways. Free Radical Biology and Medicine, 2007, 43, 557-567.	1.3	22
60	Myocardial gene expression of matched hibernating and control tissue from patients with ischemic left ventricular dysfunction. Heart and Vessels, 2008, 23, 230-242.	0.5	4
61	PTP μ has a critical role in signaling transduction pathways and phosphoprotein network topology in red cells. Proteomics, 2008, 8, 4695-4708.	1.3	37
62	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. Proteomics, 2008, 8, 4534-4546.	1.3	93
63	Integrated Analysis of the Cerebrospinal Fluid Peptidome and Proteome. Journal of Proteome Research, 2008, 7, 386-399.	1.8	162
64	Mapping the human protein interactome. Cell Research, 2008, 18, 716-724.	5.7	44
65	Global monitoring of autumn gene expression within and among phenotypically divergent populations of Sitka spruce (<i>Picea sitchensis</i>). New Phytologist, 2008, 178, 103-122.	3.5	111
66	Comprehensive gene expression atlas for the <i>Arabidopsis</i> MAP kinase signalling pathways. New Phytologist, 2008, 179, 643-662.	3.5	105
67	Functional characterization of the <i>Arabidopsis</i> ubiquitin-specific protease gene family reveals specific role and redundancy of individual members in development. Plant Journal, 2008, 55, 844-856.	2.8	101
68	GeneTrailExpress: a web-based pipeline for the statistical evaluation of microarray experiments. BMC Bioinformatics, 2008, 9, 552.	1.2	69
69	A cross-species transcriptomics approach to identify genes involved in leaf development. BMC Genomics, 2008, 9, 589.	1.2	37
70	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. BMC Genomics, 2008, 9, 630.	1.2	55
71	Annotation of expressed sequence tags for the East African cichlid fish <i>Astatotilapia burtoni</i> and evolutionary analyses of cichlid ORFs. BMC Genomics, 2008, 9, 96.	1.2	48
72	Identification of a set of genes showing regionally enriched expression in the mouse brain. BMC Neuroscience, 2008, 9, 66.	0.8	25
73	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
74	Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. BMC Systems Biology, 2008, 2, 17.	3.0	121

#	ARTICLE	IF	CITATIONS
75	Extracting expression modules from perturbational gene expression compendia. BMC Systems Biology, 2008, 2, 33.	3.0	16
76	Relationships among carbohydrate intermediate metabolites and DNA damage and repair in yeast from a systems biology perspective. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 642, 43-56.	0.4	14
77	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. Journal of Proteome Research, 2008, 7, 5314-5326.	1.8	132
78	Perceiving molecular evolution processes in Escherichia coli by comprehensive metabolite and gene expression profiling. Genome Biology, 2008, 9, R72.	13.9	17
79	Exploring Biological Networks with Cytoscape Software. Current Protocols in Bioinformatics, 2008, 23, Unit 8.13.	25.8	60
81	A systems biology analysis of protein-protein interactions in the APOBEC family. Life Sciences, 2008, 83, 521-530.	2.0	2
82	The Expression Level of the Chromatin-Associated HMGB1 Protein Influences Growth, Stress Tolerance, and Transcriptome in Arabidopsis. Journal of Molecular Biology, 2008, 384, 9-21.	2.0	56
83	Canonical WNT/ β^2 -catenin signaling is required for ureteric branching. Developmental Biology, 2008, 317, 83-94.	0.9	141
84	Identification of dilated cardiomyopathy signature genes through gene expression and network data integration. Genomics, 2008, 92, 404-413.	1.3	43
85	Global Sequencing of Proteolytic Cleavage Sites in Apoptosis by Specific Labeling of Protein N Termini. Cell, 2008, 134, 866-876.	13.5	429
86	Application of a Translational Profiling Approach for the Comparative Analysis of CNS Cell Types. Cell, 2008, 135, 749-762.	13.5	807
87	Differential H3K4 Methylation Identifies Developmentally Poised Hematopoietic Genes. Developmental Cell, 2008, 14, 798-809.	3.1	134
88	Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context. IEEE Transactions on Visualization and Computer Graphics, 2008, 14, 1253-1260.	2.9	89
89	Cigarette smoke is an endothelial stressor and leads to cell cycle arrest. Atherosclerosis, 2008, 201, 298-305.	0.4	28
90	TiO ₂ -Based Phosphoproteomic Analysis of the Plasma Membrane and the Effects of Phosphatase Inhibitor Treatment. Journal of Proteome Research, 2008, 7, 3304-3313.	1.8	94
91	Network integration and graph analysis in mammalian molecular systems biology. IET Systems Biology, 2008, 2, 206-221.	0.8	42
92	Determining Nucleolar Association from Sequence by Leveraging Protein-Protein Interactions. Journal of Computational Biology, 2008, 15, 291-304.	0.8	5
93	Up-Regulation of Genes Related to the Ubiquitin-Proteasome System in the Brown Adipose Tissue of 24-h-Fasted Rats. Bioscience, Biotechnology and Biochemistry, 2008, 72, 139-148.	0.6	34

#	ARTICLE	IF	CITATIONS
94	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
95	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
96	Phosphoproteome Analysis of <i>E. coli</i> Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	2.5	385
97	Transcriptional Profiling of Mature Arabidopsis Trichomes Reveals That <i>NOECK</i> Encodes the MIXTA-Like Transcriptional Regulator MYB106. <i>Plant Physiology</i> , 2008, 148, 1583-1602.	2.3	205
98	Global Characterization of Cell-Specific Gene Expression through Fluorescence-Activated Sorting of Nuclei. <i>Plant Physiology</i> , 2008, 147, 30-40.	2.3	114
100	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. <i>Nucleic Acids Research</i> , 2008, 36, W452-W459.	6.5	81
101	A Specificity Map for the PDZ Domain Family. <i>PLoS Biology</i> , 2008, 6, e239.	2.6	410
102	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. <i>Genome Research</i> , 2008, 18, 1092-1099.	2.4	105
103	The Interaction Between Two Arabidopsis Polyadenylation Factor Subunits Involves an Evolutionarily-Conserved Motif and Has Implications for the Assembly and Function of the Polyadenylation Complex. <i>Protein and Peptide Letters</i> , 2008, 15, 76-88.	0.4	8
104	Genome-Wide Occupancy of SREBP1 and Its Partners NFY and SP1 Reveals Novel Functional Roles and Combinatorial Regulation of Distinct Classes of Genes. <i>PLoS Genetics</i> , 2008, 4, e1000133.	1.5	191
105	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. <i>PLoS Pathogens</i> , 2008, 4, e1000195.	2.1	191
106	Proteome-wide identification of poly(ADP-ribose) binding proteins and poly(ADP-ribose)-associated protein complexes. <i>Nucleic Acids Research</i> , 2008, 36, 6959-6976.	6.5	359
107	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
108	Mapping methyl jasmonate-mediated transcriptional reprogramming of metabolism and cell cycle progression in cultured <i>Arabidopsis</i> cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1380-1385.	3.3	367
109	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. <i>Nucleic Acids Research</i> , 2008, 36, W358-W363.	6.5	569
110	Knowledge environments representing molecular entities for the virtual physiological human. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3091-3110.	1.6	19
111	Ubiquitin E3 Ligase Ring1b/Rnf2 of Polycomb Repressive Complex 1 Contributes to Stable Maintenance of Mouse Embryonic Stem Cells. <i>PLoS ONE</i> , 2008, 3, e2235.	1.1	97
112	Yeast Features: Identifying Significant Features Shared Among Yeast Proteins for Functional Genomics. <i>Nature Precedings</i> , 2008, , .	0.1	0

#	ARTICLE	IF	CITATIONS
113	A Genome-Wide Characterization of MicroRNA Genes in Maize. PLoS Genetics, 2009, 5, e1000716.	1.5	318
114	Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. PLoS Genetics, 2009, 5, e1000740.	1.5	145
115	Network-Based Inference of Cancer Progression from Microarray Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 200-212.	1.9	22
116	ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. Bioinformatics, 2009, 25, 1091-1093.	1.8	5,348
117	CTFMinig: A Method to Predict Candidate Disease Genes Based on the Combined Network Topological Features Mining. , 2009, , .		1
118	Creation of the two isoforms of rodent NKG2D was driven by a B1 retrotransposon insertion. Nucleic Acids Research, 2009, 37, 3032-3043.	6.5	13
119	GS2: an efficiently computable measure of GO-based similarity of gene sets. Bioinformatics, 2009, 25, 1178-1184.	1.8	40
120	Evaluation Model for Breast Cancer Susceptibly Gene and its Implementation Using Cytoscape. , 2009, , .		2
121	Prediction of therapeutic mechanisms of tripterygium wilfordii in rheumatoid arthritis using text mining and network-based analysis. , 2009, , .		4
122	Phytochromes promote seedling light responses by inhibiting four negatively-acting phytochrome-interacting factors. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7660-7665.	3.3	412
123	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. Human Molecular Genetics, 2009, 18, 2078-2090.	1.4	371
124	Complex Networks. Studies in Computational Intelligence, 2009, , .	0.7	9
125	An integrated network approach identifies the isobutanol response network of <i>Escherichia coli</i> . Molecular Systems Biology, 2009, 5, 277.	3.2	175
126	Coexpression network based on natural variation in human gene expression reveals gene interactions and functions. Genome Research, 2009, 19, 1953-1962.	2.4	112
127	Clustering of Gene Expression Data Based on Shape Similarity. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 195712.	1.4	22
128	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap011.	1.4	18
129	Blocking the Metabolism of Starch Breakdown Products in Arabidopsis Leaves Triggers Chloroplast Degradation. Molecular Plant, 2009, 2, 1233-1246.	3.9	127
130	Variable locus length in the human genome leads to ascertainment bias in functional inference for non-coding elements. Bioinformatics, 2009, 25, 578-584.	1.8	22

#	ARTICLE	IF	CITATIONS
131	Sys-BodyFluid: a systematical database for human body fluid proteome research. Nucleic Acids Research, 2009, 37, D907-D912.	6.5	79
132	An Integrated Systems Analysis Implicates EGR1 Downregulation in Simian Immunodeficiency Virus Encephalitis-Induced Neural Dysfunction. Journal of Neuroscience, 2009, 29, 12467-12476.	1.7	37
133	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2009, 8, 1908-1920.	2.5	94
134	Graph Partitioning Method for Functional Module Detections of Protein Interaction Network. , 2009, , .		9
135	Novel Regulators of Fgf23 Expression and Mineralization in Hyp Bone. Molecular Endocrinology, 2009, 23, 1505-1518.	3.7	110
136	An Integrated Genomics Approach to Define Niche Establishment by <i>Rhodococcus fascians</i> . Plant Physiology, 2009, 149, 1366-1386.	2.3	81
137	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. Nucleic Acids Research, 2009, 37, W115-W121.	6.5	170
138	Function Annotation of an SBP-box Gene in Arabidopsis Based on Analysis of Co-expression Networks and Promoters. International Journal of Molecular Sciences, 2009, 10, 116-132.	1.8	55
139	A Regulated Response to Impaired Respiration Slows Behavioral Rates and Increases Lifespan in <i>Caenorhabditis elegans</i> . PLoS Genetics, 2009, 5, e1000450.	1.5	142
140	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. Science Signaling, 2009, 2, ra39.	1.6	171
141	A Truncated Arabidopsis NUCLEOSOME ASSEMBLY PROTEIN 1, AtNAP1;3T, Alters Plant Growth Responses to Abscicic Acid and Salt in the Atnap1;3-2 Mutant. Molecular Plant, 2009, 2, 688-699.	3.9	45
142	Human Cancer Protein-Protein Interaction Network: A Structural Perspective. PLoS Computational Biology, 2009, 5, e1000601.	1.5	202
143	Gene expression trends and protein features effectively complement each other in gene function prediction. Bioinformatics, 2009, 25, 322-330.	1.8	5
144	A Comparative Genomics, Network-Based Approach to Understanding Virulence in <i>Vibrio cholerae</i> . Journal of Bacteriology, 2009, 191, 6262-6272.	1.0	10
145	Genome-Wide Analysis of Genes Targeted by PHYTOCHROME INTERACTING FACTOR 3-LIKE5 during Seed Germination in <i>Arabidopsis</i> . Plant Cell, 2009, 21, 403-419.	3.1	336
146	MicroRNA-125b Promotes Neuronal Differentiation in Human Cells by Repressing Multiple Targets. Molecular and Cellular Biology, 2009, 29, 5290-5305.	1.1	260
147	Large-scale Proteomics Analysis of the Human Kinome. Molecular and Cellular Proteomics, 2009, 8, 1751-1764.	2.5	257
148	MMP-9 Sheds the β 2 Integrin Subunit (CD18) from Macrophages. Molecular and Cellular Proteomics, 2009, 8, 1044-1060.	2.5	76

#	ARTICLE	IF	CITATIONS
149	The human protein coevolution network. <i>Genome Research</i> , 2009, 19, 1861-1871.	2.4	48
150	Convergence of biomarkers, bioinformatics and nanotechnology for individualized cancer treatment. <i>Trends in Biotechnology</i> , 2009, 27, 350-358.	4.9	83
151	Aging defined by a chronologicâ€“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
152	Arabidopsis gene co-expression network and its functional modules. <i>BMC Bioinformatics</i> , 2009, 10, 346.	1.2	163
153	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. <i>BMC Bioinformatics</i> , 2009, 10, 48.	1.2	3,032
154	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. <i>BMC Genomics</i> , 2009, 10, 13.	1.2	80
155	Early iron-deficiency-induced transcriptional changes in Arabidopsis roots as revealed by microarray analyses. <i>BMC Genomics</i> , 2009, 10, 147.	1.2	160
156	Colorectal cancer cell-derived microvesicles are enriched in cell cycle-related mRNAs that promote proliferation of endothelial cells. <i>BMC Genomics</i> , 2009, 10, 556.	1.2	361
157	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. <i>BMC Genomics</i> , 2009, 10, 596.	1.2	11
158	Identification of tyrosine-phosphorylated proteins associated with metastasis and functional analysis of FER in human hepatocellular carcinoma cells. <i>BMC Cancer</i> , 2009, 9, 366.	1.1	63
159	Human synthetic lethal inference as potential anti-cancer target gene detection. <i>BMC Systems Biology</i> , 2009, 3, 116.	3.0	45
160	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
161	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
162	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
163	Formulating and testing hypotheses in functional genomics. <i>Artificial Intelligence in Medicine</i> , 2009, 45, 97-107.	3.8	21
164	Bioinformatics analysis of mass spectrometryâ€“based proteomics data sets. <i>FEBS Letters</i> , 2009, 583, 1703-1712.	1.3	147
165	Potential of deoxynivalenol to induce transcription factors in human hepatoma cells. <i>Molecular Nutrition and Food Research</i> , 2009, 53, 479-491.	1.5	27
166	Shotgun proteomic analysis of the microsomal fraction of eukaryotic cells using a twoâ€“dimensional reversedâ€“phaseâ€“ionâ€“pair reversedâ€“phase HPLC setup. <i>Journal of Separation Science</i> , 2009, 32, 1165-1174.	1.3	5

#	ARTICLE	IF	CITATIONS
167	Mass spectrometric and computational analysis of cytokine-induced alterations in the astrocyte secretome. <i>Proteomics</i> , 2009, 9, 768-782.	1.3	66
168	A three-way proteomics strategy allows differential analysis of yeast mitochondrial membrane protein complexes under anaerobic and aerobic conditions. <i>Proteomics</i> , 2009, 9, 4787-4798.	1.3	39
169	Comparative proteome and transcriptome analyses of embryonic stem cells during embryoid body-based differentiation. <i>Proteomics</i> , 2009, 9, 4859-4870.	1.3	58
170	High-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
171	Bioinformatic analysis of xenobiotic reactive metabolite target proteins and their interacting partners. <i>BMC Chemical Biology</i> , 2009, 9, 5.	1.6	20
172	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
173	Nitric oxide modulates ozone-induced cell death, hormone biosynthesis and gene expression in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2009, 58, 1-12.	2.8	182
174	Identification of the <i>Arabidopsis dry2/sqe1</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
175	Genetic architecture of mouse skin inflammation and tumour susceptibility. <i>Nature</i> , 2009, 458, 505-508.	13.7	120
176	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009, 6, 741-744.	9.0	141
177	Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009, 22, 2430-2437.	0.8	19
178	Comparative proteome analysis to explore p53 pathway disruption in head and neck carcinogenesis. <i>Journal of Proteomics</i> , 2009, 72, 803-814.	1.2	10
179	Chemical Inhibition of a Subset of <i>Arabidopsis thaliana</i> GSK3-like Kinases Activates Brassinosteroid Signaling. <i>Chemistry and Biology</i> , 2009, 16, 594-604.	6.2	240
180	Integrating Proteomic, Transcriptional, and Interactome Data Reveals Hidden Components of Signaling and Regulatory Networks. <i>Science Signaling</i> , 2009, 2, ra40.	1.6	161
181	Functional Profiling Methods in Cancer. <i>Methods in Molecular Biology</i> , 2009, 576, 363-374.	0.4	2
182	Transcriptional Changes and Oxidative Stress Associated with the Synergistic Interaction Between <i>Potato virus X</i> and <i>Potato virus Y</i> and Their Relationship with Symptom Expression. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1431-1444.	1.4	75
183	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
184	ATP-Sensitive K ⁺ Channel Knockout Induces Cardiac Proteome Remodeling Predictive of Heart Disease Susceptibility. <i>Journal of Proteome Research</i> , 2009, 8, 4823-4834.	1.8	33

#	ARTICLE	IF	CITATIONS
185	Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. <i>Nucleic Acids Research</i> , 2009, 37, 1-13.	6.5	13,313
186	Assessing the impact of network depth on the analysis of PPI networks: A case study. , 2009, , .		2
187	<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
188	Global Quantitative Proteomic Profiling through 18O-Labeling in Combination with MS/MS Spectra Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 3653-3665.	1.8	20
189	Enabling a systems biology approach to immunology: focus on innate immunity. <i>Trends in Immunology</i> , 2009, 30, 249-262.	2.9	122
190	Primary biliary cirrhosis is associated with altered hepatic microRNA expression. <i>Journal of Autoimmunity</i> , 2009, 32, 246-253.	3.0	191
191	Transcript Elongation Factor TFIIS Is Involved in Arabidopsis Seed Dormancy. <i>Journal of Molecular Biology</i> , 2009, 386, 598-611.	2.0	73
192	Global Map of SUMO Function Revealed by Protein-Protein Interaction and Genetic Networks. <i>Molecular Cell</i> , 2009, 33, 124-135.	4.5	109
193	Cytoscape: A Community-Based Framework for Network Modeling. <i>Methods in Molecular Biology</i> , 2009, 563, 219-239.	0.4	191
194	Transcription regulatory networks in <i>Caenorhabditis elegans</i> inferred through reverse-engineering of gene expression profiles constitute biological hypotheses for metazoan development. <i>Molecular BioSystems</i> , 2009, 5, 1817.	2.9	23
195	Protein Networks and Pathway Analysis. <i>Methods in Molecular Biology</i> , 2009, 563, v-vii.	0.4	33
196	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
197	Breaking the hierarchy - a new cluster selection mechanism for hierarchical clustering methods. <i>Algorithms for Molecular Biology</i> , 2009, 4, 12.	0.3	14
198	Expansion of the human mitochondrial proteome by intra- and inter-compartmental protein duplication. <i>Genome Biology</i> , 2009, 10, R135.	13.9	23
199	On the basic computational structure of gene regulatory networks. <i>Molecular BioSystems</i> , 2009, 5, 1617.	2.9	36
200	A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. , 2009, , .		0
201	Integration of signals from the B-cell antigen receptor and the IL-4 receptor leads to a cooperative shift in the cellular response axis. <i>Molecular BioSystems</i> , 2009, 5, 1661.	2.9	3
202	An automatic gene ontology software tool for bicluster and cluster comparisons. , 2009, , .		1

#	ARTICLE	IF	CITATIONS
203	Transcript stability in the protein interaction network of Escherichia coli. Molecular BioSystems, 2009, 5, 154-162.	2.9	14
204	Interaction Based Functional Clustering of Genomic Data. , 2009, , .		1
205	Isolation stress for 30 days alters hepatic gene expression profiles, especially with reference to lipid metabolism in mice. Physiological Genomics, 2009, 37, 79-87.	1.0	21
206	Increased Leaf Size: Different Means to an End. Plant Physiology, 2010, 153, 1261-1279.	2.3	222
207	The <i>RON1</i> / <i>FRY1</i> / <i>SAL1</i> Gene Is Required for Leaf Morphogenesis and Venation Patterning in Arabidopsis. Plant Physiology, 2010, 152, 1357-1372.	2.3	91
208	Quality improvement of rule-based gene group descriptions using information about GO terms importance occurring in premises of determined rules. International Journal of Applied Mathematics and Computer Science, 2010, 20, 555-570.	1.5	5
209	An introduction to effective use of enrichment analysis software. Human Genomics, 2010, 4, 202.	1.4	60
210	Protein-Protein Interaction Network and Gene Ontology. , 2010, , 159-169.		1
211	The use of network analyses for elucidating mechanisms in cardiovascular disease. Molecular BioSystems, 2010, 6, 289-304.	2.9	81
212	MIR152, MIR200B, and MIR338, human positional and functional neuroblastoma candidates, are involved in neuroblast differentiation and apoptosis. Journal of Molecular Medicine, 2010, 88, 1041-1053.	1.7	37
213	Relationship between endoplasmic reticulum- and Golgi-associated calcium homeostasis and 4-NQO-induced DNA repair in Saccharomyces cerevisiae. Archives of Microbiology, 2010, 192, 247-257.	1.0	6
214	Interaction networks as a tool to investigate the mechanisms of aging. Biogerontology, 2010, 11, 463-473.	2.0	14
215	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
216	A linear programming model based on network flow for pathway inference. Journal of Systems Science and Complexity, 2010, 23, 971-977.	1.6	0
217	Degradome sequencing reveals endogenous small RNA targets in rice (Oryza sativa L. ssp. indica). Frontiers in Biology, 2010, 5, 67-90.	0.7	152
218	Response network analysis of differential gene expression in human epithelial lung cells during avian influenza infections. BMC Bioinformatics, 2010, 11, 170.	1.2	18
219	GOAL: A software tool for assessing biological significance of genes groups. BMC Bioinformatics, 2010, 11, 229.	1.2	27
220	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. BMC Bioinformatics, 2010, 11, 265.	1.2	16

#	ARTICLE	IF	CITATIONS
221	PCA2GO: a new multivariate statistics based method to identify highly expressed GO-Terms. BMC Bioinformatics, 2010, 11, 336.	1.2	4
222	MetNetGE: interactive views of biological networks and ontologies. BMC Bioinformatics, 2010, 11, 469.	1.2	6
223	A temporal precedence based clustering method for gene expression microarray data. BMC Bioinformatics, 2010, 11, 68.	1.2	9
224	ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. BMC Bioinformatics, 2010, 11, S8.	1.2	7
225	Unified translation repression mechanism for microRNAs and upstream AUGs. BMC Genomics, 2010, 11, 155.	1.2	21
226	Response of the mosquito protein interaction network to dengue infection. BMC Genomics, 2010, 11, 380.	1.2	59
227	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in Arabidopsis thaliana. BMC Genomics, 2010, 11, 411.	1.2	21
228	A potential role for intragenic miRNAs on their hosts' interactome. BMC Genomics, 2010, 11, 533.	1.2	142
229	Gene prioritization in Type 2 Diabetes using domain interactions and network analysis. BMC Genomics, 2010, 11, 84.	1.2	24
230	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. BMC Genomics, 2010, 11, S4.	1.2	10
231	Investigation of PARP-1, PARP-2, and PARG interactomes by affinity-purification mass spectrometry. Proteome Science, 2010, 8, 22.	0.7	133
232	Dynamic functional modules in co-expressed protein interaction networks of dilated cardiomyopathy. BMC Systems Biology, 2010, 4, 138.	3.0	45
233	An information-flow-based model with dissipation, saturation and direction for active pathway inference. BMC Systems Biology, 2010, 4, 72.	3.0	5
234	Loss of Caenorhabditis elegans UNG-1 uracil-DNA glycosylase affects apoptosis in response to DNA damaging agents. DNA Repair, 2010, 9, 861-870.	1.3	17
235	Systems biology of human benzene exposure. Chemico-Biological Interactions, 2010, 184, 86-93.	1.7	82
236	Uncoupling JAK3 activation induces apoptosis in human lymphoid cancer cells via regulating critical survival pathways. FEBS Letters, 2010, 584, 1515-1520.	1.3	6
237	Quantitative proteome profiling of respiratory virus-infected lung epithelial cells. Journal of Proteomics, 2010, 73, 1680-1693.	1.2	48
238	eNelator: A simulation system for large-scale vulnerability analysis of species-, disease- and process-specific protein networks. Journal of Computational Science, 2010, 1, 197-205.	1.5	6

#	ARTICLE	IF	CITATIONS
239	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
240	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. <i>Proteomics</i> , 2010, 10, 1316-1327.	1.3	55
241	Undifferentiated Embryonic Cell Transcription Factor 1 Regulates ESC Chromatin Organization and Gene Expression. <i>Stem Cells</i> , 2010, 28, 1703-1714.	1.4	30
242	Genome-wide analysis of caesium and strontium accumulation in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2010, 27, 817-835.	0.8	15
243	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
244	A role for pectin de-methylesterification in a developmentally regulated growth acceleration in dark-grown <i>Arabidopsis</i> hypocotyls. <i>New Phytologist</i> , 2010, 188, 726-739.	3.5	147
245	Constitutive salicylic acid defences do not compromise seed yield, drought tolerance and water productivity in the <i>Arabidopsis</i> accession C24. <i>Plant, Cell and Environment</i> , 2010, 33, 1959-1973.	2.8	67
246	Supra-optimal expression of the cold-regulated <i>OsMyb4</i> transcription factor in transgenic rice changes the complexity of transcriptional network with major effects on stress tolerance and panicle development. <i>Plant, Cell and Environment</i> , 2010, 33, 2209-2230.	2.8	106
247	PHF8 mediates histone H4 lysine 20 demethylation events involved in cell cycle progression. <i>Nature</i> , 2010, 466, 508-512.	13.7	367
248	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
249	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
250	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
251	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
252	The ang3 mutation identified the ribosomal protein gene RPL5B with a role in cell expansion during organ growth. <i>Physiologia Plantarum</i> , 2010, 138, 91-101.	2.6	15
255	Module Network Inference from a Cancer Gene Expression Data Set Identifies MicroRNA Regulated Modules. <i>PLoS ONE</i> , 2010, 5, e10162.	1.1	46
256	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. <i>PLoS ONE</i> , 2010, 5, e13984.	1.1	1,883
257	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
258	Article Commentary: Rough Set Soft Computing Cancer Classification and Network: One Stone, Two Birds. <i>Cancer Informatics</i> , 2010, 9, CIN.S4874.	0.9	4

#	ARTICLE	IF	CITATIONS
259	Factor XIII-A is involved in the regulation of gene expression in alternatively activated human macrophages. <i>Thrombosis and Haemostasis</i> , 2010, 104, 709-717.	1.8	32
260	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
261	Cyclin D1/Cyclin-Dependent Kinase 4 Interacts with Filamin A and Affects the Migration and Invasion Potential of Breast Cancer Cells. <i>Cancer Research</i> , 2010, 70, 2105-2114.	0.4	144
262	CpG_ML: a novel approach for identifying functional CpG islands in mammalian genomes. <i>Nucleic Acids Research</i> , 2010, 38, e6-e6.	6.5	40
263	SHORT-ROOT and SCARECROW Regulate Leaf Growth in Arabidopsis by Stimulating S-Phase Progression of the Cell Cycle. <i>Plant Physiology</i> , 2010, 154, 1183-1195.	2.3	98
264	Measuring the physical cohesiveness of proteins using physical interaction enrichment. <i>Bioinformatics</i> , 2010, 26, 2737-2743.	1.8	18
265	Deciphering Membrane-Associated Molecular Processes in Target Tissue of Autoimmune Uveitis by Label-Free Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2292-2305.	2.5	181
266	Deep mRNA Sequencing for In Vivo Functional Analysis of Cardiac Transcriptional Regulators. <i>Circulation Research</i> , 2010, 106, 1459-1467.	2.0	76
267	VisualRTC: A New View on Lateral Root Initiation by Combining Specific Transcriptome Data Sets. <i>Plant Physiology</i> , 2010, 153, 34-40.	2.3	56
268	Mapping Plant Interactomes Using Literature Curated and Predicted Protein-Protein Interaction Data Sets. <i>Plant Cell</i> , 2010, 22, 997-1005.	3.1	33
269	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
270	A Poisson model for random multigraphs. <i>Bioinformatics</i> , 2010, 26, 2004-2011.	1.8	25
271	Multilevel support vector regression analysis to identify condition-specific regulatory networks. <i>Bioinformatics</i> , 2010, 26, 1416-1422.	1.8	20
273	Lipid Signaling in Plants. <i>Plant Cell Monographs</i> , 2010, , .	0.4	14
274	AtMetExpress Development: A Phytochemical Atlas of Arabidopsis Development. <i>Plant Physiology</i> , 2010, 152, 566-578.	2.3	161
275	Functional genomics and networks: new approaches in the extraction of complex gene modules. <i>Expert Review of Proteomics</i> , 2010, 7, 55-63.	1.3	10
276	A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series. <i>Journal of Computational Biology</i> , 2010, 17, 355-367.	0.8	84
277	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1314-1323.	2.5	225

#	ARTICLE	IF	CITATIONS
278	Application of Genomics and Bioinformatics Analysis in Exploratory Study of Functional Food. , 2010, , 61-72.		0
279	TreeHugger: A New Test for Enrichment of Gene Ontology Terms. INFORMS Journal on Computing, 2010, 22, 210-221.	1.0	4
280	Metabolomic, Transcriptional, Hormonal, and Signaling Cross-Talk in Superroot2. Molecular Plant, 2010, 3, 192-211.	3.9	38
281	The MCM-Binding Protein ETG1 Aids Sister Chromatid Cohesion Required for Postreplicative Homologous Recombination Repair. PLoS Genetics, 2010, 6, e1000817.	1.5	58
282	Prediction of a gene regulatory network linked to prostate cancer from gene expression, microRNA and clinical data. Bioinformatics, 2010, 26, i638-i644.	1.8	30
283	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. Genome Research, 2010, 20, 1689-1699.	2.4	309
284	Conservation and canalization of gene expression during angiosperm diversification accompany the origin and evolution of the flower. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22570-22575.	3.3	68
285	A Systemic Network for <i>Chlamydia pneumoniae</i> Entry into Human Cells. Journal of Bacteriology, 2010, 192, 2809-2815.	1.0	21
286	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. Journal of Proteome Research, 2010, 9, 3280-3289.	1.8	253
287	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
288	Identification and analysis of unitary pseudogenes: historic and contemporary gene losses in humans and other primates. Genome Biology, 2010, 11, R26.	13.9	150
290	Proteome scanning to predict PDZ domain interactions using support vector machines. BMC Bioinformatics, 2010, 11, 507.	1.2	33
291	Phosphoproteome Analysis of Rat L6 Myotubes Using Reversed-Phase C18 Prefractionation and Titanium Dioxide Enrichment. Journal of Proteome Research, 2010, 9, 777-788.	1.8	38
292	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
293	Plant Elongator regulates auxin-related genes during RNA polymerase II transcription elongation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1678-1683.	3.3	112
294	Changes in Protein Expression Profiles between a Low Phytic Acid Rice (<i>Oryza sativa</i> L. Ssp.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T69 Agricultural and Food Chemistry, 2010, 58, 6912-6922.	2.4	16
295	Association weight matrix for the genetic dissection of puberty in beef cattle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13642-13647.	3.3	127
296	Phospholipid Transfer Protein in Human Plasma Associates with Proteins Linked to Immunity and Inflammation. Biochemistry, 2010, 49, 7314-7322.	1.2	47

#	ARTICLE	IF	CITATIONS
297	Advanced Identification of Proteins in Uncharacterized Proteomes by Pulsed in Vivo Stable Isotope Labeling-based Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1157-1166.	2.5	45
298	Transcriptional Control of a Plant Stem Cell Niche. <i>Developmental Cell</i> , 2010, 18, 841-853.	3.1	221
299	Genome-wide Analysis of the Host Intracellular Network that Regulates Survival of <i>Mycobacterium tuberculosis</i> . <i>Cell</i> , 2010, 140, 731-743.	13.5	337
300	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	13.5	789
301	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650.	13.5	200
302	A Macrophage Sterol-Responsive Network Linked to Atherogenesis. <i>Cell Metabolism</i> , 2010, 11, 125-135.	7.2	69
303	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. <i>Science Signaling</i> , 2010, 3, rs3.	1.6	245
304	Hyperglycemia Alters the Schwann Cell Mitochondrial Proteome and Decreases Coupled Respiration in the Absence of Superoxide Production. <i>Journal of Proteome Research</i> , 2010, 9, 458-471.	1.8	56
305	agriGO: a GO analysis toolkit for the agricultural community. <i>Nucleic Acids Research</i> , 2010, 38, W64-W70.	6.5	2,289
306	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
308	Network inference and network response identification: moving genome-scale data to the next level of biological discovery. <i>Molecular BioSystems</i> , 2010, 6, 469-480.	2.9	41
309	Quantitative Proteome and Transcriptome Analysis of the Archaeon <i>Thermoplasma acidophilum</i> Cultured under Aerobic and Anaerobic Conditions. <i>Journal of Proteome Research</i> , 2010, 9, 4839-4850.	1.8	42
310	Methodologies and Results in Grapevine Research. , 2010, , .		20
311	Conserved developmental transcriptomes in evolutionarily divergent species. <i>Genome Biology</i> , 2010, 11, R35.	13.9	164
312	Proteomic Profiling of Early Life Stages of European Grayling (<i>Thymallus thymallus</i>). <i>Journal of Proteome Research</i> , 2010, 9, 4790-4800.	1.8	9
313	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3638-3646.	1.8	108
314	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. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2010, 23, 261-280.	0.7	74
315	Secretory pathway genes assessed by high-throughput microscopy and synthetic genetic array analysis. <i>Molecular BioSystems</i> , 2011, 7, 2589.	2.9	39

#	ARTICLE	IF	CITATIONS
316	FINDING GENOME-TRANSCRIPTOME-PHENOME ASSOCIATION WITH STRUCTURED ASSOCIATION MAPPING AND VISUALIZATION IN GENAMAP. , 2011, , .		3
317	FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6680-6685.	3.3	325
318	The <i>Arabidopsis thaliana</i> Checkpoint Kinase WEE1 Protects against Premature Vascular Differentiation during Replication Stress. Plant Cell, 2011, 23, 1435-1448.	3.1	81
319	Label-free Proteomics and Systems Biology Analysis of Mycobacterial Phagosomes in Dendritic Cells and Macrophages. Journal of Proteome Research, 2011, 10, 2425-2439.	1.8	19
320	Genome-Wide Analysis of MuDR-Related Transposable Elements Insertion Population in Maize. Acta Agronomica Sinica, 2011, 37, 772-777.	0.3	2
321	Integrating Omics Data for Signaling Pathways, Interactome Reconstruction, and Functional Analysis. Methods in Molecular Biology, 2011, 719, 415-433.	0.4	24
323	Visualizing and Characterizing In Vivo DNA-Binding Events and Direct Target Genes of Plant Transcription Factors. Methods in Molecular Biology, 2011, 754, 293-305.	0.4	6
324	Mass Spectrometry-Driven Proteomics: An Introduction. Methods in Molecular Biology, 2011, 753, 1-27.	0.4	6
325	Plant Transcription Factors. Methods in Molecular Biology, 2011, , .	0.4	5
327	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. Cancer Genetics, 2011, 204, 252-259.	0.2	12
328	BLBP-expression in astrocytes during experimental demyelination and in human multiple sclerosis lesions. Brain, Behavior, and Immunity, 2011, 25, 1554-1568.	2.0	69
329	Assembling global maps of cellular function through integrative analysis of physical and genetic networks. Nature Protocols, 2011, 6, 1308-1323.	5.5	23
330	Proteomics of Lipoprotein(a) identifies a protein complement associated with response to wounding. Journal of Proteomics, 2011, 74, 2881-2891.	1.2	54
331	Functional analysis of beef tenderness. Journal of Proteomics, 2011, 75, 352-365.	1.2	106
332	Comprehensive Gene Expression Analysis of Human Embryonic Stem Cells during Differentiation into Neural Cells. PLoS ONE, 2011, 6, e22856.	1.1	72
333	Improving reverse vaccinology with a machine learning approach. Vaccine, 2011, 29, 8156-8164.	1.7	52
334	Effects of pooling RNA from samples treated with different compounds for determining class specific biomarkers and processes in toxicogenomics. Toxicology in Vitro, 2011, 25, 1841-1847.	1.1	7
335	Cytoscape: Software for Visualization and Analysis of Biological Networks. Methods in Molecular Biology, 2011, 696, 291-303.	0.4	1,068

#	ARTICLE	IF	CITATION
336	Identification of 1463â€³12 in human gastric cancer cells and its potency as a diagnostic and prognostic biomarker. Proteomics, 2011, 11, 2423-2439.	1.3	38
337	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. Journal of Cell Biology, 2011, 192, 615-629.	2.3	439
338	The function of histamine receptor H4R in the brain revealed by interaction partners. Frontiers in Bioscience - Scholar, 2011, S3, 1058-1066.	0.8	4
339	Identify potential chronic heart failure related transcription factors by network analysis. African Journal of Microbiology Research, 2011, 5, 3862-3869.	0.4	4
340	Data Retrieval and Visualization for Setting Research Priorities in Biomedical Research. , 2011, , .		0
341	Comparative Transcriptome and Network Biology Analyses Demonstrate Antiproliferative and Hyperapoptotic Phenotypes in Human Keratoconus Corneas. , 2011, 52, 6181.		40
342	Seeking colorectal carcinoma related genes based on regulation network. African Journal of Pharmacy and Pharmacology, 2011, 5, 1467-1474.	0.2	0
343	Defining the Role of Essential Genes in Human Disease. PLoS ONE, 2011, 6, e27368.	1.1	89
344	Polycomb Repressive Complex 2 Controls the Embryo-to-Seedling Phase Transition. PLoS Genetics, 2011, 7, e1002014.	1.5	318
345	The Light Responsive Transcriptome of the Zebrafish: Function and Regulation. PLoS ONE, 2011, 6, e17080.	1.1	90
346	Quantitative Proteomic and Interaction Network Analysis of Cisplatin Resistance in HeLa Cells. PLoS ONE, 2011, 6, e19892.	1.1	37
347	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. PLoS ONE, 2011, 6, e24709.	1.1	88
348	A New Methodology to Associate SNPs with Human Diseases According to Their Pathway Related Context. PLoS ONE, 2011, 6, e26277.	1.1	52
349	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
350	A Network-Based Approach on Elucidating the Multi-Faceted Nature of Chronological Aging in S. cerevisiae. PLoS ONE, 2011, 6, e29284.	1.1	10
351	Prediction of the Mechanisms of Salvia Miltiorrhiza against Atherosclerosis Using Text Mining and Network-Based Analysis. Journal of Algorithms and Computational Technology, 2011, 5, 139-144.	0.4	3
352	Transcriptome network analysis reveals potential candidate genes for squamous lung cancer. International Journal of Molecular Medicine, 2011, 29, 95-101.	1.8	9
353	Obtain osteoarthritis related molecular signature genes through regulation network. Molecular Medicine Reports, 2011, 5, 177-83.	1.1	2

#	ARTICLE	IF	CITATIONS
354	Exploring and challenging the network of angiogenesis. Scientific Reports, 2011, 1, 61.	1.6	10
355	Genome-wide mapping of the <i>HY5</i> -mediated gene networks in Arabidopsis that involve both transcriptional and post-transcriptional regulation. Plant Journal, 2011, 65, 346-358.	2.8	274
356	The effects of mitochondrial genotype on hypoxic survival and gene expression in a hybrid population of the killifish, <i>Fundulus heteroclitus</i> . Molecular Ecology, 2011, 20, 4503-4520.	2.0	27
357	Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671.	1.4	17
358	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. Nature Biotechnology, 2011, 29, 505-511.	9.4	90
359	Predicting triplet of transcription factor "mediating enzyme" target gene by functional profiles. Neurocomputing, 2011, 74, 3677-3681.	3.5	8
360	Medusa: A tool for exploring and clustering biological networks. BMC Research Notes, 2011, 4, 384.	0.6	49
361	COMMA: a component-based infrastructure for managing and analyzing life science ontologies and their evolution. Journal of Biomedical Semantics, 2011, 2, 6.	0.9	49
362	Reconstruction and crosstalk of protein-protein interaction networks of Wnt and Hedgehog signaling in <i>Drosophila melanogaster</i> . Computational Biology and Chemistry, 2011, 35, 282-292.	1.1	12
363	The physiological, transcriptional and genetic responses of an ozone-sensitive and an ozone tolerant poplar and selected extremes of their F2 progeny. Environmental Pollution, 2011, 159, 45-54.	3.7	32
364	The influence of scaffold elasticity on germ layer specification of human embryonic stem cells. Biomaterials, 2011, 32, 9612-9621.	5.7	130
365	Proteomic Analysis of Virus-Host Interactions in an Infectious Context Using Recombinant Viruses. Molecular and Cellular Proteomics, 2011, 10, M110.007443.	2.5	45
366	Biochemical investigation and gene expression analysis of the immunostimulatory functions of an edible <i>Salacia</i> extract in rat small intestine. BioFactors, 2011, 37, 31-39.	2.6	13
367	Heterologous production of polyunsaturated fatty acids in <i>Saccharomyces cerevisiae</i> causes a global transcriptional response resulting in reduced proteasomal activity and increased oxidative stress. Biotechnology Journal, 2011, 6, 343-356.	1.8	51
369	Analysis of Phosphoproteomics Data. Methods in Molecular Biology, 2011, 696, 41-57.	0.4	12
370	Genome-wide screen for inositol auxotrophy in <i>Saccharomyces cerevisiae</i> implicates lipid metabolism in stress response signaling. Molecular Genetics and Genomics, 2011, 285, 125-149.	1.0	53
371	The developmental aging and origins of health and disease hypotheses explained by different protein networks. Biogerontology, 2011, 12, 293-308.	2.0	25
372	Correlation between cold and hot pattern in traditional Chinese medicine and gene expression profiles in rheumatoid arthritis. Frontiers of Medicine, 2011, 5, 219-228.	1.5	42

#	ARTICLE	IF	CITATIONS
373	Ai2NU: A Cytoscape plugin for uniformization of biomolecular accession identifiers. Journal of Shanghai University, 2011, 15, 456-462.	0.1	0
374	Field transcriptome revealed critical developmental and physiological transitions involved in the expression of growth potential in japonicarice. BMC Plant Biology, 2011, 11, 10.	1.6	130
375	Dengue-2 Structural Proteins Associate with Human Proteins to Produce a Coagulation and Innate Immune Response Biased Interactome. BMC Infectious Diseases, 2011, 11, 34.	1.3	23
376	Evolution combined with genomic study elucidates genetic bases of isobutanol tolerance in Escherichia coli. Microbial Cell Factories, 2011, 10, 18.	1.9	160
377	Construction of gene regulatory networks using biclustering and bayesian networks. Theoretical Biology and Medical Modelling, 2011, 8, 39.	2.1	18
378	Sig2BioPAX: Java tool for converting flat files to BioPAX Level 3 format. Source Code for Biology and Medicine, 2011, 6, 5.	1.7	6
379	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
380	Removing bias against membrane proteins in interaction networks. BMC Systems Biology, 2011, 5, 169.	3.0	13
381	Codon usage variability determines the correlation between proteome and transcriptome fold changes. BMC Systems Biology, 2011, 5, 33.	3.0	33
382	A Boolean-based systems biology approach to predict novel genes associated with cancer: Application to colorectal cancer. BMC Systems Biology, 2011, 5, 35.	3.0	59
383	Systems biological approach on neurological disorders: a novel molecular connectivity to aging and psychiatric diseases. BMC Systems Biology, 2011, 5, 6.	3.0	18
384	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. BMC Systems Biology, 2011, 5, 93.	3.0	4
385	Differentially co-expressed interacting protein pairs discriminate samples under distinct stages of HIV type 1 infection. BMC Systems Biology, 2011, 5, S1.	3.0	9
386	Development of a blood-based gene expression algorithm for assessment of obstructive coronary artery disease in non-diabetic patients. BMC Medical Genomics, 2011, 4, 26.	0.7	117
387	GO-based Functional Dissimilarity of Gene Sets. BMC Bioinformatics, 2011, 12, 360.	1.2	17
388	GOMotif: A web server for investigating the biological role of protein sequence motifs. BMC Bioinformatics, 2011, 12, 379.	1.2	0
389	iRefScape. A Cytoscape plug-in for visualization and data mining of protein interaction data from iRefIndex. BMC Bioinformatics, 2011, 12, 388.	1.2	13
390	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541

#	ARTICLE	IF	CITATIONS
391	Comparative tissue transcriptomics reveal prompt inter-organ communication in response to local bacterial kidney infection. <i>BMC Genomics</i> , 2011, 12, 123.	1.2	16
392	Common and unique elements of the ABA-regulated transcriptome of <i>Arabidopsis</i> guard cells. <i>BMC Genomics</i> , 2011, 12, 216.	1.2	189
393	MicroRNA genes preferentially expressed in dendritic cells contain sites for conserved transcription factor binding motifs in their promoters. <i>BMC Genomics</i> , 2011, 12, 330.	1.2	26
394	<i>Drosophila</i> selenophosphate synthetase 1 regulates vitamin B6 metabolism: prediction and confirmation. <i>BMC Genomics</i> , 2011, 12, 426.	1.2	18
395	New resources for functional analysis of omics data for the genus <i>Aspergillus</i> . <i>BMC Genomics</i> , 2011, 12, 486.	1.2	28
396	Protease-associated cellular networks in malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, S9.	1.2	22
397	Proteomic analysis of urinary exosomes from patients of early IgA nephropathy and thin basement membrane nephropathy. <i>Proteomics</i> , 2011, 11, 2459-2475.	1.3	211
398	Comprehensive proteomic analysis of human bile. <i>Proteomics</i> , 2011, 11, 4443-4453.	1.3	44
399	Computational systems biology of aging. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 414-428.	6.6	28
400	The Forkhead factor FoxQ1 influences epithelial differentiation. <i>Journal of Cellular Physiology</i> , 2011, 226, 710-719.	2.0	55
401	Induction and selection of the most interesting Gene Ontology based multiattribute rules for descriptions of gene groups. <i>Pattern Recognition Letters</i> , 2011, 32, 258-269.	2.6	16
402	Popeye strikes again: The deep proteome of spinach leaves. <i>Journal of Proteomics</i> , 2011, 74, 127-136.	1.2	45
403	A high-quality secretome of A549 cells aided the discovery of C4b-binding protein as a novel serum biomarker for non-small cell lung cancer. <i>Journal of Proteomics</i> , 2011, 74, 528-538.	1.2	38
404	Unraveling tobacco BY-2 protein complexes with BN PAGE/LC-MS/MS and clustering methods. <i>Journal of Proteomics</i> , 2011, 74, 1201-1217.	1.2	15
405	Adaptation of a 2D in-gel kinase assay to trace phosphotransferase activities in the human pathogen <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2011, 74, 1644-1651.	1.2	7
406	Proteomics – The key to understanding systems biology of <i>Arabidopsis</i> trichomes. <i>Phytochemistry</i> , 2011, 72, 1061-1070.	1.4	10
407	Next generation functional proteomics in non-model plants: A survey on techniques and applications for the analysis of protein complexes and post-translational modifications. <i>Phytochemistry</i> , 2011, 72, 1192-1218.	1.4	28
408	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

#	ARTICLE	IF	CITATIONS
409	Genome-wide discovery and analysis of microRNAs and other small RNAs from rice embryogenic callus. <i>RNA Biology</i> , 2011, 8, 538-547.	1.5	125
410	A molecular systems analysis of HOX PPI networks in hematopoiesis and leukemogenesis. , 2011, , .		0
411	Generation and Comprehensive Analysis of an Influenza Virus Polymerase Cellular Interaction Network. <i>Journal of Virology</i> , 2011, 85, 13010-13018.	1.5	69
412	Gene Discovery and Tissue-Specific Transcriptome Analysis in Chickpea with Massively Parallel Pyrosequencing and Web Resource Development Â Â. <i>Plant Physiology</i> , 2011, 156, 1661-1678.	2.3	213
413	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. <i>Nucleic Acids Research</i> , 2011, 39, W316-W322.	6.5	3,897
414	High-Resolution Temporal Profiling of Transcripts during <i>Arabidopsis</i> Leaf Senescence Reveals a Distinct Chronology of Processes and Regulation Â Â. <i>Plant Cell</i> , 2011, 23, 873-894.	3.1	776
415	A Physical Interaction Network of Dengue Virus and Human Proteins. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012187.	2.5	153
416	PiNGO: a Cytoscape plugin to find candidate genes in biological networks. <i>Bioinformatics</i> , 2011, 27, 1030-1031.	1.8	41
417	Receptor-independent Protein Kinase C \pm (PKC \pm) Signaling by Calpain-generated Free Catalytic Domains Induces HDAC5 Nuclear Export and Regulates Cardiac Transcription. <i>Journal of Biological Chemistry</i> , 2011, 286, 26943-26951.	1.6	38
418	Identification of Nuclear Phosphatidylinositol 4,5-Bisphosphate-Interacting Proteins by Neomycin Extraction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S15.	2.5	107
419	Cap2-HAP Complex Is a Critical Transcriptional Regulator That Has Dual but Contrasting Roles in Regulation of Iron Homeostasis in <i>Candida albicans</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 25154-25170.	1.6	104
420	A Systemic Network Triggered by Human Cytomegalovirus Entry. <i>Advances in Virology</i> , 2011, 2011, 1-11.	0.5	3
421	Insight into Bacterial Virulence Mechanisms against Host Immune Response via the <i>Yersinia pestis</i> -Human Protein-Protein Interaction Network. <i>Infection and Immunity</i> , 2011, 79, 4413-4424.	1.0	52
422	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
423	Molecular Characterization of Propolis-Induced Cell Death in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2011, 10, 398-411.	3.4	49
424	RISC RNA Sequencing for Context-Specific Identification of In Vivo MicroRNA Targets. <i>Circulation Research</i> , 2011, 108, 18-26.	2.0	99
425	REVIGO Summarizes and Visualizes Long Lists of Gene Ontology Terms. <i>PLoS ONE</i> , 2011, 6, e21800.	1.1	5,347
426	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

#	ARTICLE	IF	CITATIONS
427	Mitotic Substrates of the Kinase Aurora with Roles in Chromatin Regulation Identified Through Quantitative Phosphoproteomics of Fission Yeast. <i>Science Signaling</i> , 2011, 4, rs6.	1.6	105
428	Proteomic analysis of peritoneal fluid of patients treated by peritoneal dialysis: effect of glucose concentration. <i>Nephrology Dialysis Transplantation</i> , 2011, 26, 1990-1999.	0.4	24
429	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. <i>Plant Cell</i> , 2011, 23, 4221-4233.	3.1	189
430	Nuclear Effects of G-Protein Receptor Kinase 5 on Histone Deacetylase 5â€œRegulated Gene Transcription in Heart Failure. <i>Circulation: Heart Failure</i> , 2011, 4, 659-668.	1.6	48
431	Translational Analysis of Mouse and Human Placental Protein and mRNA Reveals Distinct Molecular Pathologies in Human Preeclampsia. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012526.	2.5	44
432	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	6.5	101
433	Genome-level identification of targets of Hox protein Ultrabithorax in <i>Drosophila</i> : novel mechanisms for target selection. <i>Scientific Reports</i> , 2011, 1, 205.	1.6	32
434	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
435	Predicting potential disease-related genes using the network topological features. , 2011, , .		0
436	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
437	Bioinformatics approaches in the discovery and understanding of reproduction-related biomarkers. <i>Expert Review of Proteomics</i> , 2011, 8, 187-195.	1.3	4
438	Functional Network Construction in <i>Arabidopsis</i> Using Rule-Based Machine Learning on Large-Scale Data Sets. <i>Plant Cell</i> , 2011, 23, 3101-3116.	3.1	91
439	An Integrated Approach to Elucidate the Intra-Viral and Viral-Cellular Protein Interaction Networks of a Gamma-Herpesvirus. <i>PLoS Pathogens</i> , 2011, 7, e1002297.	2.1	37
440	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
441	Prognostic transcriptional association networks: a new supervised approach based on regression trees. <i>Bioinformatics</i> , 2011, 27, 252-258.	1.8	12
442	Evolutionary design principles and functional characteristics based on kingdom-specific network motifs. <i>Bioinformatics</i> , 2011, 27, 245-251.	1.8	17
443	AgBase: supporting functional modeling in agricultural organisms. <i>Nucleic Acids Research</i> , 2011, 39, D497-D506.	6.5	56
444	A single nucleotide polymorphism-derived regulatory gene network underlying puberty in 2 tropical breeds of beef cattle1. <i>Journal of Animal Science</i> , 2011, 89, 1669-1683.	0.2	90

#	ARTICLE	IF	CITATIONS
445	RuleGO: a logical rules-based tool for description of gene groups by means of Gene Ontology. <i>Nucleic Acids Research</i> , 2011, 39, W293-W301.	6.5	12
446	ELK1 Uses Different DNA Binding Modes to Regulate Functionally Distinct Classes of Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002694.	1.5	66
447	Transcriptome network analysis reveals candidate genes for renal cell carcinoma. <i>Journal of Cancer Research and Therapeutics</i> , 2012, 8, 28.	0.3	3
448	Rif2 Promotes a Telomere Fold-Back Structure through Rpd3L Recruitment in Budding Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002960.	1.5	30
449	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
450	Cadmium-Induced Proteome Remodeling Regulated by Spc1/Sty1 and Zip1 in Fission Yeast. <i>Toxicological Sciences</i> , 2012, 129, 200-212.	1.4	15
451	Large-scale phosphotyrosine proteomic profiling of rat renal collecting duct epithelium reveals predominance of proteins involved in cell polarity determination. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 302, C27-C45.	2.1	11
452	Proteome Sampling by the HLA Class I Antigen Processing Pathway. <i>PLoS Computational Biology</i> , 2012, 8, e1002517.	1.5	41
453	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
454	Tcf7 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
455	PHYSIOLOGY AND ENDOCRINOLOGY SYMPOSIUM: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females1,2,3,4. <i>Journal of Animal Science</i> , 2012, 90, 1152-1165.	0.2	43
456	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. <i>PLoS Genetics</i> , 2012, 8, e1003100.	1.5	266
457	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
458	Constructing the angiome: a global angiogenesis protein interaction network. <i>Physiological Genomics</i> , 2012, 44, 915-924.	1.0	30
459	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012, 3, 236.	1.7	41
460	Coiled-coil networking shapes cell molecular machinery. <i>Molecular Biology of the Cell</i> , 2012, 23, 3911-3922.	0.9	69
461	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
462	Evaluation and Properties of the Budding Yeast Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009555.	2.5	44

#	ARTICLE	IF	CITATIONS
463	Leveraging input and output structures for joint mapping of epistatic and marginal eQTLs. <i>Bioinformatics</i> , 2012, 28, i137-i146.	1.8	39
464	Direct and Indirect Involvement of MicroRNA-499 in Clinical and Experimental Cardiomyopathy. <i>Circulation Research</i> , 2012, 111, 521-531.	2.0	133
465	The Grapevine Expression Atlas Reveals a Deep Transcriptome Shift Driving the Entire Plant into a Maturation Program. <i>Plant Cell</i> , 2012, 24, 3489-3505.	3.1	371
466	The transcriptome of <i>Verticillium dahliae</i> -infected <i>Nicotiana benthamiana</i> determined by deep RNA sequencing. <i>Plant Signaling and Behavior</i> , 2012, 7, 1065-1069.	1.2	42
467	A unique histone deacetylase inhibitor alters microRNA expression and signal transduction in chemoresistant ovarian cancer cells. <i>Cancer Biology and Therapy</i> , 2012, 13, 681-693.	1.5	17
468	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
469	Discriminating response groups in metabolic and regulatory pathway networks. <i>Bioinformatics</i> , 2012, 28, 947-954.	1.8	1
470	Gradual Increase of miR156 Regulates Temporal Expression Changes of Numerous Genes during Leaf Development in Rice. <i>Plant Physiology</i> , 2012, 158, 1382-1394.	2.3	198
471	Evolutionary analysis of functional modules in dynamic PPI networks. , 2012, , .		6
472	Grass MicroRNA Gene Paleohistory Unveils New Insights into Gene Dosage Balance in Subgenome Partitioning after Whole-Genome Duplication. <i>Plant Cell</i> , 2012, 24, 1776-1792.	3.1	53
473	Prediction of novel systems components in cell cycle regulation in malaria parasite by subnetwork alignments. , 2012, , .		0
474	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
475	Hyperactivity of the Ero1 α Oxidase Elicits Endoplasmic Reticulum Stress but No Broad Antioxidant Response. <i>Journal of Biological Chemistry</i> , 2012, 287, 39513-39523.	1.6	54
476	Clinical Proteomics. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 377-377.	5.1	4
477	INFERRING THE REGULATORY INTERACTION MODELS OF TRANSCRIPTION FACTORS IN TRANSCRIPTIONAL REGULATORY NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250012.	0.3	5
478	Mining hub-based protein complexes in massive biological networks. , 2012, , .		0
479	SEMI-ROLLED LEAF1 Encodes a Putative Glycosylphosphatidylinositol-Anchored Protein and Modulates Rice Leaf Rolling by Regulating the Formation of Bulliform Cells. <i>Plant Physiology</i> , 2012, 159, 1488-1500.	2.3	114
480	Peroxisomal L-bifunctional enzyme (Ehhadh) is essential for the production of medium-chain dicarboxylic acids. <i>Journal of Lipid Research</i> , 2012, 53, 1296-1303.	2.0	127

#	ARTICLE	IF	CITATIONS
481	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
482	Transcriptional Regulations on the Low-Temperature-Induced Floral Transition in an <i>Orchidaceae</i> Species, <i>Dendrobium nobile</i> : An Expressed Sequence Tags Analysis. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-14.	2.0	24
483	Proteomic and Bioinformatics Analyses of Mouse Liver Microsomes. <i>International Journal of Proteomics</i> , 2012, 2012, 1-24.	2.0	11
484	Systems Proteomics for Translational Network Medicine. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 478-478.	5.1	24
485	Plant neighbor detection through touching leaf tips precedes phytochrome signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14705-14710.	3.3	89
486	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
487	What has proteomics taught us about <i>Leishmania</i> development?. <i>Parasitology</i> , 2012, 139, 1146-1157.	0.7	31
488	Characterization of SOC1's Central Role in Flowering by the Identification of Its Upstream and Downstream Regulators. <i>Plant Physiology</i> , 2012, 160, 433-449.	2.3	169
489	Genetical Genomics Identifies the Genetic Architecture for Growth and Weevil Resistance in Spruce. <i>PLoS ONE</i> , 2012, 7, e44397.	1.1	21
490	Tale of a tegument transactivator: the past, present and future of human CMV pp71. <i>Future Virology</i> , 2012, 7, 855-869.	0.9	31
491	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
492	Transcriptional profiling of <i>Saccharomyces cerevisiae</i> exposed to propolis. <i>BMC Complementary and Alternative Medicine</i> , 2012, 12, 194.	3.7	19
493	High Hydrostatic Pressure Activates Transcription Factors Involved in <i>Saccharomyces cerevisiae</i> Stress Tolerance. <i>Current Pharmaceutical Biotechnology</i> , 2012, 13, 2712-2720.	0.9	12
494	A Simple Method for Analyzing Actives in Random RNAi Screens: Introducing the "H Score" for Hit Nomination & Gene Prioritization. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2012, 15, 686-704.	0.6	24
495	Genomics of estradiol-3-sulfate action in the ovine fetal hypothalamus. <i>Physiological Genomics</i> , 2012, 44, 669-677.	1.0	23
496	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
497	A travel guide to Cytoscape plugins. <i>Nature Methods</i> , 2012, 9, 1069-1076.	9.0	1,289
498	Transcriptional repression of the APC/C activator CCS52A1 promotes active termination of cell growth. <i>EMBO Journal</i> , 2012, 31, 4488-4501.	3.5	60

#	ARTICLE	IF	CITATIONS
499	Identification of a complex genetic network underlying <i>Saccharomyces cerevisiae</i> colony morphology. <i>Molecular Microbiology</i> , 2012, 86, 225-239.	1.2	71
500	Histone H2B monoubiquitination is required to reach maximal transcript levels of circadian clock genes in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2012, 72, 249-260.	2.8	76
501	Evaluation of the Cell Viability of Human Wharton's Jelly Stem Cells for Use in Cell Therapy. <i>Tissue Engineering - Part C: Methods</i> , 2012, 18, 408-419.	1.1	36
502	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
503	Conserved Noncoding Sequences Highlight Shared Components of Regulatory Networks in Dicotyledonous Plants. <i>Plant Cell</i> , 2012, 24, 3949-3965.	3.1	64
504	Comparative Analysis of Transcriptomic and Hormonal Responses to Compatible and Incompatible Plant-Virus Interactions that Lead to Cell Death. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 709-723.	1.4	53
505	Candidate Pathways for Promoting Differentiation or Quiescence of Oligodendrocyte Progenitor-like Cells in Glioma. <i>Cancer Research</i> , 2012, 72, 4856-4868.	0.4	68
506	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
507	<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
508	FACS Purification and Transcriptome Analysis of <i>Drosophila</i> Neural Stem Cells Reveals a Role for Klumpfuss in Self-Renewal. <i>Cell Reports</i> , 2012, 2, 407-418.	2.9	122
509	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	2.9	102
510	Quantitative proteomic analysis reveals protein expression changes in the murine neuronal secretome during apoptosis. <i>Journal of Proteomics</i> , 2012, 77, 394-405.	1.2	17
511	A combined analysis of microarray gene expression studies of the human prefrontal cortex identifies genes implicated in schizophrenia. <i>Journal of Psychiatric Research</i> , 2012, 46, 1464-1474.	1.5	68
512	Integration of multiple data sources for identifying functional modules using Bayesian network. , 2012, , .		0
513	DEFOG: discrete enrichment of functionally organized genes. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 795.	0.6	3
514	Identifying core features of adaptive metabolic mechanisms for chronic heat stress attenuation contributing to systems robustness. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 480.	0.6	65
515	ANAP: An Integrated Knowledge Base for <i>Arabidopsis</i> Protein Interaction Network Analysis. <i>Plant Physiology</i> , 2012, 158, 1523-1533.	2.3	31
516	Protein Profiling in Potato (<i>Solanum tuberosum</i> L.) Leaf Tissues by Differential Centrifugation. <i>Journal of Proteome Research</i> , 2012, 11, 2594-2601.	1.8	26

#	ARTICLE	IF	CITATIONS
517	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. <i>Blood</i> , 2012, 119, e22-e34.	0.6	84
518	In Vitro Generation of Long-lived Human Plasma Cells. <i>Journal of Immunology</i> , 2012, 189, 5773-5785.	0.4	111
519	Quantitative Proteome Analysis Reveals RNA Processing Factors As Modulators of Ionizing Radiation-Induced Apoptosis in the <i>C. elegans</i> Germline.. <i>Journal of Proteome Research</i> , 2012, 11, 4277-4288.	1.8	9
521	Construction of large signaling pathways using an adaptive perturbation approach with phosphoproteomic data. <i>Molecular BioSystems</i> , 2012, 8, 1571.	2.9	15
522	Sorafenib-Induced Mitochondrial Complex I Inactivation and Cell Death in Human Neuroblastoma Cells. <i>Journal of Proteome Research</i> , 2012, 11, 1609-1620.	1.8	29
523	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. <i>Journal of Proteome Research</i> , 2012, 11, 1475-1484.	1.8	68
524	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
525	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
526	Charting the Landscape of Tandem BRCT Domain-Mediated Protein Interactions. <i>Science Signaling</i> , 2012, 5, rs6.	1.6	88
527	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
528	Understanding MicroRNA Regulation: A computational perspective. <i>IEEE Signal Processing Magazine</i> , 2012, 29, 77-88.	4.6	7
529	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis. <i>Plant Cell</i> , 2012, 24, 3530-3557.	3.1	337
530	<i>Arabidopsis</i> E2FA stimulates proliferation and endocycle separately through RBR-bound and RBR-free complexes. <i>EMBO Journal</i> , 2012, 31, 1480-1493.	3.5	142
531	Mapping N-Glycosylation Sites across Seven Evolutionarily Distant Species Reveals a Divergent Substrate Proteome Despite a Common Core Machinery. <i>Molecular Cell</i> , 2012, 46, 542-548.	4.5	238
532	QUICK identification and SPR validation of signal transducers and activators of transcription 3 (Stat3) interacting proteins. <i>Journal of Proteomics</i> , 2012, 75, 1055-1066.	1.2	17
533	Protein profiling reveals energy metabolism and cytoskeletal protein alterations in LMNA mutation carriers. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012, 1822, 970-979.	1.8	16
534	Acclimation increases freezing stress response of <i>Arabidopsis thaliana</i> at proteome level. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 813-825.	1.1	26
535	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

#	ARTICLE	IF	CITATIONS
536	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
537	A Systems Genetics Approach Identifies Genes and Pathways for Type 2 Diabetes in Human Islets. <i>Cell Metabolism</i> , 2012, 16, 122-134.	7.2	323
538	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
539	5-HT ₆ receptor recruitment of mTOR as a mechanism for perturbed cognition in schizophrenia. <i>EMBO Molecular Medicine</i> , 2012, 4, 1043-1056.	3.3	152
540	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
541	Gene expression analysis of a murine model with pulmonary vascular remodeling compared to end-stage IPAH lungs. <i>Respiratory Research</i> , 2012, 13, 103.	1.4	8
542	OLSVis: an animated, interactive visual browser for bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 116.	1.2	20
543	Gene regulatory network modeling via global optimization of high-order dynamic Bayesian network. <i>BMC Bioinformatics</i> , 2012, 13, 131.	1.2	42
544	Methods for visual mining of genomic and proteomic data atlases. <i>BMC Bioinformatics</i> , 2012, 13, 58.	1.2	8
545	Gravitational and magnetic field variations synergize to cause subtle variations in the global transcriptional state of Arabidopsis in vitro callus cultures. <i>BMC Genomics</i> , 2012, 13, 105.	1.2	43
546	De novo sequencing and characterization of <i>Picrohiza kurrooa</i> transcriptome at two temperatures showed major transcriptome adjustments. <i>BMC Genomics</i> , 2012, 13, 126.	1.2	124
547	Genetic variation and metabolic pathway intricacy govern the active compound content and quality of the Chinese medicinal plant <i>Lonicera japonica</i> thunb. <i>BMC Genomics</i> , 2012, 13, 195.	1.2	74
548	Comparison of Atlantic salmon individuals with different outcomes of cardiomyopathy syndrome (CMS). <i>BMC Genomics</i> , 2012, 13, 205.	1.2	32
549	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
550	A comparison of E15.5 fetus and newborn rat serum proteomes. <i>Proteome Science</i> , 2012, 10, 64.	0.7	3
551	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
552	A whole blood gene expression-based signature for smoking status. <i>BMC Medical Genomics</i> , 2012, 5, 58.	0.7	76
553	Murine colon proteome and characterization of the protein pathways. <i>BioData Mining</i> , 2012, 5, 11.	2.2	36

#	ARTICLE	IF	CITATIONS
554	A comparison and evaluation of five biclustering algorithms by quantifying goodness of biclusters for gene expression data. <i>BioData Mining</i> , 2012, 5, 8.	2.2	26
555	An Always Correlated gene expression landscape for ovine skeletal muscle, lessons learnt from comparison with an “equivalent” bovine landscape. <i>BMC Research Notes</i> , 2012, 5, 632.	0.6	4
556	A taxonomy of organ-specific breast cancer metastases based on a protein–protein interaction network. <i>Molecular BioSystems</i> , 2012, 8, 2085.	2.9	11
557	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
558	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
559	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
560	Differential gene expression pattern in early gastric cancer by an integrative systematic approach. <i>International Journal of Oncology</i> , 2012, 41, 1675-1682.	1.4	16
561	Computational-Based Analysis to Associate the Function of Plant Signaling Peptides with Distinct Biological Processes. <i>Signaling and Communication in Plants</i> , 2012, , 257-277.	0.5	0
562	Development of a diagnostic algorithm in periodontal disease and identification of genetic expression patterns: A preliminary report. <i>Journal of Dental Sciences</i> , 2012, 7, 48-56.	1.2	1
563	Preliminary characterization of the murine membrane reticulocyte proteome. <i>Blood Cells, Molecules, and Diseases</i> , 2012, 49, 74-82.	0.6	15
564	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
565	Effect of iron on the proliferation of lung adenocarcinoma cells in vitro. <i>African Journal of Pharmacy and Pharmacology</i> , 2012, 6, .	0.2	0
566	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
567	An Integrative Clustering Approach Combining Particle Swarm Optimization and Formal Concept Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 84-98.	1.0	2
568	Embryonic Stem Cell Interactomics: The Beginning of a Long Road to Biological Function. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 1138-1154.	5.6	8
569	Molecular basis for fungicidal action of neothyonidioside, a triterpene glycoside from the sea cucumber, <i>Australostichopus mollis</i> . <i>Molecular BioSystems</i> , 2012, 8, 902.	2.9	19
570	Plant Signaling Peptides. <i>Signaling and Communication in Plants</i> , 2012, , .	0.5	2
572	Statistical Human Genetics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	13

#	ARTICLE	IF	CITATIONS
573	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
574	Module-based subnetwork alignments reveal novel transcriptional regulators in malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Systems Biology</i> , 2012, 6, S5.	3.0	11
575	A new therapy for drug-resistant malaria using <i>Plasmodium</i> synthetic lethality inference. <i>Malaria Journal</i> , 2012, 11, .	0.8	0
576	Functional repertoire, molecular pathways and diseases associated with 3D domain swapping in the human proteome. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 8.	1.2	12
577	Gene Properties and Chromatin State Influence the Accumulation of Transposable Elements in Genes. <i>PLoS ONE</i> , 2012, 7, e30158.	1.1	10
578	Computational Identification of Phospho-Tyrosine Sub-Networks Related to Acanthocyte Generation in Neuroacanthocytosis. <i>PLoS ONE</i> , 2012, 7, e31015.	1.1	19
579	The Transcriptome of Compatible and Incompatible Interactions of Potato (<i>Solanum tuberosum</i>) with <i>Phytophthora infestans</i> Revealed by DeepSAGE Analysis. <i>PLoS ONE</i> , 2012, 7, e31526.	1.1	54
580	Unique Proteomic Signatures Distinguish Macrophages and Dendritic Cells. <i>PLoS ONE</i> , 2012, 7, e33297.	1.1	91
581	Functional Annotation of Hierarchical Modularity. <i>PLoS ONE</i> , 2012, 7, e33744.	1.1	4
582	Searching for Cellular Partners of Hantaviral Nonstructural Protein NSs: Y2H Screening of Mouse cDNA Library and Analysis of Cellular Interactome. <i>PLoS ONE</i> , 2012, 7, e34307.	1.1	10
583	Digital Gene Expression Profiling by 5' End Sequencing of cDNAs during Reprogramming in the Moss <i>Physcomitrella patens</i> . <i>PLoS ONE</i> , 2012, 7, e36471.	1.1	27
584	Transcriptomes Reveal Genetic Signatures Underlying Physiological Variations Imposed by Different Fermentation Conditions in <i>Lactobacillus plantarum</i> . <i>PLoS ONE</i> , 2012, 7, e38720.	1.1	50
585	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
586	Discovery of Genes Related to Insecticide Resistance in <i>Bactrocera dorsalis</i> by Functional Genomic Analysis of a De Novo Assembled Transcriptome. <i>PLoS ONE</i> , 2012, 7, e40950.	1.1	46
587	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
588	Porcine Tissue-Specific Regulatory Networks Derived from Meta-Analysis of the Transcriptome. <i>PLoS ONE</i> , 2012, 7, e46159.	1.1	23
589	Wiki-Pi: A Web-Server of Annotated Human Protein-Protein Interactions to Aid in Discovery of Protein Function. <i>PLoS ONE</i> , 2012, 7, e49029.	1.1	67
590	Protein Interaction Network of <i>Arabidopsis thaliana</i> Female Gametophyte Development Identifies Novel Proteins and Relations. <i>PLoS ONE</i> , 2012, 7, e49931.	1.1	36

#	ARTICLE	IF	CITATIONS
591	Circadian Clock Genes Per1 and Per2 Regulate the Response of Metabolism-Associated Transcripts to Sleep Disruption. PLoS ONE, 2012, 7, e52983.	1.1	75
592	Interactomic and Pharmacological Insights on Human Sirt-1. Frontiers in Pharmacology, 2012, 3, 40.	1.6	26
593	The Impact of Classification of Interest on Predictive Toxicogenomics. Frontiers in Genetics, 2012, 3, 14.	1.1	8
594	Infection Strategies of Bacterial and Viral Pathogens through Pathogenâ€‘Human Proteinâ€‘Protein Interactions. Frontiers in Microbiology, 2012, 3, 46.	1.5	63
595	Wnt Signaling Network in Homo Sapiens. , 0, , .		2
596	Analysis of Gene Expression Data Using Biclustering Algorithms. , 0, , .		1
597	Systemic Approach to the Genome Integration Process of Human Lentivirus. , 2012, , .		1
598	Potential Candidate Genes for Alveolar Hypoxia Identified by Transcriptome Network Analysis. Medicina (Lithuania), 2012, 48, 84.	0.8	1
599	In silico analysis strategies and resources for psychiatric genetics research. , 0, , 34-48.		0
600	The nuclear proteome of the green alga <i>Chlamydomonas reinhardtii</i> . Proteomics, 2012, 12, 95-100.	1.3	16
601	Tutorial on biological networks. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2012, 2, 298-325.	4.6	11
602	Toward a systems level view of the ECM and related proteins: A framework for the systematic definition and analysis of biological systems. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1522-1544.	1.5	26
603	The Local Transcriptome in the Synaptic Neuropil Revealed by Deep Sequencing and High-Resolution Imaging. Neuron, 2012, 74, 453-466.	3.8	626
604	Identification of Novel miR-21 Target Proteins in Multiple Myeloma Cells by Quantitative Proteomics. Journal of Proteome Research, 2012, 11, 2078-2090.	1.8	66
605	Analyzing Proteinâ€‘Protein Interaction Networks. Journal of Proteome Research, 2012, 11, 2014-2031.	1.8	145
606	Transcriptome profiling of genes involved in neural tube closure during human embryonic development using long serial analysis of gene expression (longâ€‘SAGE). Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 683-692.	1.6	18
607	Sequencing of neuroblastoma identifies chromothripsis and defects in neuritogenesis genes. Nature, 2012, 483, 589-593.	13.7	775
608	Genomics and Successful Aging: Grounds for Renewed Optimism?. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2012, 67A, 511-519.	1.7	16

#	ARTICLE	IF	CITATIONS
609	Temporal and Fluoride Control of Secondary Metabolism Regulates Cellular Organofluorine Biosynthesis. ACS Chemical Biology, 2012, 7, 1576-1585.	1.6	18
610	Subgroup-specific alternative splicing in medulloblastoma. Acta Neuropathologica, 2012, 123, 485-499.	3.9	28
611	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. New Phytologist, 2012, 193, 755-769.	3.5	305
612	A subcellular localization compendium of hydrogen peroxide-induced proteins. Plant, Cell and Environment, 2012, 35, 308-320.	2.8	86
613	Day length is a key regulator of transcriptomic responses to both CO ₂ and H ₂ O ₂ in <i>Arabidopsis</i> . Plant, Cell and Environment, 2012, 35, 374-387.	2.8	83
614	Mice heterozygous for CREB binding protein are hypersensitive to ³ -radiation and invariably develop myelodysplastic/myeloproliferative neoplasm. Experimental Hematology, 2012, 40, 295-306.e5.	0.2	28
615	Post-transcriptional regulatory networks play a key role in noise reduction that is conserved from microorganisms to mammals. FEBS Journal, 2012, 279, 3501-3512.	2.2	20
616	Identification of potential host proteins for influenza A virus based on topological and biological characteristics by proteome-wide network approach. Journal of Proteomics, 2012, 75, 2500-2513.	1.2	10
617	A proteomics approach reveals divergent molecular responses to salinity in populations of European whitefish (<i>Coregonus lavaretus</i>). Molecular Ecology, 2012, 21, 3516-3530.	2.0	54
618	CK2-defective Arabidopsis plants exhibit enhanced double-strand break repair rates and reduced survival after exposure to ionizing radiation. Plant Journal, 2012, 71, 627-638.	2.8	28
619	Tools for protein-protein interaction network analysis in cancer research. Clinical and Translational Oncology, 2012, 14, 3-14.	1.2	35
620	Cold and heat pattern of rheumatoid arthritis in traditional Chinese medicine: distinct molecular signatures identified by microarray expression profiles in CD4-positive T cell. Rheumatology International, 2012, 32, 61-68.	1.5	74
621	Spatial and temporal transcriptomic analysis of the Arabidopsis thaliana-Botrytis cinerea interaction. Molecular Biology Reports, 2012, 39, 4039-4049.	1.0	47
622	Angiogenin induces modifications in the astrocyte secretome: Relevance to amyotrophic lateral sclerosis. Journal of Proteomics, 2013, 91, 274-285.	1.2	40
623	Differential proteomic analysis of drought stress response in leaves of common bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.2	118
624	The plasticity of the grapevine berry transcriptome. Genome Biology, 2013, 14, r54.	3.8	168
625	Identification of pathways directly regulated by SHORT VEGETATIVE PHASE during vegetative and reproductive development in Arabidopsis. Genome Biology, 2013, 14, R56.	3.8	134
626	Global Proteome Analysis of the NCI-60 Cell Line Panel. Cell Reports, 2013, 4, 609-620.	2.9	276

#	ARTICLE	IF	CITATIONS
627	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
628	Efficiency of siRNA delivery by lipid nanoparticles is limited by endocytic recycling. <i>Nature Biotechnology</i> , 2013, 31, 653-658.	9.4	660
629	COntoDiff: generation of complex evolution mappings for life science ontologies. <i>Journal of Biomedical Informatics</i> , 2013, 46, 15-32.	2.5	60
630	STOP using just GO: a multi-ontology hypothesis generation tool for high throughput experimentation. <i>BMC Bioinformatics</i> , 2013, 14, 53.	1.2	17
631	Predicting PDZ domain mediated protein interactions from structure. <i>BMC Bioinformatics</i> , 2013, 14, 27.	1.2	32
632	Visualization of protein interaction networks: problems and solutions. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	70
633	Multiscale modeling of the causal functional roles of nsSNPs in a genome-wide association study: application to hypoxia. <i>BMC Genomics</i> , 2013, 14, S9.	1.2	6
634	Analysis and annotation of the hexaploid oat seed transcriptome. <i>BMC Genomics</i> , 2013, 14, 471.	1.2	62
635	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013, 14, 449.	1.2	118
636	MicroRNAs and their putative targets in <i>Brassica napus</i> seed maturation. <i>BMC Genomics</i> , 2013, 14, 140.	1.2	99
637	Gene expression in human fungal pathogen <i>Coccidioides immitis</i> changes as arthroconidia differentiate into spherules and mature. <i>BMC Microbiology</i> , 2013, 13, 121.	1.3	31
638	Cluster and propensity based approximation of a network. <i>BMC Systems Biology</i> , 2013, 7, 21.	3.0	8
639	Global Phosphoproteomic Analysis Reveals Diverse Functions of Serine/Threonine/Tyrosine Phosphorylation in the Model Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. <i>Journal of Proteome Research</i> , 2013, 12, 1909-1923.	1.8	72
640	Complex Adaptive Systems Modeling: A multidisciplinary Roadmap. <i>Complex Adaptive Systems Modeling</i> , 2013, 1, .	1.6	45
641	Effects of early life exposure to ultraviolet C radiation on mitochondrial DNA content, transcription, ATP production, and oxygen consumption in developing <i>Caenorhabditis elegans</i> . <i>BMC Pharmacology & Toxicology</i> , 2013, 14, 9.	1.0	42
642	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90.	0.3	29
643	Digital gene expression analysis of early root infection resistance to <i>Sporisorium reilianum</i> f. sp. <i>zeae</i> in maize. <i>Molecular Genetics and Genomics</i> , 2013, 288, 21-37.	1.0	20
644	A genome scale metabolic network for rice and accompanying analysis of tryptophan, auxin and serotonin biosynthesis regulation under biotic stress. <i>Rice</i> , 2013, 6, 15.	1.7	101

#	ARTICLE	IF	CITATIONS
645	Screening of osteoprotegerin-related feature genes in osteoporosis and functional analysis with DNA microarray. <i>European Journal of Medical Research</i> , 2013, 18, 15.	0.9	4
646	The Drosophila Transcription Factor Adf-1 (nalyot) Regulates Dendrite Growth by Controlling FasII and Staufen Expression Downstream of CaMKII and Neural Activity. <i>Journal of Neuroscience</i> , 2013, 33, 11916-11931.	1.7	26
647	Rewiring of human lung cell lineage and mitotic networks in lung adenocarcinomas. <i>Nature Communications</i> , 2013, 4, 1701.	5.8	42
648	An Arrayed Genome-Scale Lentiviral-Enabled Short Hairpin RNA Screen Identifies Lethal and Rescuer Gene Candidates. <i>Assay and Drug Development Technologies</i> , 2013, 11, 173-190.	0.6	15
649	Gene expression profiling of HGF/Met activation in neonatal mouse heart. <i>Transgenic Research</i> , 2013, 22, 579-593.	1.3	12
650	Sequencing of Sitka spruce (<i>Picea sitchensis</i>) cDNA libraries constructed from autumn buds and foliage reveals autumn-specific spruce transcripts. <i>Tree Genetics and Genomes</i> , 2013, 9, 683-691.	0.6	6
651	Connecting the Dots: Applications of Network Medicine in Pharmacology and Disease. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 94, 659-669.	2.3	35
652	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
653	Chronic high glucose induced INS-1 β cell mitochondrial dysfunction: A comparative mitochondrial proteome with SILAC. <i>Proteomics</i> , 2013, 13, 3030-3039.	1.3	16
654	Differential gene expression in HIV-infected individuals following ART. <i>Antiviral Research</i> , 2013, 100, 420-428.	1.9	32
655	A draft genome sequence of the pulse crop chickpea (<i>Cicer arietinum</i> L.). <i>Plant Journal</i> , 2013, 74, 715-729.	2.8	382
656	Checkpoint Kinases Regulate a Global Network of Transcription Factors in Response to DNA Damage. <i>Cell Reports</i> , 2013, 4, 174-188.	2.9	61
657	Refinement in Localization and Identification of Gene Regions Associated with Crohn Disease. <i>American Journal of Human Genetics</i> , 2013, 92, 107-113.	2.6	24
658	Rule based functional description of genes – Estimation of the multicriteria rule interestingness measure by the UTA method. <i>Biocybernetics and Biomedical Engineering</i> , 2013, 33, 222-234.	3.3	8
659	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
660	Proteins and Domains Vary in Their Tolerance of Non-Synonymous Single Nucleotide Polymorphisms (nsSNPs). <i>Journal of Molecular Biology</i> , 2013, 425, 1274-1286.	2.0	32
661	Tissue damage in organic rainbow trout muscle investigated by proteomics and bioinformatics. <i>Proteomics</i> , 2013, 13, 2180-2190.	1.3	0
662	Unraveling the Phosphoproteome Dynamics in Mammal Mitochondria from a Network Perspective. <i>Journal of Proteome Research</i> , 2013, 12, 4257-4267.	1.8	16

#	ARTICLE	IF	CITATIONS
663	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
664	Mitochondria proteome profiling: A comparative analysis between gel- and gel-free approaches. <i>Talanta</i> , 2013, 115, 277-283.	2.9	12
665	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
666	Network2Canvas: network visualization on a canvas with enrichment analysis. <i>Bioinformatics</i> , 2013, 29, 1872-1878.	1.8	34
667	Artificial Selection on Brain-Expressed Genes during the Domestication of Dog. <i>Molecular Biology and Evolution</i> , 2013, 30, 1867-1876.	3.5	74
668	ERF115 Controls Root Quiescent Center Cell Division and Stem Cell Replenishment. <i>Science</i> , 2013, 342, 860-863.	6.0	263
669	Colitis-accelerated colorectal cancer and metabolic dysregulation in a mouse model. <i>Carcinogenesis</i> , 2013, 34, 1861-1869.	1.3	29
670	Jasmonate Signaling. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	5
671	SubNet: a Java application for subnetwork extraction. <i>Bioinformatics</i> , 2013, 29, 2509-2511.	1.8	18
672	RManI: Regulatory Module Network Inference framework. <i>BMC Bioinformatics</i> , 2013, 14, S14.	1.2	6
673	Integrated analysis, transcriptome-lipidome, reveals the effects of INO- level (INO2 and INO4) on lipid metabolism in yeast. <i>BMC Systems Biology</i> , 2013, 7, S7.	3.0	22
674	Identification of a neuronal transcription factor network involved in medulloblastoma development. <i>Acta Neuropathologica Communications</i> , 2013, 1, 35.	2.4	40
675	The Oct1 homolog Nubbin is a repressor of NF- κ B-dependent immune gene expression that increases the tolerance to gut microbiota. <i>BMC Biology</i> , 2013, 11, 99.	1.7	48
676	Arginine rich short linear motif of HIV-1 regulatory proteins inhibits Dicer dependent RNA interference. <i>Retrovirology</i> , 2013, 10, 97.	0.9	9
677	Transcriptomic characterization of cold acclimation in larval zebrafish. <i>BMC Genomics</i> , 2013, 14, 612.	1.2	174
678	Research prioritization through prediction of future impact on biomedical science: a position paper on inference-analytics. <i>GigaScience</i> , 2013, 2, 11.	3.3	6
679	Arabidopsis Polycomb Repressive Complex 2 binding sites contain putative GAGA factor binding motifs within coding regions of genes. <i>BMC Genomics</i> , 2013, 14, 593.	1.2	94
680	Human growth is associated with distinct patterns of gene expression in evolutionarily conserved networks. <i>BMC Genomics</i> , 2013, 14, 547.	1.2	56

#	ARTICLE	IF	CITATIONS
681	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . BMC Genomics, 2013, 14, 563.	1.2	115
682	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
683	Prediction of protein interaction types based on sequence and network features. BMC Systems Biology, 2013, 7, S5.	3.0	5
684	Transcriptome signatures of class I and III stress response deregulation in <i>Lactobacillus plantarum</i> reveal pleiotropic adaptation. Microbial Cell Factories, 2013, 12, 112.	1.9	21
685	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. Molecular Cancer, 2013, 12, 140.	7.9	59
686	A patient tumor transplant model of squamous cell cancer identifies PI3K inhibitors as candidate therapeutics in defined molecular bins. Molecular Oncology, 2013, 7, 776-790.	2.1	140
688	Assessment of crosstalks between the Snf1 kinase complex and sphingolipid metabolism in <i>S. cerevisiae</i> via systems biology approaches. Molecular BioSystems, 2013, 9, 2914.	2.9	7
689	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. EMBO Journal, 2013, 32, 1478-1488.	3.5	1,130
690	Phytochrome-Interacting Factors Have Both Shared and Distinct Biological Roles. Molecules and Cells, 2013, 35, 371-380.	1.0	74
691	Screening of differentially expressed miRNAs related to muscle strain and their target gene. Molecular Biology, 2013, 47, 758-764.	0.4	1
692	Atopic dermatitis-associated protein interaction network lead to new insights in chronic sulfur mustard skin lesion mechanisms. Expert Review of Proteomics, 2013, 10, 449-460.	1.3	14
693	Combining small molecules for cell reprogramming through an interatomic analysis. Molecular BioSystems, 2013, 9, 2741.	2.9	2
694	Recombinant Antibody Production in Arabidopsis Seeds Triggers an Unfolded Protein Response. Plant Physiology, 2013, 161, 1021-1033.	2.3	30
695	Laulimalide and peloruside A inhibit mitosis of <i>Saccharomyces cerevisiae</i> by preventing microtubule depolymerisation-dependent steps in chromosome separation and nuclear positioning. Molecular BioSystems, 2013, 9, 2842.	2.9	9
696	Transcriptional remodelling in response to changing copper levels in the Wilson and Menkes disease model of <i>Saccharomyces cerevisiae</i> . Molecular BioSystems, 2013, 9, 2889.	2.9	24
697	Analysis of Incrementally Generated Clusters in Biological Networks Using Graph-Theoretic Filters and Ontology Enrichment. , 2013, , .		1
698	Proteomics-Based Methods for Discovery, Quantification, and Validation of Protein-Protein Interactions. Analytical Chemistry, 2013, 85, 749-768.	3.2	85
699	Molecular evolutionary and population genomic analysis of the nine-spined stickleback using a modified restriction-site-associated DNA tag approach. Molecular Ecology, 2013, 22, 565-582.	2.0	85

#	ARTICLE	IF	CITATIONS
700	Discovery of Potential Bladder Cancer Biomarkers by Comparative Urine Proteomics and Analysis. <i>Clinical Genitourinary Cancer</i> , 2013, 11, 56-62.	0.9	70
701	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. <i>Journal of Proteomics</i> , 2013, 78, 486-498.	1.2	103
702	Salivary Proteome and Peptidome Profiling in Type 1 Diabetes Mellitus Using a Quantitative Approach. <i>Journal of Proteome Research</i> , 2013, 12, 1700-1709.	1.8	50
703	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
704	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2898-2903.	3.3	351
705	Activation of protein kinase C delta by RACK peptide promotes embryonic stem cell proliferation through ERK 1/2. <i>Journal of Proteomics</i> , 2013, 94, 497-512.	1.2	7
706	Increased expression of fatty acid binding protein 4 and leptin in resident macrophages characterises atherosclerotic plaque rupture. <i>Atherosclerosis</i> , 2013, 226, 74-81.	0.4	66
707	Transcription factor complex AP-1 mediates inflammation initiated by <i>Chlamydia pneumoniae</i> infection. <i>Cellular Microbiology</i> , 2013, 15, 779-794.	1.1	70
708	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
709	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
710	Enrichment of Leishmania donovani ATP-binding proteins using a staurosporine capture compound. <i>Journal of Proteomics</i> , 2013, 86, 97-104.	1.2	3
711	Differential lysine acetylation profiles of Erwinia amylovora strains revealed by proteomics. <i>Journal of Proteomics</i> , 2013, 79, 60-71.	1.2	78
712	Enrichment map profiling of the cancer invasion front suggests regulation of colorectal cancer progression by the bone morphogenetic protein antagonist, gremlin-1. <i>Molecular Oncology</i> , 2013, 7, 826-839.	2.1	50
713	Discovery of MicroRNAs Associated with the S Type Cytoplasmic Male Sterility in Maize. <i>Journal of Integrative Agriculture</i> , 2013, 12, 229-238.	1.7	14
714	Exploring biological processes involved in embryonic stem cell differentiation by analyzing proteomic data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1063-1069.	1.1	12
715	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
716	Transcriptional regulatory network for psoriasis. <i>Journal of Dermatology</i> , 2013, 40, 48-53.	0.6	22
717	Proteomic analysis of endothelial cell secretome: A means of studying the pleiotropic effects of Hmg-CoA reductase inhibitors. <i>Journal of Proteomics</i> , 2013, 78, 346-361.	1.2	37

#	ARTICLE	IF	CITATIONS
718	Mutation of a Short Variable Region in HCpro Protein of Potato virus A Affects Interactions with a Microtubule-Associated Protein and Induces Necrotic Responses in Tobacco. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 721-733.	1.4	34
719	Systemic analysis of inducible target of rapamycin mutants reveal a general metabolic switch controlling growth in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2013, 73, 897-909.	2.8	205
720	Deep sequencing analysis of the transcriptomes of peanut aerial and subterranean young pods identifies candidate genes related to early embryo abortion. <i>Plant Biotechnology Journal</i> , 2013, 11, 115-127.	4.1	75
721	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
722	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. <i>Plant Cell</i> , 2013, 25, 780-793.	3.1	91
723	A global view of transcriptome dynamics during flower development in chickpea by deep sequencing. <i>Plant Biotechnology Journal</i> , 2013, 11, 691-701.	4.1	104
724	Yeast Systems Biology. , 2013, , 343-365.		6
725	Host microRNA molecular signatures associated with human H1N1 and H3N2 influenza A viruses reveal an unanticipated antiviral activity for miR-146a. <i>Journal of General Virology</i> , 2013, 94, 985-995.	1.3	76
726	Global Proteomic Profiling and Enrichment Maps of Dilated Cardiomyopathy. <i>Methods in Molecular Biology</i> , 2013, 1005, 53-66.	0.4	1
727	Large-scale global identification of protein lysine methylation in vivo. <i>Epigenetics</i> , 2013, 8, 477-485.	1.3	125
728	Laser microdissection and microarray analysis of <i>Truber melanosporum</i> ectomycorrhizas reveal functional heterogeneity between mantle and <i>Hartig net</i> compartments. <i>Environmental Microbiology</i> , 2013, 15, 1853-1869.	1.8	62
729	PheNetic: network-based interpretation of unstructured gene lists in <i>E. coli</i> . <i>Molecular BioSystems</i> , 2013, 9, 1594.	2.9	35
730	Inferring Biological Functions of Guanylyl Cyclases with Computational Methods. <i>Methods in Molecular Biology</i> , 2013, 1016, 225-234.	0.4	1
731	Transcriptional response of HT-29 intestinal epithelial cells to human and bovine milk oligosaccharides. <i>British Journal of Nutrition</i> , 2013, 110, 2127-2137.	1.2	53
732	A local regulatory network around three <i>NAC</i> transcription factors in stress responses and senescence in <i>Arabidopsis</i> leaves. <i>Plant Journal</i> , 2013, 75, 26-39.	2.8	202
733	Functional Annotation of Plant Genomes. , 2013, , 155-176.		0
734	Monitoring the native phosphorylation state of plasma membrane proteins from a single mouse cerebellum. <i>Journal of Neuroscience Methods</i> , 2013, 213, 153-164.	1.3	7
735	miR-296-3p, miR-298-5p and their downstream networks are causally involved in the higher resistance of mammalian pancreatic β cells to cytokine-induced apoptosis as compared to β^2 cells. <i>BMC Genomics</i> , 2013, 14, 62.	1.2	48

#	ARTICLE	IF	CITATIONS
736	Perception of low red:farâ€red ratio compromises both salicylic acidâ€and jasmonic acidâ€dependent pathogen defences in <scp>A</scp>rabidopsis. <i>Plant Journal</i> , 2013, 75, 90-103.	2.8	181
737	Visualization and Analysis of Biological Networks. <i>Methods in Molecular Biology</i> , 2013, 1021, 63-88.	0.4	21
738	The proteinâ€protein interaction network of the human Sirtuin family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1998-2009.	1.1	27
739	Testicular phosphoproteome in perfluorododecanoic acid-exposed rats. <i>Toxicology Letters</i> , 2013, 221, 91-101.	0.4	14
740	A Guide to CORNET for the Construction of Coexpression and Proteinâ€Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2013, 1011, 327-343.	0.4	4
741	Proteomic analysis of a decellularized human vocal fold mucosa scaffold using 2D electrophoresis and high-resolution mass spectrometry. <i>Biomaterials</i> , 2013, 34, 669-676.	5.7	40
742	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
743	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
745	Transcriptome Responses to Combinations of Stresses in Arabidopsis Â Â. <i>Plant Physiology</i> , 2013, 161, 1783-1794.	2.3	478
746	Unraveling toxicological mechanisms and predicting toxicity classes with gene dysregulation networks. <i>Journal of Applied Toxicology</i> , 2013, 33, 1407-1415.	1.4	6
747	Suberoylanilide hydroxamic acid induces limited changes in the transcriptome of primary CD4+ T cells. <i>Aids</i> , 2013, 27, 29-37.	1.0	23
748	Identification of Novel in vivo MAP Kinase Substrates in Arabidopsis thaliana Through Use of Tandem Metal Oxide Affinity Chromatography. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 369-380.	2.5	122
749	Thiouracil Cross-Linking Mass Spectrometry: a Cell-Based Method To Identify Host Factors Involved in Viral Amplification. <i>Journal of Virology</i> , 2013, 87, 8697-8712.	1.5	39
750	NOA: a cytoscape plugin for network ontology analysis. <i>Bioinformatics</i> , 2013, 29, 2066-2067.	1.8	24
751	Dynamics of the Saccharomyces cerevisiae Transcriptome during Bread Dough Fermentation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7325-7333.	1.4	24
752	MicroRNA Expression Profile in Human Macrophages in Response to Leishmania major Infection. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2478.	1.3	125
753	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
754	A Global In Vivo Drosophila RNAi Screen Identifies a Key Role of Ceramide Phosphoethanolamine for Glial Ensheatment of Axons. <i>PLoS Genetics</i> , 2013, 9, e1003980.	1.5	44

#	ARTICLE	IF	CITATIONS
755	Genome scale transcriptional response diversity among ten ecotypes of <i>Arabidopsis thaliana</i> during heat stress. <i>Frontiers in Plant Science</i> , 2013, 4, 532.	1.7	43
756	Reconstruction and Analysis of Human Kidney-Specific Metabolic Network Based on Omics Data. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	11
757	Cell Reprogramming Requires Silencing of a Core Subset of Polycomb Targets. <i>PLoS Genetics</i> , 2013, 9, e1003292.	1.5	59
758	Novel Positive Regulatory Role for the SPL6 Transcription Factor in the N TIR-NB-LRR Receptor-Mediated Plant Innate Immunity. <i>PLoS Pathogens</i> , 2013, 9, e1003235.	2.1	154
759	Phosphoproteomic Analyses Reveal Signaling Pathways That Facilitate Lytic Gammaherpesvirus Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003583.	2.1	24
760	Glucocorticoids Suppress T Cell Function by Upregulating MicroRNA-98. <i>Arthritis and Rheumatism</i> , 2013, 65, 1882-1890.	6.7	52
761	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003202.	1.5	84
762	N-Glycoprotein SRMatlas. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1005-1016.	2.5	48
763	Proteomics of Genetically Engineered Mouse Mammary Tumors Identifies Fatty Acid Metabolism Members as Potential Predictive Markers for Cisplatin Resistance. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1319-1334.	2.5	24
764	Computational Translation of Nonmammalian Species Data to Mammalian Species to Meet REACH and Next Generation Risk Assessment Needs. , 2013, , 113-136.		1
765	Translational profiling of hypocretin neurons identifies candidate molecules for sleep regulation. <i>Genes and Development</i> , 2013, 27, 565-578.	2.7	87
766	High-Throughput Sequencing Reveals Principles of Adeno-Associated Virus Serotype 2 Integration. <i>Journal of Virology</i> , 2013, 87, 8559-8568.	1.5	33
767	Analysis of functional redundancies within the <i>Arabidopsis</i> TCP transcription factor family. <i>Journal of Experimental Botany</i> , 2013, 64, 5673-5685.	2.4	124
768	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
769	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. <i>Nucleic Acids Research</i> , 2013, 41, 4378-4391.	6.5	684
770	Expression profiling of mouse subplate reveals a dynamic gene network and disease association with autism and schizophrenia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3555-3560.	3.3	108
771	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
772	Beyond the Binding Site: In Vivo Identification of <i>tbx2</i> , <i>smarca5</i> and <i>wnt5b</i> as Molecular Targets of CNBP during Embryonic Development. <i>PLoS ONE</i> , 2013, 8, e63234.	1.1	17

#	ARTICLE	IF	CITATIONS
773	Dmrta1 regulates proneural gene expression downstream of $Pax6$ in the mammalian telencephalon. <i>Genes To Cells</i> , 2013, 18, 636-649.	0.5	45
774	Combining animal personalities with transcriptomics resolves individual variation within a wild-type zebrafish population and identifies underpinning molecular differences in brain function. <i>Molecular Ecology</i> , 2013, 22, 6100-6115.	2.0	66
775	Network analysis reveals complex interactions in heat shock response in the malaria parasite. , 2013, , .		0
776	ETHYLENE RESPONSE FACTOR6 Acts as a Central Regulator of Leaf Growth under Water-Limiting Conditions in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 162, 319-332.	2.3	210
777	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
778	Network-based Analysis of Genome Wide Association Data Provides Novel Candidate Genes for Lipid and Lipoprotein Traits. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3398-3408.	2.5	28
779	Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19639-19644.	3.3	131
780	Differential effect of aneuploidy on the X chromosome and genes with sex-biased expression in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16514-16519.	3.3	41
781	Genes that Respond to H ₂ O ₂ Are Also Evoked Under Light in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2013, 6, 226-228.	3.9	18
783	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
784	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
785	Determination of an Angiotensin II-regulated Proteome in Primary Human Kidney Cells by Stable Isotope Labeling of Amino Acids in Cell Culture (SILAC). <i>Journal of Biological Chemistry</i> , 2013, 288, 24834-24847.	1.6	37
786	Uridylation prevents 3' trimming of oligoadenylated mRNAs. <i>Nucleic Acids Research</i> , 2013, 41, 7115-7127.	6.5	83
787	inv(16)/t(16;16) acute myeloid leukemia with non- $t(16;16)$ type A CBFB-MYH11 fusions associate with distinct clinical and genetic features and lack KIT mutations. <i>Blood</i> , 2013, 121, 385-391.	0.6	39
788	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
789	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
790	Genomics of the fetal hypothalamic cellular response to transient hypoxia: endocrine, immune, and metabolic responses. <i>Physiological Genomics</i> , 2013, 45, 521-527.	1.0	29
791	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013, 14, 722.	1.2	73

#	ARTICLE	IF	CITATIONS
792	Temporal clustering of gene expression links the metabolic transcription factor HNF4 α to the ER stress-dependent gene regulatory network. <i>Frontiers in Genetics</i> , 2013, 4, 188.	1.1	22
793	HMGB3 characterization in gastric cancer. <i>Genetics and Molecular Research</i> , 2013, 12, 6032-6039.	0.3	28
794	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
795	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	2.8	379
796	Network Characteristic Analysis of ADR-related Proteins and Identification of ADR-ADR Associations. <i>Scientific Reports</i> , 2013, 3, 1744.	1.6	15
797	Identifying potential cancer driver genes by genomic data integration. <i>Scientific Reports</i> , 2013, 3, 3538.	1.6	60
798	Systems-Level Analysis of Proteolytic Events in Increased Vascular Permeability and Complement Activation in Skin Inflammation. <i>Science Signaling</i> , 2013, 6, rs2.	1.6	99
799	Transcriptome network analysis of potential candidate genes for heart failure. <i>Genetics and Molecular Research</i> , 2013, 12, 4687-4697.	0.3	7
800	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 526-575.	1.0	13
801	Biclustor and regulatory network analysis of differentially expressed genes in adenocarcinoma and squamous cell carcinoma. <i>Genetics and Molecular Research</i> , 2013, 12, 1710-1719.	0.3	2
802	2D Depiction of Biological Interactions and Its Applications in Drug Design. <i>Current Medical Imaging</i> , 2013, 9, 18-24.	0.4	1
803	BREEDING AND GENETICS SYMPOSIUM: Building single nucleotide polymorphism-derived gene regulatory networks: Towards functional genomewide association studies ^{1,2} . <i>Journal of Animal Science</i> , 2013, 91, 530-536.	0.2	34
804	Identification of New Protein Interactions between Dengue Fever Virus and Its Hosts, Human and Mosquito. <i>PLoS ONE</i> , 2013, 8, e53535.	1.1	118
805	Mechanisms of Intron Loss and Gain in the Fission Yeast <i>Schizosaccharomyces</i> . <i>PLoS ONE</i> , 2013, 8, e61683.	1.1	27
806	Revealing the Hidden Relationship by Sparse Modules in Complex Networks with a Large-Scale Analysis. <i>PLoS ONE</i> , 2013, 8, e66020.	1.1	3
807	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus <i>Puccinia monoica</i> in <i>Boechera stricta</i> . <i>PLoS ONE</i> , 2013, 8, e75293.	1.1	25
808	Genome-Wide Computational Prediction and Analysis of Core Promoter Elements across Plant Monocots and Dicots. <i>PLoS ONE</i> , 2013, 8, e79011.	1.1	45
809	Novel Factors in the Pathogenesis of Psoriasis and Potential Drug Candidates Are Found with Systems Biology Approach. <i>PLoS ONE</i> , 2013, 8, e80751.	1.1	24

#	ARTICLE	IF	CITATIONS
810	PPAR β Interprets a Chromatin Signature of Pluripotency to Promote Embryonic Differentiation at Gastrulation. PLoS ONE, 2013, 8, e83300.	1.1	7
811	RNA Sequencing of the Exercise Transcriptome in Equine Athletes. PLoS ONE, 2013, 8, e83504.	1.1	55
812	Link Clustering with Extended Link Similarity and EQ Evaluation Division. PLoS ONE, 2013, 8, e66005.	1.1	33
813	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
814	Using an Isolated Rat Kidney Model to Identify Kidney Origin Proteins in Urine. PLoS ONE, 2013, 8, e66911.	1.1	14
815	Molecular Signatures in Arabidopsis thaliana in Response to Insect Attack and Bacterial Infection. PLoS ONE, 2013, 8, e58987.	1.1	67
816	Construction and Analysis of the Cell Surface Proteins Protein Network for Human Sperm-Egg Interaction. , 2013, 2013, 1-8.		8
817	Comprehensive Analysis of Alternative Splicing in Digitalis purpurea by Strand-Specific RNA-Seq. PLoS ONE, 2014, 9, e106001.	1.1	12
818	Footprints of Directional Selection in Wild Atlantic Salmon Populations: Evidence for Parasite-Driven Evolution?. PLoS ONE, 2014, 9, e91672.	1.1	37
819	Integrative Gene Network Construction to Analyze Cancer Recurrence Using Semi-Supervised Learning. PLoS ONE, 2014, 9, e86309.	1.1	44
820	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
821	GWAS in a Box: Statistical and Visual Analytics of Structured Associations via GenAMap. PLoS ONE, 2014, 9, e97524.	1.1	7
822	Transcriptome Analysis of Catharanthus roseus for Gene Discovery and Expression Profiling. PLoS ONE, 2014, 9, e103583.	1.1	60
823	Response of Saccharomyces cerevisiae to the Stimulation of Lipopolysaccharide. PLoS ONE, 2014, 9, e104428.	1.1	10
824	Angiogenesis Interactome and Time Course Microarray Data Reveal the Distinct Activation Patterns in Endothelial Cells. PLoS ONE, 2014, 9, e110871.	1.1	17
825	Effects and Mechanism of Bufe Yishen Formula in a Rat Chronic Obstructive Pulmonary Disease Model. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-10.	0.5	9
826	KEGGscape: a Cytoscape app for pathway data integration. F1000Research, 2014, 3, 144.	0.8	65
827	Enrichment Map – a Cytoscape app to visualize and explore OMICs pathway enrichment results. F1000Research, 2014, 3, 141.	0.8	128

#	ARTICLE	IF	CITATIONS
828	Systems Biology Analyses of the Placenta. , 2014, , 259-274.		4
829	Analysis of protein-protein interaction network in chronic obstructive pulmonary disease. Genetics and Molecular Research, 2014, 13, 8862-8869.	0.3	8
830	Rad9 interacts with Aft1 to facilitate genome surveillance in fragile genomic sites under non-DNA damage-inducing conditions in <i>S. cerevisiae</i> . Nucleic Acids Research, 2014, 42, 12650-12667.	6.5	19
831	Arabidopsis JAGGED links floral organ patterning to tissue growth by repressing Kip-related cell cycle inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2830-2835.	3.3	94
832	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. Molecular and Cellular Proteomics, 2014, 13, 1828-1843.	2.5	45
833	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. BMC Plant Biology, 2014, 14, 370.	1.6	105
834	Transcriptome analysis highlights changes in the leaves of maize plants cultivated in acidic soil containing toxic levels of Al ³⁺ . Molecular Biology Reports, 2014, 41, 8107-8116.	1.0	26
835	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. Genome Biology, 2014, 15, 512.	3.8	475
836	Genome-wide analysis of gene expression in human embryonic tooth germ. Journal of Molecular Histology, 2014, 45, 609-617.	1.0	11
837	DNA copy number evolution in <i>Drosophila</i> cell lines. Genome Biology, 2014, 15, R70.	3.8	96
838	Pogo-like Transposases Have Been Repeatedly Domesticated into CENP-B-Related Proteins. Genome Biology and Evolution, 2014, 6, 2008-2016.	1.1	38
839	Activation of RidA chaperone function by N-chlorination. Nature Communications, 2014, 5, 5804.	5.8	70
840	A conserved extraordinarily long serine homopolymer in Dictyostelid amoebae. Heredity, 2014, 112, 215-218.	1.2	3
841	A taxonomy for bioinformatics tools. , 2014, , .		0
842	iRegulon: From a Gene List to a Gene Regulatory Network Using Large Motif and Track Collections. PLoS Computational Biology, 2014, 10, e1003731.	1.5	787
843	Wigwams: identifying gene modules co-regulated across multiple biological conditions. Bioinformatics, 2014, 30, 962-970.	1.8	36
844	Locus heterogeneity disease genes encode proteins with high interconnectivity in the human protein interaction network. Frontiers in Genetics, 2014, 5, 434.	1.1	8
845	Integrated network analysis and effective tools in plant systems biology. Frontiers in Plant Science, 2014, 5, 598.	1.7	55

#	ARTICLE	IF	CITATIONS
846	Global transcriptome analysis of developing chickpea (<i>Cicer arietinum</i> L.) seeds. <i>Frontiers in Plant Science</i> , 2014, 5, 698.	1.7	50
847	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
848	The Hypervariable Amino-Terminus of P1 Protease Modulates Potyviral Replication and Host Defense Responses. <i>PLoS Pathogens</i> , 2014, 10, e1003985.	2.1	104
849	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
850	Deregulation of the Replisome Factor MCMBP Prompts Oncogenesis in Colorectal Carcinomas through Chromosomal Instability. <i>Neoplasia</i> , 2014, 16, 694-709.	2.3	14
851	A Virulent Strain of Deformed Wing Virus (DWV) of Honeybees (<i>Apis mellifera</i>) Prevails after Varroa destructor-Mediated, or In Vitro, Transmission. <i>PLoS Pathogens</i> , 2014, 10, e1004230.	2.1	294
852	Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. <i>PLoS Genetics</i> , 2014, 10, e1004402.	1.5	93
853	Identification of Human Tissue Kallikrein 6 as a Potential Marker of Laryngeal Cancer Based on the Relevant Secretory/Releasing Protein Database. <i>Disease Markers</i> , 2014, 2014, 1-8.	0.6	10
854	RNA Sequencing Analysis Reveals Transcriptomic Variations in Tobacco (<i>Nicotiana tabacum</i>) Leaves Affected by Climate, Soil, and Tillage Factors. <i>International Journal of Molecular Sciences</i> , 2014, 15, 6137-6160.	1.8	17
855	Comparative Transcriptome Analysis of Leaves and Roots in Response to Sudden Increase in Salinity in <i>Brassica napus</i> by RNA-seq. <i>BioMed Research International</i> , 2014, 2014, 1-19.	0.9	48
856	Protein-protein interaction network analysis of osteoarthritis-related differentially expressed genes. <i>Genetics and Molecular Research</i> , 2014, 13, 9343-9351.	0.3	4
857	Exploring systems affected by the heat shock response in <i>Plasmodium falciparum</i> via protein association networks. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 369.	0.3	5
858	Transcriptome profiling of gene expression in fall dormant and nondormant alfalfa. <i>Genomics Data</i> , 2014, 2, 282-284.	1.3	2
859	On the impact of data integration and edge enrichment in mining significant signals from biological networks. , 2014, , .		0
860	Annotation of gene function in citrus using gene expression information and co-expression networks. <i>BMC Plant Biology</i> , 2014, 14, 186.	1.6	38
861	FunMod: A Cytoscape Plugin for Identifying Functional Modules in Undirected Protein-Protein Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 178-186.	3.0	6
862	Jasmonoyl-isoleucine Coordinates Metabolic Networks Required for Anthesis and Floral Attractant Emission in Wild Tobacco (<i>Nicotiana attenuata</i>) Å Å. <i>Plant Cell</i> , 2014, 26, 3964-3983.	3.1	58
863	The GalNAc-type O-Glycoproteome of CHO Cells Characterized by the SimpleCell Strategy. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3224-3235.	2.5	72

#	ARTICLE	IF	CITATIONS
864	Acetylome Analysis Reveals Diverse Functions of Lysine Acetylation in Mycobacterium tuberculosis. Molecular and Cellular Proteomics, 2014, 13, 3352-3366.	2.5	170
865	Investigation of Maternal Genotype Effects in Autism by Genome-Wide Association. Autism Research, 2014, 7, 245-253.	2.1	6
866	Mechanisms for the adverse effects of late gestational increases in maternal cortisol on the heart revealed by transcriptomic analyses of the fetal septum. Physiological Genomics, 2014, 46, 547-559.	1.0	32
867	A distinct set of long non-coding RNAs in childhood MLL-rearranged acute lymphoblastic leukemia: biology and epigenetic target. Human Molecular Genetics, 2014, 23, 3278-3288.	1.4	49
868	Neurolysin Knockout Mice Generation and Initial Phenotype Characterization. Journal of Biological Chemistry, 2014, 289, 15426-15440.	1.6	41
869	Comparison of Transcriptional Profiles Between CD4+ and CD8+ T Cells in HIV Type 1-Infected Patients. AIDS Research and Human Retroviruses, 2014, 30, 134-141.	0.5	11
870	Separate enrichment analysis of pathways for up- and downregulated genes. Journal of the Royal Society Interface, 2014, 11, 20130950.	1.5	159
871	Mineralocorticoid effects in the late gestation ovine fetal lung. Physiological Reports, 2014, 2, e12066.	0.7	6
872	Advances in urinary proteome analysis and applications in systems biology. Bioanalysis, 2014, 6, 2549-2569.	0.6	17
873	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. Stem Cell Reports, 2014, 3, 858-875.	2.3	32
874	<i>Nasonia vitripennis</i> venom causes targeted gene expression changes in its fly host. Molecular Ecology, 2014, 23, 5918-5930.	2.0	63
875	Dynamics of chromatin accessibility and gene regulation by MADS-domain transcription factors in flower development. Genome Biology, 2014, 15, R41.	13.9	210
876	Enscosin/Map7 promotes microtubule growth and centrosome separation in <i>Drosophila</i> neural stem cells. Journal of Cell Biology, 2014, 204, 1111-1121.	2.3	60
877	A Flexible Bayesian Model for Testing for Transmission Ratio Distortion. Genetics, 2014, 198, 1357-1367.	1.2	21
878	Mechanism of action of Salvianolic Acid B by module-based network analysis. Bio-Medical Materials and Engineering, 2014, 24, 1333-1340.	0.4	11
879	Integrating the interactome and the transcriptome of <i>Drosophila</i> . BMC Bioinformatics, 2014, 15, 177.	1.2	4
880	Categorizer: a tool to categorize genes into user-defined biological groups based on semantic similarity. BMC Genomics, 2014, 15, 1091.	1.2	28
881	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. Molecular and Cellular Proteomics, 2014, 13, 1753-1768.	2.5	165

#	ARTICLE	IF	CITATIONS
882	Cell Type-Specific Expression Analysis to Identify Putative Cellular Mechanisms for Neurogenetic Disorders. <i>Journal of Neuroscience</i> , 2014, 34, 1420-1431.	1.7	261
883	Genome-wide analysis of histone modifications in latently HIV-1 infected T cells. <i>Aids</i> , 2014, 28, 1719-1728.	1.0	27
884	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. <i>Molecular and Cellular Oncology</i> , 2014, 1, e957981.	0.3	1
885	Prognostic Impact of Bcl-2 Depends on Tumor Histology and Expression of MALAT-1 lncRNA in Non-Small-Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2014, 9, 1294-1304.	0.5	59
886	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
887	Disruption of murine Tcte3-3 induces tissue specific apoptosis via co-expression of Anxa5 and Pebp1. <i>Computational Biology and Chemistry</i> , 2014, 53, 214-225.	1.1	5
888	Deletion of the Human Cytomegalovirus US17 Gene Increases the Ratio of Genomes per Infectious Unit and Alters Regulation of Immune and Endoplasmic Reticulum Stress Response Genes at Early and Late Times after Infection. <i>Journal of Virology</i> , 2014, 88, 2168-2182.	1.5	34
889	Optimization of transcription factor binding map accuracy utilizing knockout-mouse models. <i>Nucleic Acids Research</i> , 2014, 42, 13051-13060.	6.5	25
890	Semantic Particularity Measure for Functional Characterization of Gene Sets Using Gene Ontology. <i>PLoS ONE</i> , 2014, 9, e86525.	1.1	12
891	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
892	Network-based detection of disease modules and potential drug targets in intractable epilepsy. , 2014, , .		2
893	Transcriptomics of the fetal hypothalamic response to brachiocephalic occlusion and estradiol treatment. <i>Physiological Genomics</i> , 2014, 46, 523-532.	1.0	12
894	The transcript elongation factor SPT4/SPT5 is involved in auxin-related gene expression in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2014, 42, 4332-4347.	6.5	54
895	Inferring the relation between transcriptional and posttranscriptional regulation from expression compendia. <i>BMC Microbiology</i> , 2014, 14, 14.	1.3	21
896	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
897	Nutrigenomics. , 2014, , 501-515.		0
898	Extended interaction network of procollagen C-proteinase enhancer-1 in the extracellular matrix. <i>Biochemical Journal</i> , 2014, 457, 137-149.	1.7	37
899	Identification of Biological Targets of Therapeutic Intervention for Diabetic Nephropathy with Bioinformatics Approach. <i>Experimental and Clinical Endocrinology and Diabetes</i> , 2014, 122, 587-591.	0.6	6

#	ARTICLE	IF	CITATIONS
900	<scp>ROCK</scp>1 is a potential combinatorial drug target for <scp>BRAF</scp> mutant melanoma. Molecular Systems Biology, 2014, 10, 772.	3.2	48
901	NetworkAnalyst - integrative approaches for proteinâ€“protein interaction network analysis and visual exploration. Nucleic Acids Research, 2014, 42, W167-W174.	6.5	398
902	Colorectal cancer derived organotypic spheroids maintain essential tissue characteristics but adapt their metabolism in culture. Proteome Science, 2014, 12, 39.	0.7	40
903	Clinical proteomic biomarkers: relevant issues on study design & technical considerations in biomarker development. Clinical and Translational Medicine, 2014, 3, 7.	1.7	105
904	<i>WOX13</i>-<i>like</i> genes are required for reprogramming of leaf and protoplast cells into stem cells in the moss <i>Physcomitrella patens</i>. Development (Cambridge), 2014, 141, 1660-1670.	1.2	136
905	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
906	Fetal Alcohol Syndrome, Chemo-Biology and OMICS: Ethanol Effects on Vitamin Metabolism During Neurodevelopment as Measured by Systems Biology Analysis. OMICS A Journal of Integrative Biology, 2014, 18, 344-363.	1.0	10
907	Highly Divergent Integration Profile of Adeno-Associated Virus Serotype 5 Revealed by High-Throughput Sequencing. Journal of Virology, 2014, 88, 2481-2488.	1.5	11
908	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. , 2014, , .		0
909	Exploration of the mechanism of pattern-specific treatments in coronary heart disease with network pharmacology approach. Computers in Biology and Medicine, 2014, 51, 198-204.	3.9	11
910	The 5p12 breast cancer susceptibility locus affects <i>MRPS30</i> expression in estrogenâ€“receptor positive tumors. Molecular Oncology, 2014, 8, 273-284.	2.1	26
911	An in-depth comparison of the male pediatric and adult urinary proteomes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1044-1050.	1.1	25
912	Chromatin Biology and Cancer Linked Through Proteinâ€“Protein Interactions. , 2014, , 49-63.		0
913	Study of differential effects of TGF-beta3/BMP2 on chondrogenesis in MSC cells by gene microarray data analysis. Molecular and Cellular Biochemistry, 2014, 385, 191-198.	1.4	15
914	Contribution of NAC Transcription Factors to Plant Adaptation to Land. Science, 2014, 343, 1505-1508.	6.0	222
915	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. BMC Genomics, 2014, 15, 151.	1.2	193
916	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2014, 5, 59-68.	4.8	26
917	Protein signatures of oxidative stress response in a patient specific cell line model for autism. Molecular Autism, 2014, 5, 10.	2.6	22

#	ARTICLE	IF	CITATIONS
918	Global secretome characterization of A549 human alveolar epithelial carcinoma cells during Mycoplasma pneumoniae infection. BMC Microbiology, 2014, 14, 27.	1.3	17
919	Insecticide resistance mechanisms associated with different environments in the malaria vector Anopheles gambiae: a case study in Tanzania. Malaria Journal, 2014, 13, 28.	0.8	127
920	Sex differences in the human peripheral blood transcriptome. BMC Genomics, 2014, 15, 33.	1.2	131
921	Inferring transcription factor collaborations in gene regulatory networks. BMC Systems Biology, 2014, 8, S1.	3.0	10
922	Gene expression profiling and bioinformatics analysis of gastric carcinoma. Experimental and Molecular Pathology, 2014, 96, 361-366.	0.9	20
923	Analysis of Multiple DNA Microarray Datasets. , 2014, , 223-234.		5
924	Clustering approaches for dealing with multiple DNA microarray datasets. Journal of Computational Science, 2014, 5, 368-376.	1.5	11
925	Modulation of Gene Expression Regulated by the Transcription Factor NF- κ B/RelA. Journal of Biological Chemistry, 2014, 289, 11927-11944.	1.6	28
926	The unfolded protein response governs integrity of the haematopoietic stem-cell pool during stress. Nature, 2014, 510, 268-272.	13.7	292
927	Proteomic analysis of cerebrospinal fluid extracellular vesicles: A comprehensive dataset. Journal of Proteomics, 2014, 106, 191-204.	1.2	222
928	Transcriptomics of salinity tolerance capacity in Arctic charr (<i>Salvelinus alpinus</i>): a comparison of gene expression profiles between divergent QTL genotypes. Physiological Genomics, 2014, 46, 123-137.	1.0	32
929	The tobacco genome sequence and its comparison with those of tomato and potato. Nature Communications, 2014, 5, 3833.	5.8	503
930	Characterization of the canine urinary proteome. Veterinary Clinical Pathology, 2014, 43, 193-205.	0.3	24
931	Genomewide discovery of DNA polymorphisms in rice cultivars with contrasting drought and salinity stress response and their functional relevance. Plant Biotechnology Journal, 2014, 12, 253-264.	4.1	128
932	<i>ABCC4</i> copy number variation is associated with susceptibility to esophageal squamous cell carcinoma. Carcinogenesis, 2014, 35, 1941-1950.	1.3	47
933	Global identification of O-GlcNAc transferase (OGT) interactors by a human proteome microarray and the construction of an OGT interactome. Proteomics, 2014, 14, 1020-1030.	1.3	35
934	The effect of cell subset isolation method on gene expression in leukocytes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 94-104.	1.1	63
935	Role of CYB5A in Pancreatic Cancer Prognosis and Autophagy Modulation. Journal of the National Cancer Institute, 2014, 106, djt346.	3.0	65

#	ARTICLE	IF	CITATIONS
936	Global Phosphoproteomic Analysis of <i>Daphnia pulex</i> Reveals Evolutionary Conservation of Ser/Thr/Tyr Phosphorylation. <i>Journal of Proteome Research</i> , 2014, 13, 1327-1335.	1.8	13
937	Lifelong Exercise Training Modulates Cardiac Mitochondrial Phosphoproteome in Rats. <i>Journal of Proteome Research</i> , 2014, 13, 2045-2055.	1.8	20
938	Colorectal cancer candidate biomarkers identified by tissue secretome proteome profiling. <i>Journal of Proteomics</i> , 2014, 99, 26-39.	1.2	81
939	High-Resolution Transcript Profiling of the Atypical Biotrophic Interaction between <i>Theobroma cacao</i> and the Fungal Pathogen <i>Moniliophthora perniciosa</i> . <i>Plant Cell</i> , 2014, 26, 4245-4269.	3.1	99
940	The Involvement of Cholesterol in Sepsis and Tolerance to Lipopolysaccharide Highlighted by the Transcriptome Analysis of Zebrafish (<i>Danio rerio</i>). <i>Zebrafish</i> , 2014, 11, 421-433.	0.5	20
941	An integrated transcriptomic and comparative genomic analysis of differential gene expression in Arctic charr (<i>Salvelinus alpinus</i>) following seawater exposure. <i>Journal of Experimental Biology</i> , 2014, 217, 4029-42.	0.8	16
942	RNA-seq profiling the transcriptome of secondary seed dormancy in canola (<i>Brassica napus</i> L.). <i>Science Bulletin</i> , 2014, 59, 4341-4351.	1.7	5
943	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. <i>Briefings in Bioinformatics</i> , 2014, 15, 942-952.	3.2	16
944	Functional Mapping of the Zebrafish Early Embryo Proteome and Transcriptome. <i>Journal of Proteome Research</i> , 2014, 13, 5536-5550.	1.8	39
945	Amyloid precursor protein regulates neurogenesis by antagonizing miR-574-5p in the developing cerebral cortex. <i>Nature Communications</i> , 2014, 5, 3330.	5.8	44
946	Identification of the PKR Nuclear Interactome Reveals Roles in Ribosome Biogenesis, mRNA Processing and Cell Division. <i>Journal of Cellular Physiology</i> , 2014, 229, 1047-1060.	2.0	23
947	Annotation and retrieval in protein interaction databases. <i>European Physical Journal Plus</i> , 2014, 129, 1.	1.2	0
948	Quantitative proteomics reveals novel therapeutic and diagnostic markers in hypertension. <i>BBA Clinical</i> , 2014, 2, 79-87.	4.1	26
949	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , 2014, 9, 2539-2554.	5.5	169
950	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
951	Kinetochore genes are required to fully activate secretory pathway expansion in <i>S. cerevisiae</i> under induced ER stress. <i>Molecular BioSystems</i> , 2014, 10, 1790.	2.9	8
952	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
953	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
954	Duodenal CCK Cells from Male Mice Express Multiple Hormones Including Ghrelin. <i>Endocrinology</i> , 2014, 155, 3339-3351.	1.4	58
955	Quantitative proteomics reveals olfactory input-dependent alterations in the mouse olfactory bulb proteome. <i>Journal of Proteomics</i> , 2014, 109, 125-142.	1.2	10
956	Genome Structures and Transcriptomes Signify Niche Adaptation for the Multiple-Ion-Tolerant Extremophyte <i>Schrenkiella parvula</i> . <i>Plant Physiology</i> , 2014, 164, 2123-2138.	2.3	77
957	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
958	A network perspective on nitrogen metabolism from model to crop plants using integrated “omics” approaches. <i>Journal of Experimental Botany</i> , 2014, 65, 5619-5630.	2.4	54
959	Machine Learning-Based Differential Network Analysis: A Study of Stress-Responsive Transcriptomes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 520-537.	3.1	104
960	Transcriptomic profiling revealed an important role of cell wall remodeling and ethylene signaling pathway during salt acclimation in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2014, 86, 303-317.	2.0	126
961	The Proto-MHC of Placozoans, a Region Specialized in Cellular Stress and Ubiquitination/Proteasome Pathways. <i>Journal of Immunology</i> , 2014, 193, 2891-2901.	0.4	22
963	Uncovering the defence responses of <i>Eucalyptus</i> to pests and pathogens in the genomics age. <i>Tree Physiology</i> , 2014, 34, 931-943.	1.4	48
964	Identification of Functional Modules by Integration of Multiple Data Sources Using a Bayesian Network Classifier. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 206-217.	5.1	5
965	Hepatic transcriptomic profiling reveals early toxicological mechanisms of uranium in Atlantic salmon (<i>Salmo salar</i>). <i>BMC Genomics</i> , 2014, 15, 694.	1.2	35
966	De novo assembly and characterization of the transcriptome in the desiccation-tolerant moss <i>Syntrichia caninervis</i> . <i>BMC Research Notes</i> , 2014, 7, 490.	0.6	69
967	SoxNeuro orchestrates central nervous system specification and differentiation in <i>Drosophila</i> and is only partially redundant with Dichaete. <i>Genome Biology</i> , 2014, 15, R74.	13.9	33
968	A system based network approach to ethanol tolerance in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2014, 8, 90.	3.0	19
969	Dose-dependent hepatic transcriptional responses in Atlantic salmon (<i>Salmo salar</i>) exposed to sublethal doses of gamma radiation. <i>Aquatic Toxicology</i> , 2014, 156, 52-64.	1.9	17
970	Insights into pathophysiology of dystrophy through the analysis of gene networks: an example of bronchial asthma and tuberculosis. <i>Immunogenetics</i> , 2014, 66, 457-465.	1.2	21
971	Biological Network Exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , 2014, 47, 8.13.1-24.	25.8	780
973	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

#	ARTICLE	IF	CITATIONS
974	In-depth proteomic delineation of the colorectal cancer exoproteome: Mechanistic insight and identification of potential biomarkers. <i>Journal of Proteomics</i> , 2014, 103, 121-136.	1.2	25
975	Differential impact of cumulative SES risk on methylation of protein-protein interaction pathways as a function of SLC6A4 genetic variation in African American young adults. <i>Biological Psychology</i> , 2014, 96, 28-34.	1.1	31
976	A formal concept analysis approach to consensus clustering of multi-experiment expression data. <i>BMC Bioinformatics</i> , 2014, 15, 151.	1.2	15
977	RNA-seq analysis identifies an intricate regulatory network controlling cluster root development in white lupin. <i>BMC Genomics</i> , 2014, 15, 230.	1.2	43
978	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
979	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
980	Characterization of the membrane proteome and N-glycoproteome in BV-2 mouse microglia by liquid chromatography-tandem mass spectrometry. <i>BMC Genomics</i> , 2014, 15, 95.	1.2	18
981	Proteomics analysis of the peritoneal dialysate effluent reveals the presence of calcium-regulation proteins and acute inflammatory response. <i>Clinical Proteomics</i> , 2014, 11, 17.	1.1	24
982	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
983	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
984	Information Sciences and Systems 2014. , 2014, , .		8
985	Proteomic Analysis of Mouse Testis Reveals Perfluorooctanoic Acid-Induced Reproductive Dysfunction via Direct Disturbance of Testicular Steroidogenic Machinery. <i>Journal of Proteome Research</i> , 2014, 13, 3370-3385.	1.8	85
986	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014, 5, 4392.	5.8	137
987	Metabolomic Characterization of Knockout Mutants in Arabidopsis: Development of a Metabolite Profiling Database for Knockout Mutants in Arabidopsis. <i>Plant Physiology</i> , 2014, 165, 948-961.	2.3	49
988	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
989	A high-resolution gene expression map of the Arabidopsis shoot meristem stem cell niche. <i>Development (Cambridge)</i> , 2014, 141, 2735-2744.	1.2	110
990	Deep Transcriptome Sequencing of Wild Halophyte Rice, <i>Porteresia coarctata</i> , Provides Novel Insights into the Salinity and Submergence Tolerance Factors. <i>DNA Research</i> , 2014, 21, 69-84.	1.5	137
991	Exploring the mechanisms of different treatments for endotoxic shock through literature mining and systems biology. <i>European Journal of Integrative Medicine</i> , 2014, 6, 56-63.	0.8	2

#	ARTICLE	IF	CITATIONS
992	Nasal mucus proteomic changes reflect altered immune responses and epithelial permeability in patients with allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 741-750.	1.5	74
993	Mapping genomic markers to closest feature using the R package Map2NCBI. <i>Livestock Science</i> , 2014, 162, 59-65.	0.6	18
994	Proteomics of differential extraction fractions enriched for chromatin-binding proteins from colon adenoma and carcinoma tissues. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1034-1043.	1.1	8
995	Natural antisense transcripts in <i>Plasmodium falciparum</i> isolates from patients with complicated malaria. <i>Experimental Parasitology</i> , 2014, 141, 39-54.	0.5	12
996	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
997	<i>Arabidopsis</i> Phytochrome A Directly Targets Numerous Promoters for Individualized Modulation of Genes in a Wide Range of Pathways. <i>Plant Cell</i> , 2014, 26, 1949-1966.	3.1	73
998	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
999	Interactomics of Qa-SNARE in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2014, 55, 781-789.	1.5	98
1000	The ROS/SUMO Axis Contributes to the Response of Acute Myeloid Leukemia Cells to Chemotherapeutic Drugs. <i>Cell Reports</i> , 2014, 7, 1815-1823.	2.9	86
1001	Contextualised urinary biomarker analysis facilitates diagnosis of paediatric obstructive sleep apnoea. <i>Sleep Medicine</i> , 2014, 15, 541-549.	0.8	27
1002	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
1003	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
1004	Screening of diagnostic markers for osteosarcoma. <i>Molecular Medicine Reports</i> , 2014, 10, 2415-2420.	1.1	29
1005	Construction and validation of a gene co-expression network in grapevine (<i>Vitis vinifera</i> L.). <i>Horticulture Research</i> , 2014, 1, 14040.	2.9	32
1006	Modelling epigenetic regulation of gene expression in 12 human cell types reveals combinatorial patterns of cell-type-specific genes. <i>IET Systems Biology</i> , 2014, 8, 104-115.	0.8	3
1007	Antitumor mechanism research of cryptotanshinone by module-based network analysis. , 2014, , .		0
1008	The <i>Leishmania</i> metaphylome: a comprehensive survey of <i>Leishmania</i> protein phylogenetic relationships. <i>BMC Genomics</i> , 2015, 16, 887.	1.2	21
1009	Genomewide effects of peroxisome proliferator-activated receptor gamma in macrophages and dendritic cells â€œ revealing complexity through systems biology. <i>European Journal of Clinical Investigation</i> , 2015, 45, 964-975.	1.7	11

#	ARTICLE	IF	CITATIONS
1010	Comparison of genome-wide gene expression patterns in the seedlings of nascent allohexaploid wheats produced by two combinations of hybrids. <i>Genes and Genetic Systems</i> , 2015, 90, 79-88.	0.2	3
1011	Integrative analysis of human protein, function and disease networks. <i>Scientific Reports</i> , 2015, 5, 14344.	1.6	32
1012	In silico analysis of the molecular mechanism of postmenopausal osteoporosis. <i>Molecular Medicine Reports</i> , 2015, 12, 6584-6590.	1.1	21
1013	Microarray based analysis of gene regulation by microRNA in intervertebral disc degeneration. <i>Molecular Medicine Reports</i> , 2015, 12, 4925-4930.	1.1	25
1014	Functional analysis of the nasopharyngeal carcinoma primary tumor-associated gene interaction network. <i>Molecular Medicine Reports</i> , 2015, 12, 4975-4980.	1.1	9
1015	A systems biology approach to detect key pathways and interaction networks in gastric cancer on the basis of microarray analysis. <i>Molecular Medicine Reports</i> , 2015, 12, 7139-7145.	1.1	4
1016	Co-existence of intact stemness and priming of neural differentiation programs in mES cells lacking Trim71. <i>Scientific Reports</i> , 2015, 5, 11126.	1.6	39
1017	Integrative analyses reveal transcriptome-proteome correlation in biological pathways and secondary metabolism clusters in <i>A. flavus</i> in response to temperature. <i>Scientific Reports</i> , 2015, 5, 14582.	1.6	100
1018	Direct production of XYDMYâˆ² sex reversal female medaka (<i>Oryzias latipes</i>) by embryo microinjection of TALENs. <i>Scientific Reports</i> , 2015, 5, 14057.	1.6	18
1022	Genome-wide expression analysis offers new insights into the origin and evolution of <i>Physcomitrella patens</i> stress response. <i>Scientific Reports</i> , 2015, 5, 17434.	1.6	54
1023	DATA MINING AND SYSTEMS BIOLOGY FOR IDENTIFYING KEY GENES INVOLVED IN CITRUS QUALITY. <i>Acta Horticulturae</i> , 2015, , 591-598.	0.1	0
1024	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
1025	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
1026	Genome of the facultative scuticociliatosis pathogen <i>Pseudocohnilembus persalinus</i> provides insight into its virulence through horizontal gene transfer. <i>Scientific Reports</i> , 2015, 5, 15470.	1.6	46
1027	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
1028	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	1.4	16
1029	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
1030	The yeast Î²-crystallin/NADPH:quinone oxidoreductase (Zta1p) is under nutritional control by the target of rapamycin pathway and is involved in the regulation of argininosuccinate lyase <scp>mRNA</scp> halfâ€šĆŒife. <i>FEBS Journal</i> , 2015, 282, 1953-1964.	2.2	6

#	ARTICLE	IF	CITATIONS
1031	Molecular association of pathogenetic contributors to pre-eclampsia (pre-eclampsia associome). BMC Systems Biology, 2015, 9, S4.	3.0	25
1032	Analysis of 5â€™ gene regions reveals extraordinary conservation of novel non-coding sequences in a wide range of animals. BMC Evolutionary Biology, 2015, 15, 227.	3.2	7
1033	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine (<i>Vitis vinifera</i> L.) cultivars. BMC Genomics, 2015, 16, 946.	1.2	41
1034	Transcriptomic characterization of the dorsal lobes after hepatectomy of the ventral lobe in zebrafish. BMC Genomics, 2015, 16, 979.	1.2	7
1035	The first draft genome of the aquatic model plant <i>Lemna minor</i> opens the route for future stress physiology research and biotechnological applications. Biotechnology for Biofuels, 2015, 8, 188.	6.2	112
1036	Differential sialotranscriptomes of unfed and fed <i>Rhipicephalus haemaphysaloides</i> , with particular regard to differentially expressed genes of cysteine proteases. Parasites and Vectors, 2015, 8, 597.	1.0	39
1037	Gene expression meta-analysis reveals immune response convergence on the IFNÎ³-STAT1-IRF1 axis and adaptive immune resistance mechanisms in lymphoma. Genome Medicine, 2015, 7, 96.	3.6	24
1038	Proteomic analysis of extracellular vesicles from medullospheres reveals a role for iron in the cancer progression of medulloblastoma. Molecular and Cellular Therapies, 2015, 3, 8.	0.2	19
1039	Cell type-specific responses to salinity â€” the epidermal bladder cell transcriptome of <i>Mesembryanthemum crystallinum</i> . New Phytologist, 2015, 207, 627-644.	3.5	102
1040	CD11b+Ly6C++Ly6Gâˆ’ cells with suppressive activity towards T cells accumulate in lungs of influenza A virus-infected mice. European Journal of Microbiology and Immunology, 2015, 5, 246-255.	1.5	5
1041	The origin and genetic differentiation of the socially parasitic aphid <i>Tamalia inquilinus</i> . Molecular Ecology, 2015, 24, 5751-5766.	2.0	11
1042	The wheat resistance gene <i>Lr34</i> results in the constitutive induction of multiple defense pathways in transgenic barley. Plant Journal, 2015, 84, 202-215.	2.8	45
1043	PEIMAN 1.0: Post-translational modification Enrichment, Integration and Matching ANalysis. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav037.	1.4	10
1044	Brief Exercises Affect Gene Expression in Circulating Monocytes. Scandinavian Journal of Immunology, 2015, 82, 429-435.	1.3	14
1048	The Mechanism Research of Qishen Yiqi Formula by Module-Network Analysis. Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-12.	0.5	3
1049	Tools for visualization and analysis of molecular networks, pathways, and -omics data. Advances and Applications in Bioinformatics and Chemistry, 2015, 8, 11.	1.6	50
1050	A predicted protein interactome identifies conserved global networks and disease resistance subnetworks in maize. Frontiers in Genetics, 2015, 6, 201.	1.1	35
1051	Exome sequencing of a colorectal cancer family reveals shared mutation pattern and predisposition circuitry along tumor pathways. Frontiers in Genetics, 2015, 6, 288.	1.1	11

#	ARTICLE	IF	CITATIONS
1052	A Genomic Screen Revealing the Importance of Vesicular Trafficking Pathways in Genome Maintenance and Protection against Genotoxic Stress in Diploid <i>Saccharomyces cerevisiae</i> Cells. PLoS ONE, 2015, 10, e0120702.	1.1	28
1053	Alternative Polyadenylation Allows Differential Negative Feedback of Human miRNA miR-579 on Its Host Gene ZFR. PLoS ONE, 2015, 10, e0121507.	1.1	24
1054	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. PLoS ONE, 2015, 10, e0122170.	1.1	36
1055	Consensus Comparative Analysis of Human Embryonic Stem Cell-Derived Cardiomyocytes. PLoS ONE, 2015, 10, e0125442.	1.1	1
1056	Altered Protein Expression in the Ileum of Mice Associated with the Development of Chronic Infections with <i>Echinostoma caproni</i> (Trematoda). PLoS Neglected Tropical Diseases, 2015, 9, e0004082.	1.3	22
1057	Time-Dependent Transcriptional Changes in Axenic <i>Giardia duodenalis</i> Trophozoites. PLoS Neglected Tropical Diseases, 2015, 9, e0004261.	1.3	16
1058	A de novo Assembly of the Common Frog (<i>Rana temporaria</i>) Transcriptome and Comparison of Transcription Following Exposure to Ranavirus and <i>Batrachochytrium dendrobatidis</i> . PLoS ONE, 2015, 10, e0130500.	1.1	32
1059	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. PLoS ONE, 2015, 10, e0130902.	1.1	40
1060	Transcriptome Analysis of the Emerald Ash Borer (EAB), <i>Agrilus planipennis</i> : De Novo Assembly, Functional Annotation and Comparative Analysis. PLoS ONE, 2015, 10, e0134824.	1.1	9
1061	Control of Neuronal Network in <i>Caenorhabditis elegans</i> . PLoS ONE, 2015, 10, e0139204.	1.1	18
1062	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. PLoS Genetics, 2015, 11, e1005635.	1.5	173
1063	Spatial dissection of the <i>Arabidopsis thaliana</i> transcriptional response to downy mildew using Fluorescence Activated Cell Sorting. Frontiers in Plant Science, 2015, 6, 527.	1.7	23
1064	RNA-Seq analysis identifies key genes associated with haustorial development in the root hemiparasite <i>Santalum album</i> . Frontiers in Plant Science, 2015, 6, 661.	1.7	49
1065	Comparative proteomic analysis of a membrane-enriched fraction from flag leaves reveals responses to chemical hybridization agent SQ-1 in wheat. Frontiers in Plant Science, 2015, 6, 669.	1.7	23
1066	Common protein sequence signatures associate with <i>Sclerotinia borealis</i> lifestyle and secretion in fungal pathogens of the Sclerotiniaceae. Frontiers in Plant Science, 2015, 6, 776.	1.7	16
1067	Global analysis of WRKY transcription factor superfamily in <i>Setaria</i> identifies potential candidates involved in abiotic stress signaling. Frontiers in Plant Science, 2015, 6, 910.	1.7	96
1068	A Network Flow Approach to Predict Protein Targets and Flavonoid Backbones to Treat Respiratory Syncytial Virus Infection. BioMed Research International, 2015, 2015, 1-9.	0.9	13
1069	A New Mining Algorithm of Target Genes of Anti-Aging Traditional Chinese Medicines with Complex Networks. Current Bioinformatics, 2015, 10, 85-90.	0.7	0

#	ARTICLE	IF	CITATIONS
1070	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
1071	The Avian Transcriptome Response to Malaria Infection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1255-1267.	3.5	83
1072	Developmental-stage-dependent transcriptional response to leukaemic oncogene expression. <i>Nature Communications</i> , 2015, 6, 7203.	5.8	24
1073	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . <i>Plant Cell</i> , 2015, 27, 1567-1578.	3.1	78
1074	Context dependent preferential attachment model for complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2015, 436, 499-508.	1.2	14
1075	Visual annotation display (VLAD): a tool for finding functional themes in lists of genes. <i>Mammalian Genome</i> , 2015, 26, 567-573.	1.0	37
1076	Promoter hypermethylation of let-7a-3 is relevant to its down-expression in diabetic nephropathy by targeting UHRF1. <i>Gene</i> , 2015, 570, 57-63.	1.0	41
1077	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
1078	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
1079	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
1080	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
1081	Genome-Wide Analysis Reveals Diverged Patterns of Codon Bias, Gene Expression, and Rates of Sequence Evolution in <i>Picea</i> Gene Families. <i>Genome Biology and Evolution</i> , 2015, 7, 1002-1015.	1.1	63
1082	A novel method to prioritize RNAseq data for post-hoc analysis based on absolute changes in transcript abundance. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 227-41.	0.2	0
1083	The anatomical distribution of genetic associations. <i>Nucleic Acids Research</i> , 2015, 43, 10804-10820.	6.5	37
1084	Nuclear respiratory factor 2 induces <i>SIRT3</i> expression. <i>Aging Cell</i> , 2015, 14, 818-825.	3.0	68
1085	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
1086	Systematic Determination of Human Cyclin Dependent Kinase (CDK)-9 Interactome Identifies Novel Functions in RNA Splicing Mediated by the DEAD Box (DDX)-5/17 RNA Helicases*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2701-2721.	2.5	34
1087	Comparative studies of mitochondrial proteomics reveal an intimate protein network of male sterility in wheat (<i>Triticum aestivum</i> L.). <i>Journal of Experimental Botany</i> , 2015, 66, 6191-6203.	2.4	59

#	ARTICLE	IF	CITATIONS
1088	Gene set enrichment ensemble using fold change data only. Journal of Biomedical Informatics, 2015, 57, 189-203.	2.5	5
1089	A novel phosphate-starvation response in fission yeast requires the endocytic function of Myosin I. Journal of Cell Science, 2015, 128, 3707-13.	1.2	2
1090	Comprehensive characterization of a time-course transcriptional response induced by autotoxins in Panax ginseng using RNA-Seq. BMC Genomics, 2015, 16, 1010.	1.2	35
1091	Transcriptional Dynamics Driving MAMP-Triggered Immunity and Pathogen Effector-Mediated Immunosuppression in Arabidopsis Leaves Following Infection with <i>Pseudomonas syringae</i> pv tomato DC3000. Plant Cell, 2015, 27, 3038-3064.	3.1	148
1092	The <i>IDA/IDA-LIKE</i> and <i>PIP/PIP-LIKE</i> gene families in <i>Arabidopsis</i> : phylogenetic relationship, expression patterns, and transcriptional effect of the PIPL3 peptide. Journal of Experimental Botany, 2015, 66, 5351-5365.	2.4	72
1093	Integrating prior biological knowledge and graphical LASSO for network inference. , 2015, , .		5
1094	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. Genome Biology, 2015, 16, 79.	3.8	91
1095	Comparative genomic analysis of Leishmania (Viannia) peruviana and Leishmania (Viannia) braziliensis. BMC Genomics, 2015, 16, 715.	1.2	54
1096	17 β -Ethinylestradiol (EE2) effect on global gene expression in primary rainbow trout (Oncorhynchus Tj ETQq0 0 0.rgBT /Overlock 10 Tf	1.9	31
1097	Potential microRNA biomarkers for acute ischemic stroke. International Journal of Molecular Medicine, 2015, 36, 1639-1647.	1.8	32
1098	Skeletal muscle proteomic signature and metabolic impairment in pulmonary hypertension. Journal of Molecular Medicine, 2015, 93, 573-584.	1.7	53
1099	<i>Arabidopsis</i> Ensemble Reverse-Engineered Gene Regulatory Network Discloses Interconnected Transcription Factors in Oxidative Stress. Plant Cell, 2015, 26, 4656-4679.	3.1	79
1100	Proteomics of tissue factor silencing in cardiomyocytic cells reveals a new role for this coagulation factor in splicing machinery control. Journal of Proteomics, 2015, 119, 75-89.	1.2	5
1101	Reconstruction of Canine Diffuse Large B-cell Lymphoma Gene Regulatory Network: Detection of Functional Modules and Hub Genes. Journal of Comparative Pathology, 2015, 152, 119-130.	0.1	15
1102	UDP-Arabinopyranose Mutase 3 is Required for Pollen Wall Morphogenesis in Rice (Oryza sativa). Plant and Cell Physiology, 2015, 56, 232-241.	1.5	45
1103	Hierarchical organization of fluxes in Escherichia coli metabolic network: Using flux coupling analysis for understanding the physiological properties of metabolic genes. Gene, 2015, 561, 199-208.	1.0	6
1104	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. Proteomics, 2015, 15, 1390-1404.	1.3	38
1105	The immunological consequences of pasteurisation: Comparison of the response of human intestinally-derived cells to raw versus pasteurised milk. International Dairy Journal, 2015, 40, 67-72.	1.5	5

#	ARTICLE	IF	CITATIONS
1106	Comparison of tamoxifen and letrozole response in mammary preneoplasia of ER and aromatase overexpressing mice defines an immune-associated gene signature linked to tamoxifen resistance. <i>Carcinogenesis</i> , 2015, 36, 122-132.	1.3	16
1107	Lipid droplet remodeling and interaction with mitochondria in mouse brown adipose tissue during cold treatment. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 918-928.	1.9	113
1108	Network representations of immune system complexity. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015, 7, 13-38.	6.6	75
1109	Leaf Responses to Mild Drought Stress in Natural Variants of <i>Arabidopsis</i> Å. <i>Plant Physiology</i> , 2015, 167, 800-816.	2.3	176
1110	Revealing Shared and Distinct Gene Network Organization in <i>Arabidopsis</i> Immune Responses by Integrative Analysis. <i>Plant Physiology</i> , 2015, 167, 1186-1203.	2.3	62
1111	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
1112	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
1113	Revealing the Potential Pathogenesis of Glioma by Utilizing a Glioma Associated Protein-Protein Interaction Network. <i>Pathology and Oncology Research</i> , 2015, 21, 455-462.	0.9	7
1114	Early markers of Fabry disease revealed by proteomics. <i>Molecular BioSystems</i> , 2015, 11, 1543-1551.	2.9	51
1115	Deficiency of the <i>Arabidopsis</i> Helicase RTEL1 Triggers a SOG1-Dependent Replication Checkpoint in Response to DNA Cross-Links. <i>Plant Cell</i> , 2015, 27, 149-161.	3.1	44
1116	Bisphenol A Alters Autonomic Tone and Extracellular Matrix Structure and Induces Sex-Specific Effects on Cardiovascular Function in Male and Female CD-1 Mice. <i>Endocrinology</i> , 2015, 156, 882-895.	1.4	60
1117	Clinical Proteomics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	1
1118	Basonuclin-1 modulates epithelial plasticity and TGF-Î²1-induced loss of epithelial cell integrity. <i>Oncogene</i> , 2015, 34, 1185-1195.	2.6	7
1119	The reverse evolution from multicellularity to unicellularity during carcinogenesis. <i>Nature Communications</i> , 2015, 6, 6367.	5.8	110
1120	Social odors conveying dominance and reproductive information induce rapid physiological and neuromolecular changes in a cichlid fish. <i>BMC Genomics</i> , 2015, 16, 114.	1.2	21
1121	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
1122	Permanent proteins in the urine of healthy humans during the Mars-500 experiment. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1540001.	0.3	17
1123	Plant Functional Genomics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	9

#	ARTICLE	IF	CITATIONS
1124	Systems Chemoâ€Biology and Transcriptomic Metaâ€Analysis Reveal the Molecular Roles of Bioactive Lipids in Cardiomyocyte Differentiation. <i>Journal of Cellular Biochemistry</i> , 2015, 116, 2018-2031.	1.2	1
1125	Delicate Metabolic Control and Coordinated Stress Response Critically Determine Antifungal Tolerance of <i>Candida albicans</i> Biofilm Persists. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6101-6112.	1.4	67
1126	Mis-targeted mitochondrial proteins activate a proteostatic response in the cytosol. <i>Nature</i> , 2015, 524, 485-488.	13.7	348
1127	Cmr1/WDR76 defines a nuclear genotoxic stress body linking genome integrity and protein quality control. <i>Nature Communications</i> , 2015, 6, 6533.	5.8	80
1128	Computational approaches to identify regulators of plant stress response using high-throughput gene expression data. <i>Current Plant Biology</i> , 2015, 3-4, 20-29.	2.3	16
1129	The generation of phosphoserine stretches in phosphoproteins: mechanism and significance. <i>Molecular BioSystems</i> , 2015, 11, 2666-2679.	2.9	27
1130	Non-thermal plasma treatment altered gene expression profiling in non-small-cell lung cancer A549 cells. <i>BMC Genomics</i> , 2015, 16, 435.	1.2	55
1131	Employing genome-wide SNP discovery and genotyping strategy to extrapolate the natural allelic diversity and domestication patterns in chickpea. <i>Frontiers in Plant Science</i> , 2015, 6, 162.	1.7	104
1132	IL-10 Production in Macrophages Is Regulated by a TLR-Driven CREB-Mediated Mechanism That Is Linked to Genes Involved in Cell Metabolism. <i>Journal of Immunology</i> , 2015, 195, 1218-1232.	0.4	92
1133	SCARECROW-LIKE15 interacts with HISTONE DEACETYLASE19 and is essential for repressing the seed maturation programme. <i>Nature Communications</i> , 2015, 6, 7243.	5.8	58
1134	Competency for shoot regeneration from <i>Arabidopsis</i> root explants is regulated by DNA methylation. <i>Plant Science</i> , 2015, 238, 251-261.	1.7	63
1135	Stress-caused anergy of leukocytes towards Staphylococcal enterotoxin B and exposure transcriptome signatures. <i>Genes and Immunity</i> , 2015, 16, 330-346.	2.2	1
1136	Comparative analysis of the role of CD4+ and CD8+ T cells in severe asthma development. <i>Molecular Biology</i> , 2015, 49, 427-434.	0.4	0
1137	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
1138	MicroRNA expression in BRAF-mutated and wild-type metastatic melanoma and its correlation with response duration to BRAF inhibitors. <i>Expert Opinion on Therapeutic Targets</i> , 2015, 19, 1027-1035.	1.5	27
1139	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
1140	Quantitative Circadian Phosphoproteomic Analysis of <i>Arabidopsis</i> Reveals Extensive Clock Control of Key Components in Physiological, Metabolic, and Signaling Pathways. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2243-2260.	2.5	99
1141	The Monoterpene Carvacrol Generates Endoplasmic Reticulum Stress in the Pathogenic Fungus <i>Candida albicans</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 4584-4592.	1.4	58

#	ARTICLE	IF	CITATIONS
1142	Suppression of T Cell Activation and Collagen Accumulation by an Anti-IFNAR1 mAb, Anifrolumab, in Adult Patients with Systemic Sclerosis. <i>Journal of Investigative Dermatology</i> , 2015, 135, 2402-2409.	0.3	73
1143	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
1144	Integrative Multi-omics Module Network Inference with Lemon-Tree. <i>PLoS Computational Biology</i> , 2015, 11, e1003983.	1.5	86
1145	ComPPI: a cellular compartment-specific database for protein-protein interaction network analysis. <i>Nucleic Acids Research</i> , 2015, 43, D485-D493.	6.5	116
1146	Evolutionary trends and functional anatomy of the human expanded autophagy network. <i>Autophagy</i> , 2015, 11, 1652-1667.	4.3	21
1147	The Arabidopsis SWI2/SNF2 Chromatin Remodeler BRAHMA Regulates Polycomb Function during Vegetative Development and Directly Activates the Flowering Repressor Gene SVP. <i>PLoS Genetics</i> , 2015, 11, e1004944.	1.5	111
1148	Functional Analysis and Transcriptomic Profiling of iPSC-Derived Macrophages and Their Application in Modeling Mendelian Disease. <i>Circulation Research</i> , 2015, 117, 17-28.	2.0	120
1149	Human monocyte-derived macrophages are heterogenous: Proteomic profile of different phenotypes. <i>Journal of Proteomics</i> , 2015, 124, 112-123.	1.2	33
1150	High-throughput transcriptome analysis of ISAV-infected Atlantic salmon <i>Salmo salar</i> unravels divergent immune responses associated to head-kidney, liver and gills tissues. <i>Fish and Shellfish Immunology</i> , 2015, 45, 367-377.	1.6	73
1151	Non-exclusive Clustering: A Partitioning Approach. , 2015, , .		0
1152	Network decomposition based large-scale reverse engineering of gene regulatory network. <i>Neurocomputing</i> , 2015, 160, 213-227.	3.5	8
1153	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
1154	Identification of biological processes and genes for gestational diabetes mellitus. <i>Archives of Gynecology and Obstetrics</i> , 2015, 292, 635-640.	0.8	10
1156	MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. <i>BMC Bioinformatics</i> , 2015, 16, 45.	1.2	40
1157	BiNChE: A web tool and library for chemical enrichment analysis based on the ChEBI ontology. <i>BMC Bioinformatics</i> , 2015, 16, 56.	1.2	35
1158	Predicted protein-protein interactions in the moss <i>Physcomitrella patens</i> : a new bioinformatic resource. <i>BMC Bioinformatics</i> , 2015, 16, 89.	1.2	19
1159	Tissue-specific transcriptome assemblies of the marine medaka <i>Oryzias melastigma</i> and comparative analysis with the freshwater medaka <i>Oryzias latipes</i> . <i>BMC Genomics</i> , 2015, 16, 135.	1.2	47
1160	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

#	ARTICLE	IF	CITATIONS
1161	Global analysis of the <i>Gossypium hirsutum</i> L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43.	1.6	85
1162	Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (<i>C. junos</i> cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. BMC Plant Biology, 2015, 15, 89.	1.6	120
1163	Impacts of nucleotide fixation during soybean domestication and improvement. BMC Plant Biology, 2015, 15, 81.	1.6	22
1164	Transcriptional analysis identifies key genes involved in metabolism, fibrosis/tissue repair and the immune response against <i>Fasciola hepatica</i> in sheep liver. Parasites and Vectors, 2015, 8, 124.	1.0	53
1165	The <i>J</i> - <i>S</i> Ratio Test Reveals Hundreds of Novel Putative Cancer Drivers. Molecular Biology and Evolution, 2015, 32, 2181-2185.	3.5	7
1166	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. Molecular and Cellular Biology, 2015, 35, 2448-2463.	1.1	21
1167	Transcriptional events co-regulated by hypoxia and cold stresses in Zebrafish larvae. BMC Genomics, 2015, 16, 385.	1.2	92
1168	Epigenetic reprogramming of melanoma cells by vitamin C treatment. Clinical Epigenetics, 2015, 7, 51.	1.8	74
1169	The Last Enzyme of the De Novo Purine Synthesis Pathway 5-aminoimidazole-4-carboxamide Ribonucleotide Formyltransferase/IMP Cyclohydrolase (ATIC) Plays a Central Role in Insulin Signaling and the Golgi/Endosomes Protein Network*. Molecular and Cellular Proteomics, 2015, 14, 1079-1092.	2.5	25
1170	Systems biology approach reveals possible evolutionarily conserved moonlighting functions for enolase. Computational Biology and Chemistry, 2015, 58, 1-8.	1.1	18
1171	Genetic variation of transgenerational plasticity of offspring germination in response to salinity stress and the seed transcriptome of <i>Medicago truncatula</i> . BMC Evolutionary Biology, 2015, 15, 59.	3.2	56
1172	Genome-wide conserved non-coding microsatellite (CNMS) marker-based integrative genetical genomics for quantitative dissection of seed weight in chickpea. Journal of Experimental Botany, 2015, 66, 1271-1290.	2.4	46
1173	Global genetic analysis in mice unveils central role for cilia in congenital heart disease. Nature, 2015, 521, 520-524.	13.7	357
1174	Genomic distribution and possible functional roles of putative G-quadruplex motifs in two subspecies of <i>Oryza sativa</i> . Computational Biology and Chemistry, 2015, 56, 122-130.	1.1	26
1175	The Transcriptome and Terpene Profile of <i>Eucalyptus grandis</i> Reveals Mechanisms of Defense Against the Insect Pest, <i>Leptocybe invasa</i> . Plant and Cell Physiology, 2015, 56, 1418-1428.	1.5	55
1176	Molecular Cytotoxicity Mechanisms of Allyl Alcohol (Acrolein) in Budding Yeast. Chemical Research in Toxicology, 2015, 28, 1246-1264.	1.7	22
1177	Outlier detection at the transcriptome-proteome interface. Bioinformatics, 2015, 31, 2530-2536.	1.8	12
1178	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 815-822.	1.9	103

#	ARTICLE	IF	CITATIONS
1179	Annexin A2 is SUMOylated on its N-terminal domain: Regulation by insulin. <i>FEBS Letters</i> , 2015, 589, 985-991.	1.3	18
1180	Systematically dissecting the global mechanism of miRNA functions in mouse pluripotent stem cells. <i>BMC Genomics</i> , 2015, 16, 490.	1.2	4
1181	Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant (<i>Camellia sinensis</i>). <i>BMC Genomics</i> , 2015, 16, 560.	1.2	174
1182	POTION: an end-to-end pipeline for positive Darwinian selection detection in genome-scale data through phylogenetic comparison of protein-coding genes. <i>BMC Genomics</i> , 2015, 16, 567.	1.2	44
1185	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type <i>TP53</i> . <i>Molecular Cancer Research</i> , 2015, 13, 493-501.	1.5	53
1186	Visual analysis of biological data-knowledge networks. <i>BMC Bioinformatics</i> , 2015, 16, 135.	1.2	29
1187	Ethylene negatively regulates transcript abundance of ROP-GAP rheostat-encoding genes and affects apoplastic reactive oxygen species homeostasis in epicarps of cold stored apple fruits. <i>Journal of Experimental Botany</i> , 2015, 66, 7255-7270.	2.4	42
1188	i-cisTarget 2015 update: generalized cis-regulatory enrichment analysis in human, mouse and fly. <i>Nucleic Acids Research</i> , 2015, 43, W57-W64.	6.5	169
1189	De novo transcriptome characterization and gene expression profiling of the desiccation tolerant moss <i>Bryum argenteum</i> following rehydration. <i>BMC Genomics</i> , 2015, 16, 416.	1.2	73
1190	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
1191	Updates on drug-target network; facilitating polypharmacology and data integration by growth of DrugBank database. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv094.	3.2	43
1192	A pipeline for the systematic identification of non-redundant full-ORF cDNAs for polymorphic and evolutionary divergent genomes: Application to the ascidian <i>Ciona intestinalis</i> . <i>Developmental Biology</i> , 2015, 404, 149-163.	0.9	20
1193	Chromosomal copy number variation reveals differential levels of genomic plasticity in distinct <i>Trypanosoma cruzi</i> strains. <i>BMC Genomics</i> , 2015, 16, 499.	1.2	68
1194	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
1195	Chemotherapy-induced antitumor immunity requires formyl peptide receptor 1. <i>Science</i> , 2015, 350, 972-978.	6.0	367
1196	A stochastic model dissects cell states in biological transition processes. <i>Scientific Reports</i> , 2014, 4, 3692.	1.6	24
1197	Discovery of genes related to formothion resistance in oriental fruit fly (<i>Bactrocera dorsalis</i>) by a constrained functional genomics analysis. <i>Insect Molecular Biology</i> , 2015, 24, 338-347.	1.0	7
1198	The gene expression profiling of hepatocellular carcinoma by a network analysis approach shows a dominance of intrinsically disordered proteins (IDPs) between hub nodes. <i>Molecular BioSystems</i> , 2015, 11, 2933-2945.	2.9	5

#	ARTICLE	IF	CITATIONS
1199	Genome-wide identification of CCA1 targets uncovers an expanded clock network in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4802-10.	3.3	230
1201	Placental transcriptome in development and pathology: expression, function, and methods of analysis. American Journal of Obstetrics and Gynecology, 2015, 213, S138-S151.	0.7	58
1202	The PfAlba1 RNA-binding protein is an important regulator of translational timing in <i>Plasmodium falciparum</i> blood stages. Genome Biology, 2015, 16, 212.	3.8	55
1203	Biological Relevance and Therapeutic Potential of the Hypusine Modification System. Journal of Biological Chemistry, 2015, 290, 18343-18360.	1.6	48
1204	Olive leaf components apigenin 7-glucoside and luteolin 7-glucoside direct human hematopoietic stem cell differentiation towards erythroid lineage. Differentiation, 2015, 89, 146-155.	1.0	31
1205	The effect of red light and far-red light conditions on secondary metabolism in Agarwood. BMC Plant Biology, 2015, 15, 139.	1.6	33
1206	FERAL: network-based classifier with application to breast cancer outcome prediction. Bioinformatics, 2015, 31, i311-i319.	1.8	36
1207	Dual Labeling Biotin Switch Assay to Reduce Bias Derived From Different Cysteine Subpopulations. Circulation Research, 2015, 117, 846-857.	2.0	31
1208	Computational Systems Toxicology. Methods in Pharmacology and Toxicology, 2015, , .	0.1	5
1209	Effects of Phosphorylation of \hat{P}^2 Subunits of Phycocyanins on State Transition in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. Plant and Cell Physiology, 2015, 56, 1997-2013.	1.5	37
1210	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. Journal of Proteome Research, 2015, 14, 3568-3582.	1.8	41
1212	Glioblastoma-derived Macrophage Colony-stimulating Factor (MCSF) Induces Microglial Release of Insulin-like Growth Factor-binding Protein 1 (IGFBP1) to Promote Angiogenesis. Journal of Biological Chemistry, 2015, 290, 23401-23415.	1.6	67
1213	Pleiotropic drug-resistance attenuated genomic library improves elucidation of drug mechanisms. Molecular BioSystems, 2015, 11, 3129-3136.	2.9	15
1214	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. Nucleic Acids Research, 2015, 43, 7779-7789.	6.5	30
1215	Ectopic expression a tomato KNOX Gene Tkn4 affects the formation and the differentiation of meristems and vasculature. Plant Molecular Biology, 2015, 89, 589-605.	2.0	19
1216	Detecting protein complexes using connectivity among nodes in a PPI Network. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	2
1217	Data for proteomic analysis of murine cardiomyocytic HL-1 cells treated with siRNA against tissue factor. Data in Brief, 2015, 3, 117-119.	0.5	1
1218	Open source libraries and frameworks for biological data visualisation: A guide for developers. Proteomics, 2015, 15, 1356-1374.	1.3	43

#	ARTICLE	IF	CITATIONS
1219	Deregulation of Immune Response Genes in Patients With Epstein-Barr Virus-Associated Gastric Cancer and Outcomes. <i>Gastroenterology</i> , 2015, 148, 137-147.e9.	0.6	127
1220	Viewing the proteome: How to visualize proteomics data?. <i>Proteomics</i> , 2015, 15, 1341-1355.	1.3	32
1221	Genome-Scale Transcriptomic Insights into Molecular Aspects of Abiotic Stress Responses in Chickpea. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 388-400.	1.0	69
1222	MicroRNA408 Is Critical for the <i>HY5-SPL7</i> Gene Network That Mediates the Coordinated Response to Light and Copper Å. <i>Plant Cell</i> , 2015, 26, 4933-4953.	3.1	164
1223	The metabolomics of oxidative stress. <i>Phytochemistry</i> , 2015, 112, 33-53.	1.4	199
1224	The <i>Arabidopsis thaliana</i> RNA-binding protein <i>FCA</i> regulates thermotolerance by modulating the detoxification of reactive oxygen species. <i>New Phytologist</i> , 2015, 205, 555-569.	3.5	36
1225	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
1226	Integrating Proteomics Profiling Data Sets: A Network Perspective. <i>Methods in Molecular Biology</i> , 2015, 1243, 237-253.	0.4	5
1227	Investigating the underlying mechanisms of temperature-related skin diseases in <i>Atlantic salmon</i> , <i>Salmo salar</i> L., as measured by quantitative histology, skin transcriptomics and composition. <i>Journal of Fish Diseases</i> , 2015, 38, 977-992.	0.9	29
1228	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
1229	Investigating the molecular underpinnings underlying morphology and changes in carbon partitioning during tension wood formation in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1351-1363.	3.5	27
1230	Functional annotation and biological interpretation of proteomics data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 46-54.	1.1	45
1231	Identification of Genes Involved in the Biosynthesis of <i>Tripterygium wilfordii</i> Hook.f. Secondary Metabolites by Suppression Subtractive Hybridization. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 756-769.	1.0	9
1233	How to learn about gene function: text-mining or ontologies?. <i>Methods</i> , 2015, 74, 3-15.	1.9	24
1234	Modeling Human Neural Functionality <i>In Vitro</i> : Three-Dimensional Culture for Dopaminergic Differentiation. <i>Tissue Engineering - Part A</i> , 2015, 21, 654-668.	1.6	44
1235	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
1236	Organellar proteome analyses of ricin toxin-treated HeLa cells. <i>Toxicology and Industrial Health</i> , 2016, 32, 1166-1178.	0.6	2
1237	Effects of <i>Morus alba</i> L. (Mulberry) Leaf Extract in Hypercholesterolemic Mice on Suppression of Cholesterol Synthesis. <i>Journal of Pharmacognosy & Natural Products</i> , 2016, 2, .	0.4	5

#	ARTICLE	IF	CITATIONS
1238	Systems biology analysis reveals role of MDM2 in diabetic nephropathy. JCI Insight, 2016, 1, e87877.	2.3	34
1239	Metformin increases PDH and suppresses HIF-1 α under hypoxic conditions and induces cell death in oral squamous cell carcinoma. Oncotarget, 2016, 7, 55057-55068.	0.8	81
1240	Genome-wide characterization of non-reference transposons in crops suggests non-random insertion. BMC Genomics, 2016, 17, 536.	1.2	13
1241	Allyl-isothiocyanate treatment induces a complex transcriptional reprogramming including heat stress, oxidative stress and plant defence responses in Arabidopsis thaliana. BMC Genomics, 2016, 17, 740.	1.2	32
1242	RNA-seq based transcriptomic map reveals new insights into mouse salivary gland development and maturation. BMC Genomics, 2016, 17, 923.	1.2	35
1243	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
1244	Network analysis reveals potential markers for pediatric adrenocortical carcinoma. OncoTargets and Therapy, 2016, Volume 9, 4569-4581.	1.0	33
1245	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. BMC Genomics, 2016, 17, 702.	1.2	32
1246	A Genetic Screen for Fission Yeast Gene Deletion Mutants Exhibiting Hypersensitivity to Latrunculin A. G3: Genes, Genomes, Genetics, 2016, 6, 3399-3408.	0.8	5
1247	The Impact of Serum Amyloid P-Component on Gene Expression in RAW264.7 Mouse Macrophages. BioMed Research International, 2016, 2016, 1-9.	0.9	7
1248	Integrated Analysis of DNA Methylation and mRNA Expression Profiles Data to Identify Key Genes in Lung Adenocarcinoma. BioMed Research International, 2016, 2016, 1-9.	0.9	14
1249	Exposure to various abscission-promoting treatments suggests substantial ERF subfamily transcription factors involvement in the regulation of cassava leaf abscission. BMC Genomics, 2016, 17, 538.	1.2	13
1250	The founder-cell transcriptome in the Arabidopsis apetala1 cauliflower inflorescence meristem. BMC Genomics, 2016, 17, 855.	1.2	13
1251	Lamina Associated Polypeptide 1 (LAP1) Interactome and Its Functional Features. Membranes, 2016, 6, 8.	1.4	19
1252	Spleen-Dependent Immune Protection Elicited by CpG Adjuvanted Reticulocyte-Derived Exosomes from Malaria Infection Is Associated with Changes in T cell Subsets' Distribution. Frontiers in Cell and Developmental Biology, 2016, 4, 131.	1.8	37
1253	A Network Approach of Gene Co-expression in the Zea mays/Aspergillus flavus Pathosystem to Map Host/Pathogen Interaction Pathways. Frontiers in Genetics, 2016, 7, 206.	1.1	32
1254	Ontogenetic Changes in the Bacterial Symbiont Community of the Tropical Demosponge Amphimedon queenslandica: Metamorphosis Is a New Beginning. Frontiers in Marine Science, 2016, 3, .	1.2	49
1255	Systematic Analysis of Protein Interaction Network Associated with Azoospermia. International Journal of Molecular Sciences, 2016, 17, 1857.	1.8	14

#	ARTICLE	IF	CITATIONS
1256	Structure Identification and Anti-Cancer Pharmacological Prediction of Triterpenes from <i>Ganoderma lucidum</i> . <i>Molecules</i> , 2016, 21, 678.	1.7	27
1257	Computational characterization of Iron metabolism in the Tsetse disease vector, <i>Glossina morsitans</i> : IRE stem-loops. <i>BMC Genomics</i> , 2016, 17, 561.	1.2	2
1258	Phosphoproteome Analysis of Invasion and Metastasis-Related Factors in Pancreatic Cancer Cells. <i>PLoS ONE</i> , 2016, 11, e0152280.	1.1	21
1259	Comprehensive Map of Molecules Implicated in Obesity. <i>PLoS ONE</i> , 2016, 11, e0146759.	1.1	17
1260	De Novo Assembled Wheat Transcriptomes Delineate Differentially Expressed Host Genes in Response to Leaf Rust Infection. <i>PLoS ONE</i> , 2016, 11, e0148453.	1.1	36
1261	Elucidation of the Mode of Action of a New Antibacterial Compound Active against <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0155139.	1.1	30
1262	IFNs Modify the Proteome of <i>Legionella</i> -Containing Vacuoles and Restrict Infection Via IRG1-Derived Itaconic Acid. <i>PLoS Pathogens</i> , 2016, 12, e1005408.	2.1	195
1263	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in <i>Pigeonpea</i> (<i>Cajanus cajan</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1065.	1.7	39
1264	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015, 6, 1194.	1.7	93
1265	Grapevine Rootstocks Differentially Affect the Rate of Ripening and Modulate Auxin-Related Genes in Cabernet Sauvignon Berries. <i>Frontiers in Plant Science</i> , 2016, 7, 69.	1.7	67
1266	Coupling of Physiological and Proteomic Analysis to Understand the Ethylene- and Chilling-Induced Kiwifruit Ripening Syndrome. <i>Frontiers in Plant Science</i> , 2016, 7, 120.	1.7	71
1267	Transcriptome Analysis of Soybean Leaf Abscission Identifies Transcriptional Regulators of Organ Polarity and Cell Fate. <i>Frontiers in Plant Science</i> , 2016, 7, 125.	1.7	26
1268	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
1269	Relevance of the Axis Spermidine/eIF5A for Plant Growth and Development. <i>Frontiers in Plant Science</i> , 2016, 7, 245.	1.7	14
1270	Learning from Co-expression Networks: Possibilities and Challenges. <i>Frontiers in Plant Science</i> , 2016, 7, 444.	1.7	268
1271	Different Gene Expression Patterns between Leaves and Flowers in <i>Lonicera japonica</i> Revealed by Transcriptome Analysis. <i>Frontiers in Plant Science</i> , 2016, 7, 637.	1.7	9
1272	Low Temperature Affects Stem Cell Maintenance in <i>Brassica oleracea</i> Seedlings. <i>Frontiers in Plant Science</i> , 2016, 7, 800.	1.7	12
1273	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

#	ARTICLE	IF	CITATIONS
1274	Photosynthate Regulation of the Root System Architecture Mediated by the Heterotrimeric G Protein Complex in Arabidopsis. <i>Frontiers in Plant Science</i> , 2016, 7, 1255.	1.7	31
1275	Genome-Wide Gene/Genome Dosage Imbalance Regulates Gene Expressions in Synthetic Brassica napus and Derivatives (AC, AAC, CCA, CCAA). <i>Frontiers in Plant Science</i> , 2016, 7, 1432.	1.7	25
1276	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
1277	Depletion of Key Meiotic Genes and Transcriptome-Wide Abiotic Stress Reprogramming Mark Early Preparatory Events Ahead of Apomeiotic Transition. <i>Frontiers in Plant Science</i> , 2016, 7, 1539.	1.7	60
1278	Transcriptomic Profiling of Soybean in Response to High-Intensity UV-B Irradiation Reveals Stress Defense Signaling. <i>Frontiers in Plant Science</i> , 2016, 7, 1917.	1.7	17
1279	Prediction of genetic risk factors of atherosclerosis using various bioinformatic tools. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	12
1280	Combining systems pharmacology, transcriptomics, proteomics, and metabolomics to dissect the therapeutic mechanism of Chinese herbal Bufei Jianpi formula for application to COPD. <i>International Journal of COPD</i> , 2016, 11, 553.	0.9	7
1281	The epidermis coordinates auxin-induced stem growth in response to shade. <i>Genes and Development</i> , 2016, 30, 1529-1541.	2.7	99
1282	The Arabidopsis leaf transcriptome reveals distinct but also overlapping responses to colonization by phyllosphere commensals and pathogen infection with impact on plant health. <i>New Phytologist</i> , 2016, 212, 192-207.	3.5	134
1283	Chemokine (Câ€C motif) receptor 2â€“positive monocytes aggravate the early phase of acetaminophenâ€nduced acute liver injury. <i>Hepatology</i> , 2016, 64, 1667-1682.	3.6	271
1284	An overview of innovations and industrial solutions in Protein Microarray Technology. <i>Proteomics</i> , 2016, 16, 1297-1308.	1.3	34
1285	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 70.	2.2	11
1286	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
1287	Evaluation of the antineoplastic activity of gallic acid in oral squamous cell carcinoma under hypoxic conditions. <i>Anti-Cancer Drugs</i> , 2016, 27, 407-416.	0.7	34
1288	Differential Expression of Genes Involved in Host Recognition, Attachment, and Degradation in the Mycoparasite <i>Tolypocladium ophioglossoides</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 731-741.	0.8	21
1289	Bioinformatics Analyses of Differentially Expressed Genes Associated with Acute Myocardial Infarction. <i>Cardiovascular Therapeutics</i> , 2016, 34, 67-75.	1.1	14
1290	Transcriptomic investigation of meat tenderness in two Italian cattle breeds. <i>Animal Genetics</i> , 2016, 47, 273-287.	0.6	37
1291	Uncovering the exerciseâ€related proteome signature in skeletal muscle. <i>Proteomics</i> , 2016, 16, 816-830.	1.3	24

#	ARTICLE	IF	CITATIONS
1292	Protein kinase G signaling in cardiac pathophysiology: Impact of proteomics on clinical trials. <i>Proteomics</i> , 2016, 16, 894-905.	1.3	10
1293	Characterization of inflammatory markers and transcriptome profiles of differentially activated embryonic stem cell-derived microglia. <i>Glia</i> , 2016, 64, 1007-1020.	2.5	22
1294	Cycloheximide Inhibits Actin Cytoskeletal Dynamics by Suppressing Signaling via RhoA. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 2886-2898.	1.2	4
1295	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. <i>Molecular BioSystems</i> , 2016, 12, 2394-2407.	2.9	12
1296	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
1297	Effect of prior drought and pathogen stress on <i>Arabidopsis</i> transcriptome changes to caterpillar herbivory. <i>New Phytologist</i> , 2016, 210, 1344-1356.	3.5	53
1298	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
1299	Uterine glands impact uterine receptivity, luminal fluid homeostasis and blastocyst implantation. <i>Scientific Reports</i> , 2016, 6, 38078.	1.6	65
1300	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
1301	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
1302	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
1303	Reactive oxygen species regulate leaf pulvinus abscission zone cell separation in response to water-deficit stress in cassava. <i>Scientific Reports</i> , 2016, 6, 21542.	1.6	51
1304	Genome-wide identification of cassava R2R3 MYB family genes related to abscission zone separation after environmental-stress-induced abscission. <i>Scientific Reports</i> , 2016, 6, 32006.	1.6	27
1305	Transcriptomic analysis of mouse liver reveals a potential hepato-enteric pathogenic mechanism in acute <i>Toxoplasma gondii</i> infection. <i>Parasites and Vectors</i> , 2016, 9, 427.	1.0	73
1306	Alternative splicing in tomato pollen in response to heat stress. <i>DNA Research</i> , 2017, 24, dsw051.	1.5	55
1307	Analysis of molecular networks and targets mining of Chinese herbal medicines on anti-aging. <i>BMC Complementary and Alternative Medicine</i> , 2016, 16, 520.	3.7	5
1308	Transcriptome analyses reveal genotype- and developmental stage-specific molecular responses to drought and salinity stresses in chickpea. <i>Scientific Reports</i> , 2016, 6, 19228.	1.6	188
1309	Comparative analysis of <i>Cucurbita pepo</i> metabolism throughout fruit development in acorn squash and oilseed pumpkin. <i>Horticulture Research</i> , 2016, 3, 16045.	2.9	22

#	ARTICLE	IF	CITATIONS
1310	Interactome-transcriptome analysis discovers signatures complementary to GWAS Loci of Type 2 Diabetes. <i>Scientific Reports</i> , 2016, 6, 35228.	1.6	20
1311	Gene expression profiles and protein-protein interaction networks in amyotrophic lateral sclerosis patients with C9orf72 mutation. <i>Orphanet Journal of Rare Diseases</i> , 2016, 11, 148.	1.2	38
1312	Proteomics in Human Reproduction. <i>SpringerBriefs in Reproductive Biology</i> , 2016, , .	0.0	3
1313	Schizophrenia interactome with 504 novel proteinâ€“protein interactions. <i>NPJ Schizophrenia</i> , 2016, 2, 16012.	2.0	54
1314	Global Proteome Response to Deletion of Genes Related to Mercury Methylation and Dissimilatory Metal Reduction Reveals Changes in Respiratory Metabolism in <i>Geobacter sulfurreducens</i> PCA. <i>Journal of Proteome Research</i> , 2016, 15, 3540-3549.	1.8	28
1315	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
1316	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations1. <i>Journal of Animal Science</i> , 2016, 94, 1446-1458.	0.2	11
1317	Gene expression and metabolism preceding soft scald, a chilling injury of â€“Honeycrispâ€™ apple fruit. <i>BMC Genomics</i> , 2016, 17, 798.	1.2	28
1318	Network-Based Comparative Analysis of Arabidopsis Immune Responses to <i>Golovinomyces orontii</i> and <i>Botrytis cinerea</i> Infections. <i>Scientific Reports</i> , 2016, 6, 19149.	1.6	37
1319	The N-end rule pathway regulates pathogen responses in plants. <i>Scientific Reports</i> , 2016, 6, 26020.	1.6	39
1320	Genomeâ€“wide association analysis and differential expression analysis of resistance to <i>Sclerotinia</i> stem rot in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 1368-1380.	4.1	186
1321	Firstâ€“generation HapMap in <i>Cajanus</i> spp. reveals untapped variations in parental lines of mapping populations. <i>Plant Biotechnology Journal</i> , 2016, 14, 1673-1681.	4.1	39
1322	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
1323	Proteomics of cellâ€“cell interactions in health and disease. <i>Proteomics</i> , 2016, 16, 328-344.	1.3	12
1324	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. <i>Nucleic Acids Research</i> , 2016, 44, 5529-5539.	6.5	35
1325	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
1327	Seasonal cues induce phenotypic plasticity of <i>Drosophila suzukii</i> to enhance winter survival. <i>BMC Ecology</i> , 2016, 16, 11.	3.0	155
1328	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

#	ARTICLE	IF	CITATIONS
1329	Construction of an immunorelated proteinâ€“protein interaction network for clarifying the mechanism of burn. <i>Burns</i> , 2016, 42, 405-413.	1.1	8
1330	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
1331	Global <i>De Novo</i> Proteinâ€“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
1332	Cyc17, a meiosis-specific cyclin, is essential for anaphase initiation and chromosome segregation in<i>Tetrahymena thermophila</i>. <i>Cell Cycle</i> , 2016, 15, 1855-1864.	1.3	17
1333	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
1334	Bifidobacterium thermophilum RBL67 impacts on growth and virulence gene expression of Salmonella enterica subsp. enterica serovar Typhimurium. <i>BMC Microbiology</i> , 2016, 16, 46.	1.3	33
1335	<i>Fusarium oxysporum</i> mediates systems metabolic reprogramming of chickpea roots as revealed by a combination of proteomics and metabolomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1589-1603.	4.1	63
1336	Genome-wide DNA polymorphisms in Kavuni, a traditional rice cultivar with nutritional and therapeutic properties. <i>Genome</i> , 2016, 59, 363-366.	0.9	3
1337	Transcriptomeâ€“wide sequencing provides insights into geocarpy in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2016, 14, 1215-1224.	4.1	30
1338	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals the Meristematic Nature of Arabidopsis Gynoecial Medial Domain. <i>Plant Physiology</i> , 2016, 171, 42-61.	2.3	32
1339	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
1340	Comparing human and macaque placental transcriptomes to disentangle preterm birth pathology from gestational age effects. <i>Placenta</i> , 2016, 41, 74-82.	0.7	19
1341	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
1342	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
1343	<i>De novo</i> deciphering three-dimensional chromatin interaction and topological domains by wavelet transformation of epigenetic profiles. <i>Nucleic Acids Research</i> , 2016, 44, e106-e106.	6.5	33
1344	Proteasome inhibitor-adapted myeloma cells are largely independent from proteasome activity and show complex proteomic changes, in particular in redox and energy metabolism. <i>Leukemia</i> , 2016, 30, 2198-2207.	3.3	117
1345	Hepatic transcriptional responses in Atlantic salmon (<i>Salmo salar</i>) exposed to gamma radiation and depleted uranium singly and in combination. <i>Science of the Total Environment</i> , 2016, 562, 270-279.	3.9	16
1346	AtWRKY22 promotes susceptibility to aphids and modulates salicylic acid and jasmonic acid signalling. <i>Journal of Experimental Botany</i> , 2016, 67, 3383-3396.	2.4	121

#	ARTICLE	IF	CITATIONS
1347	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. <i>Nature Genetics</i> , 2016, 48, 687-693.	9.4	193
1348	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
1349	Ganglioside GM2 mediates migration of tumor cells by interacting with integrin and modulating the downstream signaling pathway. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 1472-1489.	1.9	27
1350	Calcineurin Orchestrates Lateral Transfer of <i>Aspergillus fumigatus</i> during Macrophage Cell Death. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1127-1139.	2.5	54
1351	Analysis of the potential pathways and target genes in spinal cord injury using bioinformatics methods. <i>Genes and Genomics</i> , 2016, 38, 619-628.	0.5	2
1352	Identification of potential therapeutic targets for papillary thyroid carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 51-58.	0.8	15
1353	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
1354	The mvp2 mutation affects the generative transition through the modification of transcriptome pattern, salicylic acid and cytokinin metabolism in <i>Triticum monococcum</i> . <i>Journal of Plant Physiology</i> , 2016, 202, 21-33.	1.6	10
1355	An essential role for the IL-2 receptor in Treg cell function. <i>Nature Immunology</i> , 2016, 17, 1322-1333.	7.0	618
1356	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
1357	Cell Type-Specific Tandem Affinity Purification of the Mouse Hippocampal CB1 Receptor-Associated Proteome. <i>Journal of Proteome Research</i> , 2016, 15, 3585-3601.	1.8	15
1358	Characterization of the Translationally Controlled Tumor Protein (TCTP) Interactome Reveals Novel Binding Partners in Human Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 3741-3751.	1.8	21
1359	Systematic Genetic Screens Reveal the Dynamic Global Functional Organization of the Bacterial Translation Machinery. <i>Cell Reports</i> , 2016, 17, 904-916.	2.9	34
1360	MicroRNA expression signatures in lungs of mice infected with <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2016, 101, 151-159.	0.8	14
1361	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
1362	A Plastic Vegetative Growth Threshold Governs Reproductive Capacity in <i>Aspergillus nidulans</i> . <i>Genetics</i> , 2016, 204, 1161-1175.	1.2	2
1363	Comparative RNA-Seq profiling of berry development between table grape 'Kyoho' and its early-ripening mutant 'Fengzao'. <i>BMC Genomics</i> , 2016, 17, 795.	1.2	47
1364	A Guide to Genome-Wide In Vivo RNAi Applications in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , 2016, 1478, 117-143.	0.4	32

#	ARTICLE	IF	CITATIONS
1365	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
1366	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
1367	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3256-3269.	2.5	48
1368	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
1369	Epidermal growth factor-induced stimulation of proliferation and gene expression changes in the hypotrichous ciliate, <i>Stylonychia lemnae</i> . <i>Gene</i> , 2016, 592, 186-192.	1.0	2
1370	Histone acetyltransferase general control non-repressed protein 5 (<i>GCN5</i>) affects the fatty acid composition of <i>Arabidopsis thaliana</i> seeds by acetylating <i>fatty acid desaturase3</i> (<i>FAD3</i>). <i>Plant Journal</i> , 2016, 88, 794-808.	2.8	30
1371	Transcriptome analysis of Dlm mutants reveals the potential formation mechanism of lesion mimic in wheat. <i>European Journal of Plant Pathology</i> , 2016, 146, 987-997.	0.8	6
1372	Gene discovery and genome editing to develop cisgenic crops with improved resistance against pathogen infection. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 279-295.	0.8	17
1373	Normal human mitral valve proteome: A preliminary investigation by gel-based and gel-free proteomic approaches. <i>Electrophoresis</i> , 2016, 37, 2633-2643.	1.3	3
1374	Fast and reliable inference of semantic clusters. <i>Knowledge-Based Systems</i> , 2016, 111, 133-143.	4.0	3
1375	Deciphering hallmark processes of aging from interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2706-2715.	1.1	11
1376	Sunitinib activates Axl signaling in renal cell cancer. <i>International Journal of Cancer</i> , 2016, 138, 3002-3010.	2.3	32
1377	High-Throughput Tag-Seq 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
1378	Interaction between inflammatory mediators and miRNAs in <i>Helicobacter pylori</i> infection. <i>Cellular Microbiology</i> , 2016, 18, 1444-1458.	1.1	32
1379	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
1380	Transcriptome analysis of smooth cordgrass (<i>Spartina alterniflora</i> Loisel), a monocot halophyte, reveals candidate genes involved in its adaptation to salinity. <i>BMC Genomics</i> , 2016, 17, 657.	1.2	55
1381	Analyses of Drought-Tolerance Mechanism of Rice Based on the Transcriptome and Gene Ontology Data. , 2016, , 415-432.		2
1382	Combination of transcriptomic and proteomic approaches helps to unravel the protein composition of <i>Chelidonium majus</i> L. milky sap. <i>Planta</i> , 2016, 244, 1055-1064.	1.6	22

#	ARTICLE	IF	CITATIONS
1383	Identification of key genes associated with gastric cancer based on DNA microarray data. <i>Oncology Letters</i> , 2016, 11, 525-530.	0.8	48
1384	miRNA Profiling in Plants: Current Identification and Expression Approaches. , 2016, , 189-215.		0
1385	Applications of Quantitative Proteomics in Plant Research. , 2016, , 1-29.		5
1386	The heat-stress factor HSFA6b connects ABA signaling and ABA-mediated heat responses. <i>Plant Physiology</i> , 2016, 172, pp.00860.2016.	2.3	201
1387	Individual and molecular level effects of produced water contaminants on nauplii and adult females of <i>Calanus finmarchicus</i> . <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2016, 79, 585-601.	1.1	19
1388	The variant Polycomb Repressor Complex 1 component PCGF1 interacts with a pluripotency sub-network that includes DPPA4, a regulator of embryogenesis. <i>Scientific Reports</i> , 2016, 5, 18388.	1.6	38
1389	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016, 6, 37770.	1.6	38
1390	System biology analysis of long-term effect and mechanism of Bufe Yishen on COPD revealed by system pharmacology and 3-omics profiling. <i>Scientific Reports</i> , 2016, 6, 25492.	1.6	23
1391	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233.	5.8	106
1392	Reprogramming mouse fibroblasts into engraftable myeloerythroid and lymphoid progenitors. <i>Nature Communications</i> , 2016, 7, 13396.	5.8	22
1393	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , 2016, 17, 815.	1.2	49
1394	Manual of Cardiovascular Proteomics. , 2016, , .		4
1395	Microarray analysis of slipped capital femoral epiphysis growth plates. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2016, 29, 971-978.	0.4	4
1396	Proteomic Network Systems Analysis. , 2016, , 321-342.		2
1397	Characterization of long non-coding RNAs involved in cadmium toxic response in <i>Brassica napus</i> . <i>RSC Advances</i> , 2016, 6, 82157-82173.	1.7	32
1398	Bioinformatics Tools for Exploring the SUMO Gene Network. <i>Methods in Molecular Biology</i> , 2016, 1450, 285-301.	0.4	3
1399	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
1400	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

#	ARTICLE	IF	CITATIONS
1401	Altered expression of the bZIP transcription factor DRINK ME affects growth and reproductive development in <i>Arabidopsis thaliana</i> . Plant Journal, 2016, 88, 437-451.	2.8	40
1402	Identification of potential therapeutic targets for lung cancer by bioinformatics analysis. Molecular Medicine Reports, 2016, 13, 1975-1982.	1.1	15
1403	Cdk3, a conjugation-specific cyclin-dependent kinase, is essential for the initiation of meiosis in <i>Tetrahymena thermophila</i> . Cell Cycle, 2016, 15, 2506-2514.	1.3	17
1404	Transcriptome-based profiling of yolk sac-derived macrophages reveals a role for Irf8 in macrophage maturation. EMBO Journal, 2016, 35, 1730-1744.	3.5	108
1406	A PubMed-wide study of endometriosis. Genomics, 2016, 108, 151-157.	1.3	13
1407	Genome wide transcriptome profiling of <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> conidial germination reveals new insights into infection-related genes. Scientific Reports, 2016, 6, 37353.	1.6	45
1408	Transcriptomic Profiling Maps Anatomically Patterned Subpopulations among Single Embryonic Cardiac Cells. Developmental Cell, 2016, 39, 491-507.	3.1	218
1409	Differential Coexpression Analysis Reveals Extensive Rewiring of Arabidopsis Gene Coexpression in Response to <i>Pseudomonas syringae</i> Infection. Scientific Reports, 2016, 6, 35064.	1.6	25
1410	Cyclodextrin promotes atherosclerosis regression via macrophage reprogramming. Science Translational Medicine, 2016, 8, 333ra50.	5.8	271
1411	LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. Scientific Reports, 2016, 6, 18871.	1.6	37
1412	Genome-wide analysis of long intergenic non-coding RNAs in chickpea and their potential role in flower development. Scientific Reports, 2016, 6, 33297.	1.6	67
1413	A combination of genome-wide association and transcriptome analysis reveals candidate genes controlling harvest index-related traits in <i>Brassica napus</i> . Scientific Reports, 2016, 6, 36452.	1.6	59
1414	Genome-wide Identification and Structural, Functional and Evolutionary Analysis of WRKY Components of Mulberry. Scientific Reports, 2016, 6, 30794.	1.6	39
1415	Sex Change in Clownfish: Molecular Insights from Transcriptome Analysis. Scientific Reports, 2016, 6, 35461.	1.6	88
1416	Photoactivation and inactivation of <i>Arabidopsis</i> cryptochrome 2. Science, 2016, 354, 343-347.	6.0	149
1417	A computationally constructed ceRNA interaction network based on a comparison of the SHEE and SHEEC cell lines. Cellular and Molecular Biology Letters, 2016, 21, 21.	2.7	30
1418	Rewiring of jasmonate and phytochrome B signalling uncouples plant growth-defense tradeoffs. Nature Communications, 2016, 7, 12570.	5.8	323
1419	Quantitative proteomics study of the neuroprotective effects of B12 on hydrogen peroxide-induced apoptosis in SH-SY5Y cells. Scientific Reports, 2016, 6, 22635.	1.6	29

#	ARTICLE	IF	CITATIONS
1420	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
1421	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3927-3939.	0.8	187
1422	Functional transcription factor target discovery via compendia of binding and expression profiles. <i>Scientific Reports</i> , 2016, 6, 20649.	1.6	16
1423	High frequency of +1 programmed ribosomal frameshifting in <i>Euplotes octocarinatus</i> . <i>Scientific Reports</i> , 2016, 6, 21139.	1.6	48
1424	Using contrast patterns between true complexes and random subgraphs in PPI networks to predict unknown protein complexes. <i>Scientific Reports</i> , 2016, 6, 21223.	1.6	30
1425	Systematic analysis of the molecular mechanism underlying atherosclerosis using a text mining approach. <i>Human Genomics</i> , 2016, 10, 14.	1.4	12
1426	Fuzzy-FishNET: a highly reproducible protein complex-based approach for feature selection in comparative proteomics. <i>BMC Medical Genomics</i> , 2016, 9, 67.	0.7	9
1427	Identification of protein complexes from multi-relationship protein interaction networks. <i>Human Genomics</i> , 2016, 10, 17.	1.4	14
1428	Determination of testicular function in adolescents with varicocele – a proteomics approach. <i>Andrology</i> , 2016, 4, 447-455.	1.9	37
1429	Adaptive responses to cefotaxime treatment in ESBL-producing <i>Escherichia coli</i> and the possible use of significantly regulated pathways as novel secondary targets. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2449-2459.	1.3	9
1430	Gene expression profile analysis indicate SEPALLATA3 and AGL15 potentially involved in arabidopsis silique dehiscence by regulating glycosyl hydrolase. <i>Journal of Plant Biology</i> , 2016, 59, 133-142.	0.9	4
1431	Comparative transcriptomics and comprehensive marker resource development in mulberry. <i>BMC Genomics</i> , 2016, 17, 98.	1.2	18
1432	Small RNA and PARE sequencing in flower bud reveal the involvement of sRNAs in endodormancy release of Japanese pear (<i>Pyrus pyrifolia</i> 'Kosui'). <i>BMC Genomics</i> , 2016, 17, 230.	1.2	25
1433	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
1434	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97.	6.5	7,240
1435	Microarray Analysis to Monitor Bacterial Cell Wall Homeostasis. <i>Methods in Molecular Biology</i> , 2016, 1440, 31-46.	0.4	0
1436	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
1437	g:Profiler – a web server for functional interpretation of gene lists (2016 update). <i>Nucleic Acids Research</i> , 2016, 44, W83-W89.	6.5	1,179

#	ARTICLE	IF	CITATIONS
1438	Parkinson's disease and lactoferrin: Analysis of dependent protein networks. Gene Reports, 2016, 4, 177-183.	0.4	9
1439	Diffany: an ontology-driven framework to infer, visualise and analyse differential molecular networks. BMC Bioinformatics, 2016, 17, 18.	1.2	30
1440	Genome and network visualization facilitates the analyses of the effects of drugs and mutations on protein-protein and drug-protein networks. BMC Bioinformatics, 2016, 17, 54.	1.2	4
1441	Gene and transposable element methylation in great tit (<i>Parus major</i>) brain and blood. BMC Genomics, 2016, 17, 332.	1.2	66
1442	Exogenous auxin regulates multi-metabolic network and embryo development, controlling seed secondary dormancy and germination in <i>Nicotiana tabacum</i> L.. BMC Plant Biology, 2016, 16, 41.	1.6	18
1443	Absciscic acid transcriptomic signaling varies with grapevine organ. BMC Plant Biology, 2016, 16, 72.	1.6	45
1444	Integrative meta-analysis identifies microRNA-regulated networks in infantile hemangioma. BMC Medical Genetics, 2016, 17, 4.	2.1	18
1445	Elevated urinary urea by high-protein diet could be one of the inducements of bladder disorders. Journal of Translational Medicine, 2016, 14, 53.	1.8	12
1446	A Brief Review on the Ecological Network Analysis with Applications in the Emerging Medical Ecology. Springer Protocols, 2016, , 7-39.	0.1	7
1447	Global analysis of the developmental dynamics of <i>Gossypium hirsutum</i> based on strand-specific transcriptome. Physiologia Plantarum, 2016, 158, 106-121.	2.6	6
1448	<scp>NORE1</scp>/<scp>SAUL1</scp> integrates temperature-dependent defense programs involving <scp>SGT1b</scp> and <scp>PAD4</scp> pathways and leaf senescence in <i>Arabidopsis</i> . Physiologia Plantarum, 2016, 158, 180-199.	2.6	19
1449	Regulation of Gene Expression in <i>Shewanella oneidensis</i> MR-1 during Electron Acceptor Limitation and Bacterial Nanowire Formation. Applied and Environmental Microbiology, 2016, 82, 5428-5443.	1.4	59
1450	Exosomes Secreted by Apoptosis-Resistant Acute Myeloid Leukemia (AML) Blasts Harbor Regulatory Network Proteins Potentially Involved in Antagonism of Apoptosis. Molecular and Cellular Proteomics, 2016, 15, 1281-1298.	2.5	90
1451	Aiolos collaborates with Blimp-1 to regulate the survival of multiple myeloma cells. Cell Death and Differentiation, 2016, 23, 1175-1184.	5.0	23
1452	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
1453	Seasonal proteome changes of nasal mucus reflect perennial inflammatory response and reduced defence mechanisms and plasticity in allergic rhinitis. Journal of Proteomics, 2016, 133, 153-160.	1.2	17
1454	Protein turnover during in vitro tissue engineering. Biomaterials, 2016, 81, 104-113.	5.7	24
1455	Mitochondrial electron transport chain identified as a novel molecular target of SPIO nanoparticles mediated cancer-specific cytotoxicity. Biomaterials, 2016, 83, 102-114.	5.7	77

#	ARTICLE	IF	CITATIONS
1456	Integrative Network Analysis Combined with Quantitative Phosphoproteomics Reveals Transforming Growth Factor-beta Receptor type-2 (TGFB2) as a Novel Regulator of Glioblastoma Stem Cell Properties. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1017-1031.	2.5	16
1457	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
1458	Programming of Plant Leaf Senescence with Temporal and Inter-Organellar Coordination of Transcriptome in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 171, 452-467.	2.3	121
1459	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
1460	Exploratory Analysis of Biological Networks through Visualization, Clustering, and Functional Annotation in Cytoscape. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot077644.	0.2	31
1461	The durably resistant rice cultivar <i>Digu</i> activates defence gene expression before the full maturation of <i>Magnaporthe oryzae</i> appressorium. <i>Molecular Plant Pathology</i> , 2016, 17, 354-368.	2.0	32
1462	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
1463	Dynamics of Hippocampal Protein Expression During Long-term Spatial Memory Formation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 523-541.	2.5	19
1464	Transcriptional Framework of Male Gametogenesis in the Liverwort <i>Marchantia polymorpha</i> L.. <i>Plant and Cell Physiology</i> , 2016, 57, 325-338.	1.5	83
1465	Network stratification analysis for identifying function-specific network layers. <i>Molecular BioSystems</i> , 2016, 12, 1232-1240.	2.9	1
1466	Sperm proteomics: potential impact on male infertility treatment. <i>Expert Review of Proteomics</i> , 2016, 13, 285-296.	1.3	29
1467	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
1468	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
1469	Time-Series Transcriptomics Reveals That <i>AGAMOUS-LIKE22</i> Affects Primary Metabolism and Developmental Processes in Drought-Stressed <i>Arabidopsis</i> . <i>Plant Cell</i> , 2016, 28, 345-366.	3.1	92
1470	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
1471	Evaluation of proteomic biomarkers associated with circulating microparticles as an effective means to stratify the risk of spontaneous preterm birth. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 214, 631.e1-631.e11.	0.7	46
1472	Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms. <i>Plant Cell</i> , 2016, 28, 326-344.	3.1	202
1473	Metabolic and transcriptional response of central metabolism affected by root endophytic fungus <i>Piriformospora indica</i> under salinity in barley. <i>Plant Molecular Biology</i> , 2016, 90, 699-717.	2.0	73

#	ARTICLE	IF	CITATIONS
1474	Protein Structure Is Related to RNA Structural Reactivity In Vivo. <i>Journal of Molecular Biology</i> , 2016, 428, 758-766.	2.0	14
1475	Genomic, Proteomic, and Metabolite Characterization of Gemfibrozil-Degrading Organism <i>Bacillus</i> sp. GeD10. <i>Environmental Science & Technology</i> , 2016, 50, 744-755.	4.6	30
1476	Cumulative metabolic effects of low-dose benzo(a)pyrene exposure on human cells. <i>Toxicology Research</i> , 2016, 5, 107-115.	0.9	11
1477	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
1478	Overview of Plant Defence Systems: Lessons from <i>Arabidopsis-Botrytis cinerea</i> Systems Biology. , 2016, , 335-360.		3
1479	<i>Botrytis</i> – the Fungus, the Pathogen and its Management in Agricultural Systems. , 2016, , .		167
1480	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
1481	Determination of the substrate repertoire of ADAMTS2, 3, and 14 significantly broadens their functions and identifies extracellular matrix organization and TGF β ² signaling as primary targets. <i>FASEB Journal</i> , 2016, 30, 1741-1756.	0.2	79
1482	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
1483	In silico assessment of adverse drug reactions and associated mechanisms. <i>Drug Discovery Today</i> , 2016, 21, 58-71.	3.2	51
1484	Whole transcriptome profiling of adult and infective stages of the trematode <i>Opisthorchis felinus</i> . <i>Parasitology International</i> , 2016, 65, 12-19.	0.6	27
1485	BONLAC: A combinatorial proteomic technique to measure stimulus-induced translational profiles in brain slices. <i>Neuropharmacology</i> , 2016, 100, 76-89.	2.0	47
1486	Evolution of DNA-Binding Sites of a Floral Master Regulatory Transcription Factor. <i>Molecular Biology and Evolution</i> , 2016, 33, 185-200.	3.5	32
1487	Network Approaches to the Understanding of Alzheimer's Disease: From Model Organisms to Humans. <i>Methods in Molecular Biology</i> , 2016, 1303, 447-458.	0.4	3
1488	Comparative analysis of molecular mechanism of spinal cord injury with time based on bioinformatics data. <i>Spinal Cord</i> , 2016, 54, 431-438.	0.9	13
1489	MTHFSD and DDX58 are novel RNA-binding proteins abnormally regulated in amyotrophic lateral sclerosis. <i>Brain</i> , 2016, 139, 86-100.	3.7	40
1490	Transcriptome profiling of indole-3-butyric acid-induced adventitious root formation in softwood cuttings of the <i>Catalpa bungei</i> variety 'YU-1' at different developmental stages. <i>Genes and Genomics</i> , 2016, 38, 145-162.	0.5	29
1491	A Computational Network Biology Approach to Uncover Novel Genes Related to Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 435-446.	0.4	4

#	ARTICLE	IF	CITATIONS
1492	Proteomic analysis of naturally-sourced biological scaffolds. <i>Biomaterials</i> , 2016, 75, 37-46.	5.7	115
1494	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
1495	A bi-objective network design approach for discovering functional modules linking Golgi apparatus fragmentation and neuronal death. <i>Annals of Operations Research</i> , 2017, 258, 5-30.	2.6	2
1496	Molecular and physiological responses to titanium dioxide and cerium oxide nanoparticles in <i>Arabidopsis</i> . <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 71-82.	2.2	58
1497	Screening for potential genes associated with bone overgrowth after mid-shaft femur fracture in a rat model. <i>Journal of Orthopaedic Surgery and Research</i> , 2017, 12, 8.	0.9	10
1498	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
1499	A systems approach for the elucidation of crucial genes and network constituents of cervical intraepithelial neoplasia 1 (CIN1). <i>Molecular BioSystems</i> , 2017, 13, 549-555.	2.9	7
1500	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
1501	Key Genes in Stomach Adenocarcinoma Identified via Network Analysis of RNA-Seq Data. <i>Pathology and Oncology Research</i> , 2017, 23, 745-752.	0.9	6
1502	Stable Isotope Labeling with Amino Acids (SILAC)-Based Proteomics of Primary Human Kidney Cells Reveals a Novel Link between Male Sex Hormones and Impaired Energy Metabolism in Diabetic Kidney Disease. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 368-385.	2.5	13
1503	Gibberellin Signaling Requires Chromatin Remodeler PICKLE to Promote Vegetative Growth and Phase Transitions. <i>Plant Physiology</i> , 2017, 173, 1463-1474.	2.3	55
1504	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
1505	Normal human cell proteins that interact with the adenovirus type 5 E1B 55 kDa protein. <i>Virology</i> , 2017, 504, 12-24.	1.1	16
1506	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
1507	Comparative genomics of canine-isolated <i>Leishmania</i> (<i>Leishmania</i>) <i>amazonensis</i> from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brazil. <i>Scientific Reports</i> , 2017, 7, 40804.	1.6	65
1508	Lemna minor plants chronically exposed to ionising radiation: RNA-seq analysis indicates a dose rate dependent shift from acclimation to survival strategies. <i>Plant Science</i> , 2017, 257, 84-95.	1.7	63
1509	Global transcriptome analysis reveals extensive gene remodeling, alternative splicing and differential transcription profiles in non-seed vascular plant <i>Selaginella moellendorffii</i> . <i>BMC Genomics</i> , 2017, 18, 1042.	1.2	34
1510	Epigenetic map and genetic map basis of complex traits in cassava population. <i>Scientific Reports</i> , 2017, 7, 41232.	1.6	26

#	ARTICLE	IF	CITATIONS
1511	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
1512	A Systems Biology Methodology Combining Transcriptome and Interactome Datasets to Assess the Implications of Cytokinin Signaling for Plant Immune Networks. <i>Methods in Molecular Biology</i> , 2017, 1569, 165-173.	0.4	3
1513	Transcriptomic analysis of oyster <i>Crassostrea gigas</i> larvae illustrates the response patterns regulated by catecholaminergic system upon acute heat and bacterial stress. <i>Developmental and Comparative Immunology</i> , 2017, 73, 52-60.	1.0	21
1514	Differential Protein Expression Marks the Transition From Infection With <i>Opisthorchis viverrini</i> to Cholangiocarcinoma. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 911-923.	2.5	9
1515	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
1516	Effects of Dietary Macronutrient Composition on FNDC5 and Irisin in Mice Skeletal Muscle. <i>Metabolic Syndrome and Related Disorders</i> , 2017, 15, 161-169.	0.5	15
1517	Small <sc>RNA</sc> interactome of pathogenic <i>E.Âcoli</i> revealed through crosslinking of <sc>RN</sc>ase E. <i>EMBO Journal</i> , 2017, 36, 374-387.	3.5	153
1518	Insights into Diabetic Kidney Disease Using Urinary Proteomics and Bioinformatics. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 1050-1061.	3.0	101
1519	Molecular finds of pressure ulcer: A bioinformatics approach in pressure ulcer. <i>Journal of Tissue Viability</i> , 2017, 26, 119-124.	0.9	7
1520	ABA Suppresses Root Hair Growth via the OBP4 Transcriptional Regulator. <i>Plant Physiology</i> , 2017, 173, 1750-1762.	2.3	67
1521	The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1239-1249.	0.8	18
1522	Aberrant Epicardial Adipose Tissue Extracellular Matrix Remodeling in Patients with Severe Ischemic Cardiomyopathy: Insight from Comparative Quantitative Proteomics. <i>Scientific Reports</i> , 2017, 7, 43787.	1.6	25
1523	Auxins and Cytokinins in Plant Biology. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	15
1524	bHLH142 regulates various metabolic pathway-related genes to affect pollen development and anther dehiscence in rice. <i>Scientific Reports</i> , 2017, 7, 43397.	1.6	34
1525	Impacts of the overexpression of a tomato translationally controlled tumor protein (TCTP) in tobacco revealed by phenotypic and transcriptomic analysis. <i>Plant Cell Reports</i> , 2017, 36, 887-900.	2.8	10
1526	Parallel analysis of<i>Arabidopsis</i> circadian clock mutants reveals different scales of transcriptome and proteome regulation. <i>Open Biology</i> , 2017, 7, 160333.	1.5	52
1527	Effects of ErbB2 Overexpression on the Proteome and ErbB Ligand-specific Phosphosignaling in Mammary Luminal Epithelial Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 608-621.	2.5	6
1528	Quantitative Map of Î²-Lactone-Induced Virulence Regulation. <i>Journal of Proteome Research</i> , 2017, 16, 1180-1192.	1.8	25

#	ARTICLE	IF	CITATIONS
1529	Understanding Epstein-Barr Virus Life Cycle with Proteomics: A Temporal Analysis of Ubiquitination During Virus Reactivation. OMICS A Journal of Integrative Biology, 2017, 21, 27-37.	1.0	9
1530	An adaptation of particle swarm clustering applied in basal cell carcinoma, squamous cell carcinoma of the skin and actinic keratosis. Meta Gene, 2017, 12, 72-77.	0.3	7
1531	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. Genome Biology, 2017, 18, 27.	3.8	624
1532	Selective Autophagy of BES1 Mediated by DSK2 Balances Plant Growth and Survival. Developmental Cell, 2017, 41, 33-46.e7.	3.1	262
1533	Gene co-expression network reconstruction: a review on computational methods for inferring functional information from plant-based expression data. Plant Biotechnology Reports, 2017, 11, 71-86.	0.9	34
1534	Comparative proteomics of hydatid fluids from two Echinococcus multilocularis isolates. Journal of Proteomics, 2017, 162, 40-51.	1.2	19
1535	Dynamic chromatin accessibility modeled by Markov process of randomly-moving molecules in the 3D genome. Nucleic Acids Research, 2017, 45, e85-e85.	6.5	7
1536	Population Genomics of Paramecium Species. Molecular Biology and Evolution, 2017, 34, 1194-1216.	3.5	35
1537	Dynamic Cytology and Transcriptional Regulation of Rice Lamina Joint Development. Plant Physiology, 2017, 174, 1728-1746.	2.3	53
1538	A survey of proteomic biomarkers for heterotopic ossification in blood serum. Journal of Orthopaedic Surgery and Research, 2017, 12, 69.	0.9	13
1539	Identification of repaglinide as a therapeutic drug for glioblastoma multiforme. Biochemical and Biophysical Research Communications, 2017, 488, 33-39.	1.0	23
1540	Comprehensive profiling of rhizome-associated alternative splicing and alternative polyadenylation in moso bamboo (<i>Phyllostachys edulis</i>). Plant Journal, 2017, 91, 684-699.	2.8	170
1541	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in Arabidopsis. Nature Communications, 2017, 8, 15235.	5.8	54
1542	S100-alarmin-induced innate immune programming protects newborn infants from sepsis. Nature Immunology, 2017, 18, 622-632.	7.0	131
1543	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. Genome Biology and Evolution, 2017, 9, 1130-1147.	1.1	75
1544	Surface topology affects wetting behavior of Bacillus subtilis biofilms. Npj Biofilms and Microbiomes, 2017, 3, 11.	2.9	55
1545	Identification of HDA15-PIF1 as a key repression module directing the transcriptional network of seed germination in the dark. Nucleic Acids Research, 2017, 45, 7137-7150.	6.5	89
1546	Integrating 3-omics data analyze rat lung tissue of COPD states and medical intervention by delineation of molecular and pathway alterations. Bioscience Reports, 2017, 37, .	1.1	13

#	ARTICLE	IF	CITATIONS
1547	E2fl1 is a meiosis-specific transcription factor in the protist <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2017, 16, 123-135.	1.3	9
1548	Working with Ontologies. <i>Methods in Molecular Biology</i> , 2017, 1525, 123-135.	0.4	6
1549	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
1550	3-Bromopyruvate treatment induces alterations of metabolic and stress-related pathways in glioblastoma cells. <i>Journal of Proteomics</i> , 2017, 152, 329-338.	1.2	19
1551	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
1552	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
1553	Transcriptome-wide analysis of jasmonate-treated BY-2 cells reveals new transcriptional regulators associated with alkaloid formation in tobacco. <i>Journal of Plant Physiology</i> , 2017, 215, 1-10.	1.6	9
1554	Establishment of a Strong Link Between Smoking and Cancer Pathogenesis through DNA Methylation Analysis. <i>Scientific Reports</i> , 2017, 7, 1811.	1.6	59
1555	Nonsense-mediated mRNA decay in <i>Tetrahymena</i> is EJC independent and requires a protozoa-specific nuclease. <i>Nucleic Acids Research</i> , 2017, 45, 6848-6863.	6.5	22
1556	Identification of potential crucial genes associated with early-onset pre-eclampsia via a microarray analysis. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 812-819.	0.6	8
1557	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
1558	Integrated analysis and transcript abundance modelling of H3K4me3 and H3K27me3 in developing secondary xylem. <i>Scientific Reports</i> , 2017, 7, 3370.	1.6	32
1559	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	1.6	24
1560	Genetic and transcriptomic analyses of lignin- and lodging-related traits in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 1961-1973.	1.8	64
1561	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
1562	Global transcriptome and coexpression network analyses reveal cultivar-specific molecular signatures associated with seed development and seed size/weight determination in chickpea. <i>Plant Journal</i> , 2017, 91, 1088-1107.	2.8	108
1563	Evidence for salicylic acid signalling and histological changes in the defence response of <i>Eucalyptus grandis</i> to <i>Chrysoporthe austroafricana</i> . <i>Scientific Reports</i> , 2017, 7, 45402.	1.6	9
1564	ceRNAs in plants: computational approaches and associated challenges for target mimic research. <i>Briefings in Bioinformatics</i> , 2017, 19, 1273-1289.	3.2	16

#	ARTICLE	IF	CITATIONS
1565	The common transcriptional subnetworks of the grape berry skin in the late stages of ripening. BMC Plant Biology, 2017, 17, 94.	1.6	42
1566	Ndfip1 restricts mTORC1 signalling and glycolysis in regulatory T cells to prevent autoinflammatory disease. Nature Communications, 2017, 8, 15677.	5.8	34
1567	Widespread Down-Regulation of Cardiac Mitochondrial and Sarcomeric Genes in Patients With Sepsis*. Critical Care Medicine, 2017, 45, 407-414.	0.4	76
1568	Proteomic identification of ERP29 as a key chemoresistant factor activated by the aggregating p53 mutant Arg282Trp. Oncogene, 2017, 36, 5473-5483.	2.6	23
1569	Lysine Acetylome Analysis Reveals Photosystem II Manganese-stabilizing Protein Acetylation is Involved in Negative Regulation of Oxygen Evolution in Model Cyanobacterium Synechococcus sp. PCC 7002. Molecular and Cellular Proteomics, 2017, 16, 1297-1311.	2.5	26
1570	Data from proteome analysis of Lasiodiplodia theobromae (Botryosphaeriaceae). Data in Brief, 2017, 13, 124-128.	0.5	1
1571	vhfRNAi: a web-platform for analysis of host genes involved in viral infections discovered by genome wide RNAi screens. Molecular BioSystems, 2017, 13, 1377-1387.	2.9	3
1572	Histone H3 lysine 36 methylation affects temperature-induced alternative splicing and flowering in plants. Genome Biology, 2017, 18, 102.	3.8	146
1573	Gene networks for total number born in pigs across divergent environments. Mammalian Genome, 2017, 28, 426-435.	1.0	3
1574	Suppression of NF- κ B signal pathway by NLRC3-like protein in stony coral Acropora aculeus under heat stress. Fish and Shellfish Immunology, 2017, 67, 322-330.	1.6	15
1575	Morphoproteomic Characterization of Lung Squamous Cell Carcinoma Fragmentation, a Histological Marker of Increased Tumor Invasiveness. Cancer Research, 2017, 77, 2585-2593.	0.4	15
1576	The molecular mechanisms of androgen receptor in nephrolithiasis. Gene, 2017, 616, 16-21.	1.0	7
1577	Genome-wide transcriptome profiling of Carica papaya L. embryogenic callus. Physiology and Molecular Biology of Plants, 2017, 23, 357-368.	1.4	26
1578	Transcriptomic and metabolic analyses provide new insights into chilling injury in peach fruit. Plant, Cell and Environment, 2017, 40, 1531-1551.	2.8	92
1579	The miRNAome of Catharanthus roseus: identification, expression analysis, and potential roles of microRNAs in regulation of terpenoid indole alkaloid biosynthesis. Scientific Reports, 2017, 7, 43027.	1.6	39
1580	rNAV 2.0: a visualization tool for bacterial sRNA-mediated regulatory networks mining. BMC Bioinformatics, 2017, 18, 188.	1.2	6
1582	Populus trichocarpa encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports, 2017, 7, 382.	1.6	36
1583	Powerful differential expression analysis incorporating network topology for next-generation sequencing data. Bioinformatics, 2017, 33, 1505-1513.	1.8	20

#	ARTICLE	IF	CITATIONS
1584	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
1585	AtSLP2 is an intronless protein phosphatase that co-expresses with intronless mitochondrial pentatricopeptide repeat (PPR) and tetratricopeptide (TPR) protein encoding genes. <i>Plant Signaling and Behavior</i> , 2017, 12, e1307493.	1.2	4
1586	Reconstructing the genome of the most recent common ancestor of flowering plants. <i>Nature Genetics</i> , 2017, 49, 490-496.	9.4	203
1587	Proteomics-based network analysis characterizes biological processes and pathways activated by preconditioned mesenchymal stem cells in cardiac repair mechanisms. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 1190-1199.	1.1	9
1588	Prolonged Absence of Mechanoluminal Stimulation in Human Intestine Alters the Transcriptome and Intestinal Stem Cell Niche. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017, 3, 367-388.e1.	2.3	22
1589	Novel proteins from proteomic analysis of the trunk disease fungus <i>Lasiodiplodia theobromae</i> (Botryosphaeriaceae). <i>Biochimie Open</i> , 2017, 4, 88-98.	3.2	6
1590	Elevated ammonium reduces the negative effect of heat stress on the stony coral <i>Pocillopora damicornis</i> . <i>Marine Pollution Bulletin</i> , 2017, 118, 319-327.	2.3	27
1591	Transcriptome analysis of a wild bird reveals physiological responses to the urban environment. <i>Scientific Reports</i> , 2017, 7, 44180.	1.6	86
1592	Molecular Evidence for Differential Long-term Outcomes of Early Life Severe Acute Malnutrition. <i>EBioMedicine</i> , 2017, 18, 274-280.	2.7	15
1593	Identification of crucial genes associated with rat traumatic spinal cord injury. <i>Molecular Medicine Reports</i> , 2017, 15, 1997-2006.	1.1	12
1594	Transcriptome analysis reveals sunflower cytochrome P450 CYP93A1 responses to high salinity treatment at the seedling stage. <i>Genes and Genomics</i> , 2017, 39, 581-591.	0.5	19
1595	Placental Proteomics Provides Insights into Pathophysiology of Pre-Eclampsia and Predicts Possible Markers in Plasma. <i>Journal of Proteome Research</i> , 2017, 16, 1050-1060.	1.8	31
1596	Myofibrillar Z-discs Are a Protein Phosphorylation Hot Spot with Protein Kinase C (PKC \pm) Modulating Protein Dynamics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 346-367.	2.5	36
1597	Exosomes and Microvesicles. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	10
1598	Modellierung und Simulation von Protein-Interaktionen am Beispiel von Wirts-Pathogen-Interaktionen. , 2017, , .		0
1599	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
1600	The transcriptional regulatory network mediated by banana (<i>Musa acuminata</i>) dehydration-responsive element binding (MaDREB) transcription factors in fruit ripening. <i>New Phytologist</i> , 2017, 214, 762-781.	3.5	68
1601	Network-Based Approach to Identify Potential Targets and Drugs that Promote Neuroprotection and Neurorepair in Acute Ischemic Stroke. <i>Scientific Reports</i> , 2017, 7, 40137.	1.6	38

#	ARTICLE	IF	CITATIONS
1602	Exploring Plant Co-Expression and Gene-Gene Interactions with CORNET 3.0. <i>Methods in Molecular Biology</i> , 2017, 1533, 201-212.	0.4	11
1603	Comparative interactomics for virus–human protein–protein interactions: <scp>DNA</scp> viruses versus <scp>RNA</scp> viruses. <i>FEBS Open Bio</i> , 2017, 7, 96-107.	1.0	42
1604	Bioinformatics Tools for Extracellular Vesicles Research. <i>Methods in Molecular Biology</i> , 2017, 1545, 189-196.	0.4	16
1605	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
1607	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
1608	Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2017, 29, 2786-2800.	3.1	46
1609	H2A.Z Represses Gene Expression by Modulating Promoter Nucleosome Structure and Enhancer Histone Modifications in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2017, 10, 1274-1292.	3.9	102
1610	Transcriptomic responses to drought and salt stress in desert tree <i>Prosopis juliflora</i> . <i>Plant Gene</i> , 2017, 12, 114-122.	1.4	13
1611	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
1612	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2017, 1666, 539-556.	0.4	11
1613	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 989, 93-107.	0.8	3
1615	Screening and identification of key biomarkers in hepatocellular carcinoma: Evidence from bioinformatic analysis. <i>Oncology Reports</i> , 2017, 38, 2607-2618.	1.2	187
1616	Immuno-Oncology Integrative Networks: Elucidating the Influences of Osteosarcoma Phenotypes. <i>Cancer Informatics</i> , 2017, 16, 117693511772169.	0.9	5
1617	Monitoring storage induced changes in the platelet proteome employing label free quantitative mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 11045.	1.6	27
1618	Microarray and bioinformatics analyses of gene expression profiles in BALB/c murine macrophage polarization. <i>Molecular Medicine Reports</i> , 2017, 16, 7382-7390.	1.1	31
1619	Identification of genes associated with castration-resistant prostate cancer by gene expression profile analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 6803-6813.	1.1	13
1620	Formation of <i>Staphylococcus aureus</i> Biofilm in the Presence of Sublethal Concentrations of Disinfectants Studied via a Transcriptomic Analysis Using Transcriptome Sequencing (RNA-seq). <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	33
1621	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

#	ARTICLE	IF	CITATIONS
1622	Transcription factor 19 interacts with histone 3 lysine 4 trimethylation and controls gluconeogenesis via the nucleosome-remodeling-deacetylase complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 20362-20378.	1.6	25
1623	Ets transcription factor GABP controls T cell homeostasis and immunity. <i>Nature Communications</i> , 2017, 8, 1062.	5.8	22
1624	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
1625	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
1626	Proteomics for Drug Discovery. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	4
1627	Two plant-derived aporphinoid alkaloids exert their antifungal activity by disrupting mitochondrial iron-sulfur cluster biosynthesis. <i>Journal of Biological Chemistry</i> , 2017, 292, 16578-16593.	1.6	13
1628	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
1629	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
1630	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
1631	Identification of Nidogen 1 as a lung metastasis protein through secretome analysis. <i>Genes and Development</i> , 2017, 31, 1439-1455.	2.7	41
1632	The BABY BOOM Transcription Factor Activates the LEC1-ABI3-FUS3-LEC2 Network to Induce Somatic Embryogenesis. <i>Plant Physiology</i> , 2017, 175, 848-857.	2.3	236
1633	Downregulation of miR-136-5p in hepatocellular carcinoma and its clinicopathological significance. <i>Molecular Medicine Reports</i> , 2017, 16, 5393-5405.	1.1	28
1634	YAP/TAZ Orchestrate VEGF Signaling during Developmental Angiogenesis. <i>Developmental Cell</i> , 2017, 42, 462-478.e7.	3.1	249
1635	Transcriptome changes in <i>Arabidopsis thaliana</i> infected with <i>Pseudomonas syringae</i> during drought recovery. <i>Scientific Reports</i> , 2017, 7, 9124.	1.6	18
1636	Intracellular spectral repositioning of light enhances algal photosynthetic efficiency. <i>Science Advances</i> , 2017, 3, e1603096.	4.7	42
1637	(Re-)programming of subtype specific cardiomyocytes. <i>Advanced Drug Delivery Reviews</i> , 2017, 120, 142-167.	6.6	13
1638	Wounding Triggers Callus Formation via Dynamic Hormonal and Transcriptional Changes. <i>Plant Physiology</i> , 2017, 175, 1158-1174.	2.3	214
1639	The ClpXP protease is dispensable for degradation of unfolded proteins in <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2017, 7, 11739.	1.6	53

#	ARTICLE	IF	CITATIONS
1640	Desiccation tolerance in bryophytes: The dehydration and rehydration transcriptomes in the desiccation-tolerant bryophyte <i>Bryum argenteum</i> . <i>Scientific Reports</i> , 2017, 7, 7571.	1.6	50
1641	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
1642	Transcriptome-based network analysis reveals renal cell type-specific dysregulation of hypoxia-associated transcripts. <i>Scientific Reports</i> , 2017, 7, 8576.	1.6	62
1643	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
1644	The yeast noncoding RNA interaction network. <i>Rna</i> , 2017, 23, 1479-1492.	1.6	25
1645	Insight into synergetic mechanisms of tetracycline and the selective serotonin reuptake inhibitor, sertraline, in a tetracycline-resistant strain of <i>Escherichia coli</i> . <i>Journal of Antibiotics</i> , 2017, 70, 944-953.	1.0	25
1646	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
1647	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
1648	Computational analysis for GNAQ mutations: New insights on the molecular etiology of Sturge-Weber syndrome. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 76, 429-440.	1.3	31
1649	The inducible blockage of RNAi reveals a role for polyunsaturated fatty acids in the regulation of dsRNA-endocytic capacity in <i>Bactrocera dorsalis</i> . <i>Scientific Reports</i> , 2017, 7, 5584.	1.6	12
1650	ACCERBATIN, a small molecule at the intersection of auxin and reactive oxygen species homeostasis with herbicidal properties. <i>Journal of Experimental Botany</i> , 2017, 68, 4185-4203.	2.4	7
1651	Non-interacting proteins may resemble interacting proteins: prevalence and implications. <i>Scientific Reports</i> , 2017, 7, 40419.	1.6	12
1652	Divergently expressed gene identification and interaction prediction of long noncoding RNA and mRNA involved in duck reproduction. <i>Animal Reproduction Science</i> , 2017, 185, 8-17.	0.5	13
1653	Induction of senescence in cancer cells by 5-aza-2'-deoxycytidine: Bioinformatics and experimental insights to its targets. <i>Computational Biology and Chemistry</i> , 2017, 70, 49-55.	1.1	17
1654	Transcriptomic Analysis of Ribosome-Bound mRNA in Cortical Neurites <i>In Vivo</i> . <i>Journal of Neuroscience</i> , 2017, 37, 8688-8705.	1.7	49
1655	Transcriptome Association Identifies Regulators of Wheat Spike Architecture. <i>Plant Physiology</i> , 2017, 175, 746-757.	2.3	94
1656	Age, estrogen, and immune response in breast adenocarcinoma and adjacent normal tissue. <i>Oncolmmunology</i> , 2017, 6, e1356142.	2.1	34
1657	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1647, 267-295.	0.4	1

#	ARTICLE	IF	CITATIONS
1658	Quantitative proteomic analysis of host responses triggered by Mycobacterium tuberculosis infection in human macrophage cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 835-844.	0.9	23
1659	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
1660	A gene network regulated by FGF signalling during ear development. <i>Scientific Reports</i> , 2017, 7, 6162.	1.6	29
1661	Drought and salt stress in <i>Chrysopogon zizanioides</i> leads to common and specific transcriptomic responses and may affect essential oil composition and benzylisoquinoline alkaloids metabolism. <i>Current Plant Biology</i> , 2017, 11-12, 12-22.	2.3	14
1662	Ethylene promotes root hair growth through coordinated EIN3/EIL1 and RHD6/RSL1 activity in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13834-13839.	3.3	149
1664	Increased Phosphorylation of Ser-Gln Sites on SUPPRESSOR OF GAMMA RESPONSE1 Strengthens the DNA Damage Response in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2017, 29, 3255-3268.	3.1	54
1665	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
1666	Toxic Substances in <i>Jatropha</i> Seeds: Biosynthesis of the Most Problematic Compounds, Phorbol Esters. <i>Compendium of Plant Genomes</i> , 2017, , 97-111.	0.3	2
1667	Identifications of potential therapeutic targets and drugs in angiotensin II-induced hypertension. <i>Medicine (United States)</i> , 2017, 96, e8501.	0.4	5
1668	Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.		1
1669	3D collagen architecture induces a conserved migratory and transcriptional response linked to vasculogenic mimicry. <i>Nature Communications</i> , 2017, 8, 1651.	5.8	109
1670	Identification of regenerative roadblocks via repeat deployment of limb regeneration in axolotls. <i>Npj Regenerative Medicine</i> , 2017, 2, 30.	2.5	42
1671	Severe neonatal hyperbilirubinemia in Crigler-Najjar syndrome model mice can be reversed with zinc protoporphyrin. <i>Hepatology Communications</i> , 2017, 1, 792-802.	2.0	8
1672	Evaluating the associations between human circadian rhythms and dysregulated genes in liver cancer cells. <i>Oncology Letters</i> , 2017, 14, 7353-7359.	0.8	6
1673	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
1674	Proteome dynamics during post-desiccation recovery reveal convergence of desiccation and gamma radiation stress response pathways in <i>Deinococcus radiodurans</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1215-1226.	1.1	22
1675	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
1676	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

#	ARTICLE	IF	CITATIONS
1677	Overexpression of mir-183 and mir-494 promotes proliferation and migration in human breast cancer cell lines. <i>Oncology Letters</i> , 2017, 14, 1054-1060.	0.8	40
1678	Microbial-Host Co-metabolites Are Prodromal Markers Predicting Phenotypic Heterogeneity in Behavior, Obesity, and Impaired Glucose Tolerance. <i>Cell Reports</i> , 2017, 20, 136-148.	2.9	78
1679	A Systems Vaccinology Approach Reveals Temporal Transcriptomic Changes of Immune Responses to the Yellow Fever 17D Vaccine. <i>Journal of Immunology</i> , 2017, 199, 1476-1489.	0.4	40
1680	Protein complex finding and ranking: An application to Alzheimer's disease. <i>Journal of Biosciences</i> , 2017, 42, 383-396.	0.5	3
1681	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
1682	Avoiding the pitfalls of gene set enrichment analysis with SetRank. <i>BMC Bioinformatics</i> , 2017, 18, 151.	1.2	93
1683	Response of microRNAs to cold treatment in the young spikes of common wheat. <i>BMC Genomics</i> , 2017, 18, 212.	1.2	75
1684	Defining the transcriptomic landscape of the developing enteric nervous system and its cellular environment. <i>BMC Genomics</i> , 2017, 18, 290.	1.2	38
1685	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
1686	Comparative transcriptomics of mountain pine beetle pheromone-biosynthetic tissues and functional analysis of CYP6DE3. <i>BMC Genomics</i> , 2017, 18, 311.	1.2	30
1687	De novo sequencing and comparative transcriptome analysis of the male and hermaphroditic flowers provide insights into the regulation of flower formation in andromonoecious <i>Taihangia rupestris</i> . <i>BMC Plant Biology</i> , 2017, 17, 54.	1.6	29
1688	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
1689	Characterization of genetic aberrations in a single case of metastatic thymic adenocarcinoma. <i>BMC Cancer</i> , 2017, 17, 330.	1.1	14
1690	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
1691	The Gene Ontology Handbook. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	63
1692	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017, 89, 706-717.	2.8	145
1693	Visualization and Analysis of MiRNA-Targets Interactions Networks. <i>Methods in Molecular Biology</i> , 2017, 1509, 209-220.	0.4	16
1694	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

#	ARTICLE	IF	CITATIONS
1695	Systems genetics reveals a transcriptional network associated with susceptibility in the maize “grey leaf spot pathosystem. <i>Plant Journal</i> , 2017, 89, 746-763.	2.8	49
1696	Meta-analysis of Genome-Wide Chromatin Data. <i>Methods in Molecular Biology</i> , 2017, 1456, 33-50.	0.4	2
1697	Gene-Category Analysis. <i>Methods in Molecular Biology</i> , 2017, 1446, 175-188.	0.4	11
1698	Visualizing GO Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 207-220.	0.4	12
1700	Effects of elevated ammonium on the transcriptome of the stony coral <i>Pocillopora damicornis</i> . <i>Marine Pollution Bulletin</i> , 2017, 114, 46-52.	2.3	30
1701	New Insight Into Early Somatic Embryogenesis of Mangosteen (<i>Garcinia mangostana</i>) Through de Novo and Comparative Transcriptome Analyses. <i>Tropical Plant Biology</i> , 2017, 10, 30-44.	1.0	8
1702	Identification of key genes involved in nasopharyngeal carcinoma. <i>Brazilian Journal of Otorhinolaryngology</i> , 2017, 83, 670-676.	0.4	13
1703	Structural pliability adjacent to the kinase domain highlights contribution of FAK1 IDRs to cytoskeletal remodeling. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 43-54.	1.1	2
1704	Integrated RNA-seq and sRNA-seq analysis reveals miRNA effects on secondary metabolism in <i>Solanum tuberosum</i> L. <i>Molecular Genetics and Genomics</i> , 2017, 292, 37-52.	1.0	43
1705	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
1706	Arabidopsis NF-YCs Mediate the Light-Controlled Hypocotyl Elongation via Modulating Histone Acetylation. <i>Molecular Plant</i> , 2017, 10, 260-273.	3.9	77
1707	MicroRNA and target mRNA selection through invasion and cytotoxicity cell modeling and bioinformatics approaches in esophageal squamous cell carcinoma. <i>Oncology Reports</i> , 2017, 38, 1181-1189.	1.2	5
1708	Changes in flavonoid biosynthesis and in the berry whole transcriptome of “Sangiovese”™ under moderate air temperature increase. <i>Acta Horticulturae</i> , 2017, , 157-164.	0.1	1
1709	Analysis of expression profile data identifies key genes and pathways in hepatocellular carcinoma. <i>Oncology Letters</i> , 2018, 15, 2625-2630.	0.8	6
1710	Grapevine downy mildew dual epidemics: a leaf and inflorescence transcriptomics study. <i>Acta Horticulturae</i> , 2017, , 265-270.	0.1	2
1711	Whole-genome sequencing and SNV genotyping of “Nebbiolo”™ (<i>Vitis vinifera</i> L.) clones. <i>Scientific Reports</i> , 2017, 7, 17294.	1.6	72
1712	Identification of key genes influenced by fixation stability in early fracture hematoma and elucidation of their roles in fracture healing. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 4633-4638.	0.8	2
1713	Integrated transcriptomic analysis of <i>Trichosporon Asahii</i> uncovers the core genes and pathways of fluconazole resistance. <i>Scientific Reports</i> , 2017, 7, 17847.	1.6	7

#	ARTICLE	IF	CITATIONS
1714	Gene expression profiling reveals candidate genes related to residual feed intake in duodenum of laying ducks ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 5270-5277.	0.2	5
1715	Conserved Transcription Factors Steer Growth-Related Genomic Programs in <i>Daphnia</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1821-1842.	1.1	13
1716	Identification of new genes associated to senescent and tumorigenic phenotypes in mesenchymal stem cells. <i>Scientific Reports</i> , 2017, 7, 17837.	1.6	26
1718	Proteomic and bioinformatics analysis of human saliva for the dental-risk assessment. <i>Open Life Sciences</i> , 2017, 12, 248-265.	0.6	2
1719	In-depth PtdIns(3,4,5)P3 signalosome analysis identifies DAPP1 as a negative regulator of GPVI-driven platelet function. <i>Blood Advances</i> , 2017, 1, 918-932.	2.5	34
1720	Transcriptome Profiling in Systems Vascular Medicine. <i>Frontiers in Pharmacology</i> , 2017, 8, 563.	1.6	22
1721	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
1722	<i>Arabidopsis</i> NITRILASE 1 Contributes to the Regulation of Root Growth and Development through Modulation of Auxin Biosynthesis in Seedlings. <i>Frontiers in Plant Science</i> , 2017, 8, 36.	1.7	64
1723	Differential Gene Expression Analysis in <i>Polygonum minus</i> Leaf upon 24 h of Methyl Jasmonate Elicitation. <i>Frontiers in Plant Science</i> , 2017, 8, 109.	1.7	25
1724	Genome-Wide Association and Transcriptome Analyses Reveal Candidate Genes Underlying Yield-determining Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 206.	1.7	70
1725	Transcriptome Analysis of Flowering Time Genes under Drought Stress in Maize Leaves. <i>Frontiers in Plant Science</i> , 2017, 8, 267.	1.7	54
1726	De novo Transcriptome Analysis of <i>Miscanthus lutarioriparius</i> Identifies Candidate Genes in Rhizome Development. <i>Frontiers in Plant Science</i> , 2017, 8, 492.	1.7	18
1727	Whole Plant Temperature Manipulation Affects Flavonoid Metabolism and the Transcriptome of Grapevine Berries. <i>Frontiers in Plant Science</i> , 2017, 8, 929.	1.7	102
1728	Extra Large G-Protein Interactome Reveals Multiple Stress Response Function and Partner-Dependent XLG Subcellular Localization. <i>Frontiers in Plant Science</i> , 2017, 8, 1015.	1.7	31
1729	TGMS in Rapeseed (<i>Brassica napus</i>) Resulted in Aberrant Transcriptional Regulation, Asynchronous Microsporocyte Meiosis, Defective Tapetum, and Fused Sexine. <i>Frontiers in Plant Science</i> , 2017, 8, 1268.	1.7	9
1730	Perturbation of Auxin Homeostasis and Signaling by PINOID Overexpression Induces Stress Responses in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1308.	1.7	14
1731	Effects of Combined Low Glutathione with Mild Oxidative and Low Phosphorus Stress on the Metabolism of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1464.	1.7	16
1732	eQTLs Regulating Transcript Variations Associated with Rapid Internode Elongation in Deepwater Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1753.	1.7	29

#	ARTICLE	IF	CITATIONS
1733	Comparative muscle transcriptome associated with carcass traits of Nellore cattle. BMC Genomics, 2017, 18, 506.	1.2	51
1734	iTRAQ-Based Quantitative Proteomic Analysis Reveals Cold Responsive Proteins Involved in Leaf Senescence in Upland Cotton (<i>Gossypium hirsutum</i> L.). International Journal of Molecular Sciences, 2017, 18, 1984.	1.8	16
1735	Transcriptomic Profiling of the Allorecognition Response to Grafting in the Demosponge <i>Amphimedon queenslandica</i> . Marine Drugs, 2017, 15, 136.	2.2	3
1736	Identification of HIV-1 Tat-Associated Proteins Contributing to HIV-1 Transcription and Latency. Viruses, 2017, 9, 67.	1.5	18
1737	Handling Big Data in Precision Medicine. , 2017, , 251-268.		3
1738	Comparative transcriptome profile of the leaf elongation zone of wild barley (<i>Hordeum spontaneum</i>) <i>eib1</i> mutant and its isogenic wild type. Genetics and Molecular Biology, 2017, 40, 834-843.	0.6	0
1739	Transcriptional Analysis of <i>Acinetobacter</i> sp. <i>neg1</i> Capable of Degrading Ochratoxin A. Frontiers in Microbiology, 2016, 7, 2162.	1.5	48
1740	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	1.8	90
1741	Integrated proteomic and N-glycoproteomic analyses of doxorubicin sensitive and resistant ovarian cancer cells reveal glycoprotein alteration in protein abundance and glycosylation. Oncotarget, 2017, 8, 13413-13427.	0.8	18
1742	DegoViz: An Interactive Visualization Tool for a Differentially Expressed Genes Heatmap and Gene Ontology Graph. Applied Sciences (Switzerland), 2017, 7, 543.	1.3	4
1743	De Novo Transcriptome Characterization, Gene Expression Profiling and Ionic Responses of <i>Nitraria sibirica</i> Pall. under Salt Stress. Forests, 2017, 8, 211.	0.9	12
1744	Expression Profiling in <i>Pinus pinaster</i> in Response to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . Forests, 2017, 8, 279.	0.9	22
1745	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. Genes, 2017, 8, 8.	1.0	28
1746	A Transcriptomic Comparison of Two Bambara Groundnut Landraces under Dehydration Stress. Genes, 2017, 8, 121.	1.0	23
1747	Auxin Response Factor Genes Repertoire in Mulberry: Identification, and Structural, Functional and Evolutionary Analyses. Genes, 2017, 8, 202.	1.0	16
1748	Overexpression of Transforming Acidic Coiled Coil-Containing Protein 3 Reflects Malignant Characteristics and Poor Prognosis of Glioma. International Journal of Molecular Sciences, 2017, 18, 235.	1.8	9
1749	Semi-Quantitative Mass Spectrometry in AML Cells Identifies New Non-Genomic Targets of the EZH2 Methyltransferase. International Journal of Molecular Sciences, 2017, 18, 1440.	1.8	7
1750	The MicroRNA Interaction Network of Lipid Diseases. Frontiers in Genetics, 2017, 8, 116.	1.1	15

#	ARTICLE	IF	CITATIONS
1751	Integrating Transcriptomics, Proteomics, and Metabolomics Profiling with System Pharmacology for the Delineation of Long-Term Therapeutic Mechanisms of Bufeijianpi Formula in Treating COPD. BioMed Research International, 2017, 2017, 1-17.	0.9	11
1752	Bioactive Nutrients and Nutrigenomics in Age-Related Diseases. Molecules, 2017, 22, 105.	1.7	61
1753	The amyloid interactome: Exploring protein aggregation. PLoS ONE, 2017, 12, e0173163.	1.1	25
1754	WetA bridges cellular and chemical development in <i>Aspergillus flavus</i> . PLoS ONE, 2017, 12, e0179571.	1.1	48
1755	Genetic variation and expression changes associated with molybdate resistance from a glutathione producing wine strain of <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2017, 12, e0180814.	1.1	8
1756	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
1757	Adaptation of <i>Arabidopsis thaliana</i> to the Yangtze River basin. Genome Biology, 2017, 18, 239.	3.8	44
1758	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. BMC Biology, 2017, 15, 63.	1.7	238
1759	Multiple-trait genomewide mapping and gene network analysis for scrotal circumference growth curves in Brahman cattle1. Journal of Animal Science, 2017, 95, 3331-3345.	0.2	16
1760	Constructing and analyzing gene regulatory networks in leaf senescence of <i>Arabidopsis thaliana</i> . , 2017, , .		0
1761	Molecular Mechanisms Underlying the Nephrotoxicity of Cisplatin, Lead Acetate and Cyclosporine: Key Roles of Myc and Smad4. Biological Systems, Open Access, 2017, 06, .	0.1	1
1762	<i>miR-9a</i> mediates the role of Lethal giant larvae as an epithelial growth inhibitor in <i>Drosophila</i> . Biology Open, 2018, 7, .	0.6	6
1763	LncRNA expression in the spinal cord modulated by minocycline in a mouse model of spared nerve injury. Journal of Pain Research, 2017, Volume 10, 2503-2514.	0.8	27
1764	A comprehensive analysis of candidate gene signatures in oral squamous cell carcinoma. Neoplasma, 2017, 64, 167-174.	0.7	4
1765	Exploring autophagy with Gene Ontology. Autophagy, 2018, 14, 419-436.	4.3	64
1766	Spina bifida-predisposing heterozygous mutations in Planar Cell Polarity genes and Zic2 reduce bone mass in young mice. Scientific Reports, 2018, 8, 3325.	1.6	5
1767	Differentially expressed proteins associated with drought tolerance in bananas (<i>Musa</i> spp.). Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	12
1768	Bringing numerous methods for expression and promoter analysis to a public cloud computing service. Bioinformatics, 2018, 34, 884-886.	1.8	573

#	ARTICLE	IF	CITATIONS
1769	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
1770	Integration of transcriptomics, proteomics, metabolomics and systems pharmacology data to reveal the therapeutic mechanism underlying Chinese herbal Bufe Yishen formula for the treatment of chronic obstructive pulmonary disease. <i>Molecular Medicine Reports</i> , 2018, 17, 5247-5257.	1.1	25
1771	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
1772	Comparative transcriptome analysis to investigate the potential role of miRNAs in milk protein/fat quality. <i>Scientific Reports</i> , 2018, 8, 6250.	1.6	17
1773	Regulatory gene network from a genome-wide association study for sow lifetime productivity traits. <i>Animal Genetics</i> , 2018, 49, 254-258.	0.6	6
1774	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
1775	Deciphering the mechanism of action of 089, a compound impairing the fungal cell cycle. <i>Scientific Reports</i> , 2018, 8, 5964.	1.6	6
1776	Global H3.3 dynamic deposition defines its bimodal role in cell fate transition. <i>Nature Communications</i> , 2018, 9, 1537.	5.8	49
1777	Metallic materials ontology population from LOD based on conditional random field. <i>Computers in Industry</i> , 2018, 99, 140-155.	5.7	3
1778	MTGO: PPI Network Analysis Via Topological and Functional Module Identification. <i>Scientific Reports</i> , 2018, 8, 5499.	1.6	103
1779	Network-based meta-analysis in the identification of biomarkers for papillary thyroid cancer. <i>Gene</i> , 2018, 661, 160-168.	1.0	20
1780	Transcriptome profiling reveals regulatory mechanisms underlying corolla senescence in petunia. <i>Horticulture Research</i> , 2018, 5, 16.	2.9	28
1781	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
1782	Comparative transcriptomics with self-organizing map reveals cryptic photosynthetic differences between two accessions of North American Lake cress. <i>Scientific Reports</i> , 2018, 8, 3302.	1.6	19
1783	Functional Genome-wide Screen Identifies Pathways Restricting Central Nervous System Axonal Regeneration. <i>Cell Reports</i> , 2018, 23, 415-428.	2.9	43
1784	Deciphering the Combined Effects of Environmental Stressors on Gene Transcription: A Conceptual Approach. <i>Environmental Science & Technology</i> , 2018, 52, 5479-5489.	4.6	20
1785	Comparative transcriptome analysis in Arabidopsis <i>ein2/ore3</i> and <i>ahk3/ore12</i> mutants during dark-induced leaf senescence. <i>Journal of Experimental Botany</i> , 2018, 69, 3023-3036.	2.4	31
1786	Role of CD133 Molecule in Wnt Response and Renal Repair. <i>Stem Cells Translational Medicine</i> , 2018, 7, 283-294.	1.6	50

#	ARTICLE	IF	CITATIONS
1787	Loss of ATRX suppresses ATM dependent DNA damage repair by modulating H3K9me3 to enhance temozolomide sensitivity in glioma. <i>Cancer Letters</i> , 2018, 419, 280-290.	3.2	47
1788	Gamma radiation induces dose-dependent oxidative stress and transcriptional alterations in the freshwater crustacean <i>Daphnia magna</i> . <i>Science of the Total Environment</i> , 2018, 628-629, 206-216.	3.9	27
1789	Identifying the target genes of <scp>SUPPRESSOR OF GAMMA RESPONSE</scp> 1, a master transcription factor controlling <scp>DNA</scp> damage response in <i>Arabidopsis</i>. <i>Plant Journal</i> , 2018, 94, 439-453.	2.8	127
1790	Exploration of the platelet proteome in patients with early-stage cancer. <i>Journal of Proteomics</i> , 2018, 177, 65-74.	1.2	65
1791	Unraveling the transcriptional complexity of compactness in sistan grape cluster. <i>Plant Science</i> , 2018, 270, 198-208.	1.7	10
1792	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (G×E) on the berry transcriptome. <i>Plant Journal</i> , 2018, 93, 1143-1159.	2.8	75
1793	The Genotypeâ€“Phenotype Relationships in the Light of Natural Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 525-542.	3.5	16
1794	A DP-like transcription factor protein interacts with E2f1 to regulate meiosis in<i>Tetrahymena thermophila</i>. <i>Cell Cycle</i> , 2018, 17, 634-642.	1.3	31
1795	Antisecretory Factorâ€“Mediated Inhibition of Cell Volume Dynamics Produces Antitumor Activity in Glioblastoma. <i>Molecular Cancer Research</i> , 2018, 16, 777-790.	1.5	16
1796	A novel approach to wildlife transcriptomics provides evidence of diseaseâ€“mediated differential expression and changes to the microbiome of amphibian populations. <i>Molecular Ecology</i> , 2018, 27, 1413-1427.	2.0	32
1797	Quantitative Proteomics of Strong and Weak Biofilm Formers of <i>Enterococcus faecalis</i> Reveals Novel Regulators of Biofilm Formation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 643-654.	2.5	44
1798	Comparative proteomics of the larval and adult stages of the model cestode parasite <i>Mesocostoides corti</i> . <i>Journal of Proteomics</i> , 2018, 175, 127-135.	1.2	21
1799	Systems Biology Modeling to Study Pathogenâ€“Host Interactions. <i>Methods in Molecular Biology</i> , 2018, 1734, 97-112.	0.4	13
1800	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
1801	Desiccation tolerance in bryophytes: the rehydration proteomes of <i>Bryum argenteum</i> provide insights into the resuscitation mechanism. <i>Journal of Arid Land</i> , 2018, 10, 152-167.	0.9	9
1802	Adaptation to high zinc depends on distinct mechanisms in metalicolous populations of <i>Arabidopsis halleri</i>. <i>New Phytologist</i> , 2018, 218, 269-282.	3.5	90
1803	Contrasting cadmium resistance strategies in two metalicolous populations of <i>Arabidopsis halleri</i>. <i>New Phytologist</i> , 2018, 218, 283-297.	3.5	88
1804	Glucocorticoids induce differentiation of monocytes towards macrophages that share functional and phenotypical aspects with erythroblastic island macrophages. <i>Haematologica</i> , 2018, 103, 395-405.	1.7	65

#	ARTICLE	IF	CITATIONS
1805	Sequential feature selection and inference using multi-variate random forests. <i>Bioinformatics</i> , 2018, 34, 1336-1344.	1.8	7
1806	FunGeneNet: a web tool to estimate enrichment of functional interactions in experimental gene sets. <i>BMC Genomics</i> , 2018, 19, 76.	1.2	7
1807	A meta-analysis of public microarray data identifies biological regulatory networks in Parkinson's disease. <i>BMC Medical Genomics</i> , 2018, 11, 40.	0.7	36
1808	Transcriptome profiling of <i>Issatchenkia orientalis</i> under ethanol stress. <i>AMB Express</i> , 2018, 8, 39.	1.4	21
1809	IgG Immunocomplexes Sensitize Human Monocytes for Inflammatory Hyperactivity via Transcriptomic and Epigenetic Reprogramming in Rheumatoid Arthritis. <i>Journal of Immunology</i> , 2018, 200, 3913-3925.	0.4	15
1810	Integrative network analyses of wilt transcriptome in chickpea reveal genotype dependent regulatory hubs in immunity and susceptibility. <i>Scientific Reports</i> , 2018, 8, 6528.	1.6	14
1811	Identification of candidate resistance genes of cotton against <i>Aspergillus flavus</i> infection using a comparative transcriptomics approach. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 513-519.	1.4	3
1812	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
1813	Promyelocytic Leukemia Protein (PML) Requirement for Interferon-induced Global Cellular SUMOylation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1196-1208.	2.5	22
1814	Host-Virus Protein Interaction Network Reveals the Involvement of Multiple Host Processes in the Life Cycle of Hepatitis E Virus. <i>MSystems</i> , 2018, 3, .	1.7	40
1815	Embryophyte stress signaling evolved in the algal progenitors of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3471-E3480.	3.3	164
1816	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
1817	Protein S-Nitrosylation Controls Glycogen Synthase Kinase 3 ^β Function Independent of Its Phosphorylation State. <i>Circulation Research</i> , 2018, 122, 1517-1531.	2.0	40
1818	Key genes and regulatory networks involved in the initiation, progression and invasion of colorectal cancer. <i>Future Science OA</i> , 2018, 4, FSO278.	0.9	12
1819	Data set on G4 DNA interactions with human proteins. <i>Data in Brief</i> , 2018, 18, 348-359.	0.5	13
1820	Site-Specific Systematic Analysis of Lysine Modification Crosstalk. <i>Proteomics</i> , 2018, 18, e1700292.	1.3	6
1821	DNA methylation profiling of asbestos-treated MeT5A cell line reveals novel pathways implicated in asbestos response. <i>Archives of Toxicology</i> , 2018, 92, 1785-1795.	1.9	16
1822	Transcriptome profiling of HepG2 cells exposed to the flame retardant 9,10-dihydro-9-oxa-10-phosphaphenanthrene 10-oxide (DOPO). <i>Toxicology Research</i> , 2018, 7, 492-502.	0.9	4

#	ARTICLE	IF	CITATIONS
1823	Transcriptome landscape of a bacterial pathogen under plant immunity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3055-E3064.	3.3	166
1824	Sparse Pathway-Induced Dynamic Network Biomarker Discovery for Early Warning Signal Detection in Complex Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1028-1034.	1.9	6
1825	Adding biological meaning to human protein-protein interactions identified by yeast two-hybrid screenings: A guide through bioinformatics tools. Journal of Proteomics, 2018, 171, 127-140.	1.2	9
1826	Mechanisms of Mendelian dominance. Clinical Genetics, 2018, 93, 419-428.	1.0	70
1827	Global proteome and phosphoproteome dynamics indicate novel mechanisms of vitamin C induced dormancy in Mycobacterium smegmatis. Journal of Proteomics, 2018, 180, 1-10.	1.2	16
1828	G proteinâ€dependent signaling triggers a Î²â€arrestinâ€scaffolded p70S6K/ rpS6 module that controls 5'TOP mRNA translation. FASEB Journal, 2018, 32, 1154-1169.	0.2	24
1829	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	2.4	18
1830	Drought and salt stress in Macrotyloma uniflorum leads to common and specific transcriptomic responses and reveals importance of raffinose family oligosaccharides in stress tolerance. Gene Reports, 2018, 10, 7-16.	0.4	10
1831	Nonâ€branched Î²â€1,3â€glucan oligosaccharides trigger immune responses in Arabidopsis. Plant Journal, 2018, 93, 34-49.	2.8	112
1832	Gene expression signatures of mating system evolution. Genome, 2018, 61, 287-297.	0.9	13
1833	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
1834	Dynamic transcriptomic analysis in hircine longissimus dorsi muscle from fetal to neonatal development stages. Functional and Integrative Genomics, 2018, 18, 43-54.	1.4	25
1835	Toxicogenomics of the flame retardant tris (2-butoxyethyl) phosphate in HepG2 cells using RNA-seq. Toxicology in Vitro, 2018, 46, 178-188.	1.1	21
1836	Micro<scp>RNA</scp> profiling reveals dysregulated micro<scp>RNA</scp>s and their target gene regulatory networks in cementoâ€ossifying fibroma. Journal of Oral Pathology and Medicine, 2018, 47, 78-85.	1.4	19
1837	Functional Interpretation of Gene Sets: Semantic-Based Clustering of Gene Ontology Terms on the BioTest Platform. Advances in Intelligent Systems and Computing, 2018, , 125-136.	0.5	3
1838	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. Hepatology, 2018, 67, 1270-1283.	3.6	388
1839	Acetylome Profiling Reveals Extensive Lysine Acetylation of the Fatty Acid Metabolism Pathway in the Diatom Phaeodactylum tricornutum. Molecular and Cellular Proteomics, 2018, 17, 399-412.	2.5	26
1840	Systemic response of the stony coral Pocillopora damicornis against acute cadmium stress. Aquatic Toxicology, 2018, 194, 132-139.	1.9	28

#	ARTICLE	IF	CITATIONS
1841	HDAC11 is a regulator of diverse immune functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 54-59.	0.9	70
1842	Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. , 2018, , .		5
1844	Using a Next-Generation Sequencing Approach to Profile MicroRNAs from Human Origin. <i>Methods in Molecular Biology</i> , 2018, 1710, 203-217.	0.4	2
1845	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
1846	Potential role of lncRNAs in contributing to pathogenesis of chronic glomerulonephritis based on microarray data. <i>Gene</i> , 2018, 643, 46-54.	1.0	10
1847	Thermal acclimation in <i>Arabidopsis lyrata</i> : genotypic costs and transcriptional changes. <i>Journal of Evolutionary Biology</i> , 2018, 31, 123-135.	0.8	12
1848	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
1849	The <i>RIN-MC</i> Fusion of MADS-Box Transcription Factors Has Transcriptional Activity and Modulates Expression of Many Ripening Genes. <i>Plant Physiology</i> , 2018, 176, 891-909.	2.3	94
1850	Comparison of Disease Specific Sub-Network Identification Programs. , 2018, , .		0
1851	Distinct Diagnostic and Prognostic Values of Kinesin Family Member Genes Expression in Patients with Breast Cancer. <i>Medical Science Monitor</i> , 2018, 24, 9442-9464.	0.5	28
1852	Rule-Based Graph Repairing: Semantic and Efficient Repairing Methods. , 2018, , .		19
1853	Defining a Characteristic Gene Expression Set Responsible for Cancer Stem Cell-Like Features in a Sub-Population of Ewing Sarcoma Cells CADO-ES1. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3908.	1.8	13
1854	Hub genes and gene functions associated with postmenopausal osteoporosis predicted by an integrated method. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 1262-1267.	0.8	2
1855	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
1856	Network assessment of demethylation treatment in melanoma: Differential transcriptome-methylome and antigen profile signatures. <i>PLoS ONE</i> , 2018, 13, e0206686.	1.1	2
1857	De novo variants in congenital diaphragmatic hernia identify MYRF as a new syndrome and reveal genetic overlaps with other developmental disorders. <i>PLoS Genetics</i> , 2018, 14, e1007822.	1.5	79
1859	SyNDI: synchronous network data integration framework. <i>BMC Bioinformatics</i> , 2018, 19, 403.	1.2	1
1860	Gene Co-expression Network Reveals Potential New Genes Related to Sugarcane Bagasse Degradation in <i>Trichoderma reesei</i> RUT-30. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 151.	2.0	36

#	ARTICLE	IF	CITATIONS
1861	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
1862	Proteome Investigation of Rat Lungs subjected to Ex Vivo Perfusion (EVLP). <i>Molecules</i> , 2018, 23, 3061.	1.7	20
1863	Endangered Père David's deer genome provides insights into population recovering. <i>Evolutionary Applications</i> , 2018, 11, 2040-2053.	1.5	19
1864	gLabTrie: A Data Structure for Motif Discovery with Constraints. <i>Data-centric Systems and Applications</i> , 2018, , 71-95.	0.2	3
1866	Dysregulation of Neuronal Cholesterol Homeostasis upon Exposure to HIV-1 Tat and Cocaine Revealed by RNA-Sequencing. <i>Scientific Reports</i> , 2018, 8, 16300.	1.6	25
1867	Large scale study of anti-sense regulation by differential network analysis. <i>BMC Systems Biology</i> , 2018, 12, 95.	3.0	1
1868	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
1869	Relationship between <i>Fusobacterium nucleatum</i> , inflammatory mediators and microRNAs in colorectal carcinogenesis. <i>World Journal of Gastroenterology</i> , 2018, 24, 5351-5365.	1.4	82
1870	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
1871	Ozone-induced inhibition of kiwifruit ripening is amplified by 1-methylcyclopropene and reversed by exogenous ethylene. <i>BMC Plant Biology</i> , 2018, 18, 358.	1.6	50
1872	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
1873	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
1874	Functional Neurogenomics: A New Approach to Study Cognitive Disability in Down Syndrome Brain. , 2018, , .		0
1875	Comparative Transcriptomics of Rat and Axolotl After Spinal Cord Injury Dissects Differences and Similarities in Inflammatory and Matrix Remodeling Gene Expression Patterns. <i>Frontiers in Neuroscience</i> , 2018, 12, 808.	1.4	13
1876	Decoding Transcriptome Dynamics of Genome-Encoded Polyadenylation and Autoregulation with Small-Molecule Modulators of Alternative Polyadenylation. <i>Cell Chemical Biology</i> , 2018, 25, 1470-1484.e5.	2.5	18
1877	Approaches to the discovery of non-invasive urinary biomarkers of prostate cancer. <i>Oncotarget</i> , 2018, 9, 32534-32550.	0.8	21
1878	Identification of key genes and associated pathways in KIT/PDGFRα wild-type gastrointestinal stromal tumors through bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 4499-4515.	1.1	5
1879	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

#	ARTICLE	IF	CITATIONS
1880	Genome-wide association studies for tick resistance in <i>Bos taurus</i> – <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
1881	A transcriptomics model of estrogen action in the ovine fetal hypothalamus: evidence for estrogenic effects of ICI 182,780. <i>Physiological Reports</i> , 2018, 6, e13871.	0.7	5
1882	The receptor tyrosine kinase HIR-1 coordinates HIF-independent responses to hypoxia and extracellular matrix injury. <i>Science Signaling</i> , 2018, 11, .	1.6	19
1883	Identification of genes and signaling pathways associated with arthrogryposis-renal dysfunction-cholestasis syndrome using weighted correlation network analysis. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2238-2246.	1.8	5
1884	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
1885	Inhibition of histone methyltransferase EZH2 in <i>Schistosoma mansoni</i> in vitro by GSK343 reduces egg laying and decreases the expression of genes implicated in DNA replication and noncoding RNA metabolism. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006873.	1.3	25
1886	A Systems Analysis With a Simplified Source-Sink Model Reveals Metabolic Reprogramming in a Pair of Source-to-Sink Organs During Early Fruit Development in Tomato by LED Light Treatments. <i>Frontiers in Plant Science</i> , 2018, 9, 1439.	1.7	9
1887	Pilot Production of Mesenchymal Stem/Stromal Freeze-Dried Secretome for Cell-Free Regenerative Nanomedicine: A Validated GMP-Compliant Process. <i>Cells</i> , 2018, 7, 190.	1.8	108
1888	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
1889	The KDM4A/KDM4C/NF- κ B and WDR5 epigenetic cascade regulates the activation of B cells. <i>Nucleic Acids Research</i> , 2018, 46, 5547-5560.	6.5	34
1890	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
1891	Mrp1 is involved in lipid presentation and iNKT cell activation by <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 4279.	5.8	11
1892	Transcriptomic basis for reinforcement of elm antiherbivore defence mediated by insect egg deposition. <i>Molecular Ecology</i> , 2018, 27, 4901-4915.	2.0	18
1893	Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With Expanded Knowledge in the Gene Ontology. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001813.	1.6	24
1894	Genome-Wide Investigation of the Role of MicroRNAs in Desiccation Tolerance in the Resurrection Grass <i>Tripogon loliiformis</i> . <i>Plants</i> , 2018, 7, 68.	1.6	8
1895	<i>Saccharomyces paradoxus</i> K66 Killer System Evidences Expanded Assortment of Helper and Satellite Viruses. <i>Viruses</i> , 2018, 10, 564.	1.5	19
1896	A framework for identifying functional modules in dynamic networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 21, 1.	0.1	3
1897	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

#	ARTICLE	IF	CITATIONS
1898	Combining discovery and targeted proteomics reveals a prognostic signature in oral cancer. <i>Nature Communications</i> , 2018, 9, 3598.	5.8	134
1899	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
1900	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
1901	Neuronal heterogeneity and stereotyped connectivity in the auditory afferent system. <i>Nature Communications</i> , 2018, 9, 3691.	5.8	195
1902	SOX2OT knockdown derived changes in mitotic regulatory gene network of cancer cells. <i>Cancer Cell International</i> , 2018, 18, 129.	1.8	6
1903	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
1904	Dynamics of alternative polyadenylation in human preimplantation embryos. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 727-733.	1.0	3
1905	Small RNAs from cereal powdery mildew pathogens may target host plant genes. <i>Fungal Biology</i> , 2018, 122, 1050-1063.	1.1	41
1906	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
1907	Gene expression profile and cancer-associated pathways linked to progesterone receptor isoform α (PRA) predominance in transgenic mouse mammary glands. <i>BMC Cancer</i> , 2018, 18, 682.	1.1	6
1908	Insights into archaeal chaperone machinery: a network-based approach. <i>Cell Stress and Chaperones</i> , 2018, 23, 1257-1274.	1.2	1
1909	A Novel Differential Ion Mobility Device Expands the Depth of Proteome Coverage and the Sensitivity of Multiplex Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2051-2067.	2.5	106
1910	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
1911	Bioinformatics analysis to screen for critical genes between survived and non-survived patients with sepsis. <i>Molecular Medicine Reports</i> , 2018, 18, 3737-3743.	1.1	22
1912	Gene expression profiling of coronary artery disease and its relation with different severities. <i>Journal of Genetics</i> , 2018, 97, 853-867.	0.4	2
1913	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018, 19, 188.	1.2	2
1914	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
1915	Genetic differentiation in life history traits and thermal stress performance across a heterogeneous dune landscape in <i>Arabidopsis lyrata</i> . <i>Annals of Botany</i> , 2018, 122, 473-484.	1.4	6

#	ARTICLE	IF	CITATIONS
1916	Screening for implicated genes in colorectal cancer using whole-genome gene expression profiling. <i>Molecular Medicine Reports</i> , 2018, 17, 8260-8268.	1.1	8
1917	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
1918	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
1919	Developmental Chromatin Restriction of Proliferative Growth Genes Networks Acts as an Epigenetic Barrier to Axon Regeneration in Cortical Neurons. <i>Developmental Neurobiology</i> , 2018, 78, 960-977.	1.5	29
1920	Metabolic Reprogramming in Leaf Lettuce Grown Under Different Light Quality and Intensity Conditions Using Narrow-Band LEDs. <i>Scientific Reports</i> , 2018, 8, 7914.	1.6	77
1921	WEGO 2.0: a web tool for analyzing and plotting GO annotations, 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W71-W75.	6.5	473
1922	An Open-Source Desktop Application for Generating Arc-Routing Benchmark Instances. <i>INFORMS Journal on Computing</i> , 2018, 30, 361-370.	1.0	7
1923	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
1924	Potential mechanism and drug candidates for sepsis-induced acute lung injury. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4689-4696.	0.8	6
1925	Transcriptome and Expression Profiling Analysis of Recalcitrant Tea (<i>Camellia sinensis</i> L.) Seeds Sensitive to Dehydration. <i>International Journal of Genomics</i> , 2018, 2018, 1-11.	0.8	7
1926	Transcriptomic and Network Analyses Reveal Mechanistic-Based Biomarkers of Endocrine Disruption in the Marine Mussel, <i>Mytilus edulis</i> . <i>Environmental Science & Technology</i> , 2018, 52, 9419-9430.	4.6	42
1927	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
1928	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
1929	Function, dynamics and evolution of network motif modules in integrated gene regulatory networks of worm and plant. <i>Nucleic Acids Research</i> , 2018, 46, 6480-6503.	6.5	33
1930	Genome-wide bisulphite-sequencing reveals organ-specific methylation patterns in chickpea. <i>Scientific Reports</i> , 2018, 8, 9704.	1.6	25
1931	Maternal obesity stimulates lipotoxicity and upregulates inflammatory signaling pathways in the full-term swine placenta. <i>Animal Science Journal</i> , 2018, 89, 1310-1322.	0.6	14
1932	Wild tomato endosperm transcriptomes reveal common roles of genomic imprinting in both nuclear and cellular endosperm. <i>Plant Journal</i> , 2018, 95, 1084-1101.	2.8	38
1933	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

#	ARTICLE	IF	CITATIONS
1934	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8406-8411.	3.3	119
1935	Proteome-wide analysis of human motif-domain interactions mapped on influenza A virus. <i>BMC Bioinformatics</i> , 2018, 19, 238.	1.2	8
1936	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
1937	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
1938	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
1939	OLIGOCELLULA1/HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES15 Promotes Cell Proliferation With HISTONE DEACETYLASE9 and POWERDRESS During Leaf Development in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 580.	1.7	30
1940	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
1941	Making a Better Home: Modulation of Plant Defensive Response by <i>Brevipalpus</i> Mites. <i>Frontiers in Plant Science</i> , 2018, 9, 1147.	1.7	44
1942	Distinct Diagnostic and Prognostic Values of Minichromosome Maintenance Gene Expression in Patients with Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2018, 9, 2357-2373.	1.2	59
1943	Whole-genome re-sequencing reveals molecular mechanisms of biomass changes in 11-year-old Bt transgenic poplar. <i>Trees - Structure and Function</i> , 2018, 32, 1609-1620.	0.9	2
1944	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. <i>BMC Genomics</i> , 2018, 19, 126.	1.2	53
1945	A Systems Biology Approach for Studying Heterotopic Ossification: Proteomic Analysis of Clinical Serum and Tissue Samples. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 212-220.	3.0	9
1946	Inhibition of TOR Represses Nutrient Consumption, Which Improves Greening after Extended Periods of Etiolation. <i>Plant Physiology</i> , 2018, 178, 101-117.	2.3	27
1947	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
1948	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	1.2	51
1949	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
1950	RNA-Seq Reveals Extensive Transcriptional Response to Heat Stress in the Stony Coral <i>Galaxea fascicularis</i> . <i>Frontiers in Genetics</i> , 2018, 9, 37.	1.1	27
1951	Identification of Shared Molecular Signatures Indicate the Susceptibility of Endometriosis to Multiple Sclerosis. <i>Frontiers in Genetics</i> , 2018, 9, 42.	1.1	16

#	ARTICLE	IF	CITATIONS
1952	Infection by a Giant Virus (AaV) Induces Widespread Physiological Reprogramming in <i>Aureococcus anophagefferens</i> CCMP1984 – A Harmful Bloom Algae. <i>Frontiers in Microbiology</i> , 2018, 9, 752.	1.5	60
1953	IDPpi: Protein-Protein Interaction Analyses of Human Intrinsically Disordered Proteins. <i>Scientific Reports</i> , 2018, 8, 10563.	1.6	18
1954	Tau GSTs involved in regulation of leaf abscission by comparison the gene profiling of MeGSTs in various abscission-promoting treatments in cassava abscission zones. <i>BMC Genetics</i> , 2018, 19, 45.	2.7	3
1955	Genome-Wide Identification and Expression Analysis of the HD-Zip Gene Family in Wheat (<i>Triticum</i>) TJ ETQq1 1 0.784314 rgBT ₄₁ /Overl	1.0	41
1956	Identification of key genes and pathways for esophageal squamous cell carcinoma by bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1121-1130.	0.8	9
1957	A genetic program mediates cold-warming response and promotes stress-induced phenoptosis in <i>C. elegans</i> . <i>ELife</i> , 2018, 7, .	2.8	37
1958	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
1959	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
1960	Quantitative Proteomic Analysis of Biological Processes and Responses of the Bacterium <i>Desulfovibrio desulfuricans</i> ND132 upon Deletion of Its Mercury Methylation Genes. <i>Proteomics</i> , 2018, 18, e1700479.	1.3	22
1961	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
1962	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
1963	Direct reprogramming of fibroblasts into neural stem cells by single non-neural progenitor transcription factor Ptf1a. <i>Nature Communications</i> , 2018, 9, 2865.	5.8	72
1964	Temporal analysis of Arabidopsis genes activated by <i>Eucalyptus grandis</i> NAC transcription factors associated with xylem fibre and vessel development. <i>Scientific Reports</i> , 2018, 8, 10983.	1.6	16
1965	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
1966	Comparative proteomics of two <i>Mycoplasma hyopneumoniae</i> strains and <i>Mycoplasma flocculare</i> identified potential porcine enzootic pneumonia determinants. <i>Virulence</i> , 2018, 9, 1230-1246.	1.8	20
1967	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
1968	PD-1 axis expression in musculoskeletal tumors and antitumor effect of nivolumab in osteosarcoma model of humanized mouse. <i>Journal of Hematology and Oncology</i> , 2018, 11, 16.	6.9	96
1969	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

#	ARTICLE	IF	CITATIONS
1970	Ca ²⁺ imaging and gene expression profiling of <i>Lonicera Confusa</i> in response to calcium-rich environment. <i>Scientific Reports</i> , 2018, 8, 7068.	1.6	9
1971	Single-cell RNA-seq of human induced pluripotent stem cells reveals cellular heterogeneity and cell state transitions between subpopulations. <i>Genome Research</i> , 2018, 28, 1053-1066.	2.4	102
1972	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
1973	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
1974	A Spatiotemporal DNA Endoploidy Map of the Arabidopsis Root Reveals Roles for the Endocycle in Root Development and Stress Adaptation. <i>Plant Cell</i> , 2018, 30, 2330-2351.	3.1	107
1975	Association of DFNA5, SYK, and NELL1 variants along with HPV infection in oral cancer among the prolonged tobacco-chewers. <i>Tumor Biology</i> , 2018, 40, 101042831879302.	0.8	11
1976	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. <i>BMC Genomics</i> , 2018, 19, 588.	1.2	64
1977	KLF6 and STAT3 co-occupy regulatory DNA and functionally synergize to promote axon growth in CNS neurons. <i>Scientific Reports</i> , 2018, 8, 12565.	1.6	34
1978	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. <i>Theranostics</i> , 2018, 8, 4345-4358.	4.6	63
1979	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
1980	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
1981	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
1982	Expanding the horizons of microRNA bioinformatics. <i>Rna</i> , 2018, 24, 1005-1017.	1.6	27
1983	Developmental Origin Governs CD8+ T Cell Fate Decisions during Infection. <i>Cell</i> , 2018, 174, 117-130.e14.	13.5	132
1984	Prediction of novel target genes and pathways involved in bevacizumab-resistant colorectal cancer. <i>PLoS ONE</i> , 2018, 13, e0189582.	1.1	16
1985	A transcriptome screen for positive selection in domesticated breadfruit and its wild relatives (<i>T. ETQq1</i> 1 0.784314.rgBT / Overlock 10 0.8)	0.8	10
1986	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 390-405.	0.6	4
1987	The Pathway Coexpression Network: Revealing pathway relationships. <i>PLoS Computational Biology</i> , 2018, 14, e1006042.	1.5	41

#	ARTICLE	IF	CITATIONS
1988	Dynamic genome wide expression profiling of <i>Drosophila</i> head development reveals a novel role of Hunchback in retinal glia cell development and blood-brain barrier integrity. <i>PLoS Genetics</i> , 2018, 14, e1007180.	1.5	11
1989	A census of <i>P. longum</i> 's phytochemicals and their network pharmacological evaluation for identifying novel drug-like molecules against various diseases, with a special focus on neurological disorders. <i>PLoS ONE</i> , 2018, 13, e0191006.	1.1	35
1990	Potential role of RAB6C-AS1 long noncoding RNA in different cancers. <i>Journal of Cellular Physiology</i> , 2019, 234, 891-903.	2.0	12
1991	Functional Enrichment Analysis. , 2019, , 218-229.		2
1992	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019, 17, 517-530.	4.1	56
1993	Transcriptome Profiling of <i>Bigeloviella natans</i> in Response to Light Stress. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 316-333.	0.8	8
1994	<i>Ocimum basilicum</i> miRNOME revisited: A cross kingdom approach. <i>Genomics</i> , 2019, 111, 772-785.	1.3	12
1995	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
1996	Protein Post-Translational Modification Prediction. , 2019, , 15-27.		1
1997	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
1998	Integrated use of bioinformatic resources reveals that co-targeting of histone deacetylases, IKBK and SRC inhibits epithelial-mesenchymal transition in cancer. <i>Briefings in Bioinformatics</i> , 2019, 20, 717-731.	3.2	20
1999	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
2000	Analysis of chickpea gene co-expression networks and pathways during heavy metal stress. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	2
2001	Genomic Integrity Safeguards Self-Renewal in Embryonic Stem Cells. <i>Cell Reports</i> , 2019, 28, 1400-1409.e4.	2.9	15
2002	Integrated analysis of lncRNA-miRNA-mRNA ceRNA network in squamous cell carcinoma of tongue. <i>BMC Cancer</i> , 2019, 19, 779.	1.1	234
2003	Genetic signature related to heme-hemoglobin metabolism pathway in sepsis secondary to pneumonia. <i>Npj Systems Biology and Applications</i> , 2019, 5, 26.	1.4	18
2004	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
2005	DNA hypermethylation of aurora kinase A in hepatitis C virus-positive hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2019, 20, 2519-2532.	1.1	6

#	ARTICLE	IF	CITATIONS
2006	The evolution of gene duplicates in angiosperms and the impact of protein-protein interactions and the mechanism of duplication. <i>Genome Biology and Evolution</i> , 2019, 11, 2292-2305.	1.1	48
2007	WRKY1 Mediates Transcriptional Regulation of Light and Nitrogen Signaling Pathways. <i>Plant Physiology</i> , 2019, 181, 1371-1388.	2.3	22
2008	The Osteocyte Transcriptome Is Extensively Dysregulated in Mouse Models of Osteogenesis Imperfecta. <i>JBMR Plus</i> , 2019, 3, e10171.	1.3	29
2009	m6A mRNA methylation regulates human β -cell biology in physiological states and in type 2 diabetes. <i>Nature Metabolism</i> , 2019, 1, 765-774.	5.1	158
2010	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. <i>Molecular Medicine</i> , 2019, 25, 36.	1.9	7
2011	Identification of a thymus microRNA-mRNA regulatory network in Down syndrome. <i>Molecular Medicine Reports</i> , 2019, 20, 2063-2072.	1.1	3
2012	Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1900199.	1.3	10
2013	Polypropylene mesh implantation for hernia repair causes myeloid cell-driven persistent inflammation. <i>JCI Insight</i> , 2019, 4, .	2.3	43
2014	Genetic variants of the oppA gene are involved in metabolic regulation of surfactin in <i>Bacillus subtilis</i> . <i>Microbial Cell Factories</i> , 2019, 18, 141.	1.9	9
2015	<p><p>PRPF40A as a potential diagnostic and prognostic marker is upregulated in pancreatic cancer tissues and cell lines: an integrated bioinformatics data analysis<p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 5037-5051.	1.0	13
2016	Rhesus Brain Transcriptomic Landscape in an ex vivo Model of the Interaction of Live <i>Borrelia burgdorferi</i> With Frontal Cortex Tissue Explants. <i>Frontiers in Neuroscience</i> , 2019, 13, 651.	1.4	9
2017	Diagnostic and prognostic values of integrin β subfamily mRNA expression in colon adenocarcinoma. <i>Oncology Reports</i> , 2019, 42, 923-936.	1.2	13
2018	Exploration of the Differentially Expressed Long Noncoding RNAs and Genes of Morphine Tolerance via Bioinformatic Analysis. <i>Journal of Computational Biology</i> , 2019, 26, 1379-1393.	0.8	7
2019	Transcriptomic evidence that cortisol alters perinatal epicardial adipose tissue maturation. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E573-E585.	1.8	5
2020	Screening and Bioinformatics Analysis of IgA Nephropathy Gene Based on GEO Databases. <i>BioMed Research International</i> , 2019, 2019, 1-7.	0.9	17
2021	Diagnostic and prognostic value of WNT family gene expression in hepatitis B virus-related hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 895-910.	1.2	8
2022	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
2023	Screening and identification of hub genes in pancreatic cancer by integrated bioinformatics analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19496-19508.	1.2	39

#	ARTICLE	IF	CITATIONS
2024	Differential UVR8 Signal across the Stem Controls UV-Bâ€“Induced Inflorescence Phototropism. <i>Plant Cell</i> , 2019, 31, 2070-2088.	3.1	35
2025	Madecassic Acid Derivatives as Potential Anticancer Agents: Synthesis and Cytotoxic Evaluation. <i>Journal of Natural Products</i> , 2019, 82, 2094-2105.	1.5	17
2026	Quantitative proteomics reveals TMOD1-related proteins associated with water balance regulation. <i>PLoS ONE</i> , 2019, 14, e0219932.	1.1	5
2027	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
2028	<i>Trypanosoma brucei</i> ribonuclease H2A is an essential R-loop processing enzyme whose loss causes DNA damage during transcription initiation and antigenic variation. <i>Nucleic Acids Research</i> , 2019, 47, 9180-9197.	6.5	32
2029	Genome-Wide Profiling Reveals the Landscape of Prognostic Alternative Splicing Signatures in Pancreatic Ductal Adenocarcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 511.	1.3	26
2030	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
2031	Graph Theoretic and Pearson Correlation-Based Discovery of Network Biomarkers for Cancer. <i>Data</i> , 2019, 4, 81.	1.2	9
2032	Genome-wide association studies for heat stress response in <i>Bos taurus</i> Ã— <i>Bos indicus</i> crossbred cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8148-8158.	1.4	31
2033	Verification and Improvement of the Capability of ENSEMBLES to Predict the Winter Arctic Oscillation. <i>Earth and Space Science</i> , 2019, 6, 1887-1899.	1.1	6
2034	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
2035	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
2036	The White-Rot Basidiomycete <i>Dichomitus squalens</i> Shows Highly Specific Transcriptional Response to Lignocellulose-Related Aromatic Compounds. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 229.	2.0	21
2037	Transcriptional regulatory framework for vascular cambium development in <i>Arabidopsis</i> roots. <i>Nature Plants</i> , 2019, 5, 1033-1042.	4.7	81
2038	Comparison between the Transcriptomes of â€˜KDML105â€™ TM Rice and a Salt-Tolerant Chromosome Segment Substitution Line. <i>Genes</i> , 2019, 10, 742.	1.0	5
2039	RORÎ³ is a targetable master regulator of cholesterol biosynthesis in a cancer subtype. <i>Nature Communications</i> , 2019, 10, 4621.	5.8	81
2040	High accuracy comsol simulation method of bimorph cantilever for piezoelectric vibration energy harvesting. <i>AIP Advances</i> , 2019, 9, .	0.6	44
2041	Prognostic value of Kinesinâ€“4 family genes mRNA expression in earlyâ€“stage pancreatic ductal adenocarcinoma patients after pancreaticoduodenectomy. <i>Cancer Medicine</i> , 2019, 8, 6487-6502.	1.3	4

#	ARTICLE	IF	CITATIONS
2042	Unraveling oxidative stress response in the cestode parasite <i>Echinococcus granulosus</i> . <i>Scientific Reports</i> , 2019, 9, 15876.	1.6	13
2043	DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1981-1982.	1.8	2
2044	Transcriptional Signature Derived from Murine Tumor-Associated Macrophages Correlates with Poor Outcome in Breast Cancer Patients. <i>Cell Reports</i> , 2019, 29, 1221-1235.e5.	2.9	47
2045	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
2046	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
2047	A Genome-Wide Screen for Wortmannin-Resistant Mutants in <i>Schizosaccharomyces pombe</i> : The Phosphorylation-Impaired Mutants Are Resistant to Signaling Defect. <i>DNA and Cell Biology</i> , 2019, 38, 1427-1436.	0.9	0
2048	The prognostic value of faciogenital dysplasias as biomarkers in head and neck squamous cell carcinoma. <i>Biomarkers in Medicine</i> , 2019, 13, 1399-1415.	0.6	8
2049	Candidate Domestication-Related Genes Revealed by Expression Quantitative Trait Loci Mapping of Narrow-Leafed Lupin (<i>Lupinus angustifolius</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 5670.	1.8	23
2050	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
2051	The Interactome analysis of the Respiratory Syncytial Virus protein M2-1 suggests a new role in viral mRNA metabolism post-transcription. <i>Scientific Reports</i> , 2019, 9, 15258.	1.6	14
2052	Sex-specific changes in the aphid DNA methylation landscape. <i>Molecular Ecology</i> , 2019, 28, 4228-4241.	2.0	45
2053	Adipose Mesenchymal Extracellular Vesicles as Alpha-1-Antitrypsin Physiological Delivery Systems for Lung Regeneration. <i>Cells</i> , 2019, 8, 965.	1.8	48
2054	Stress-induced Changes in the S-palmitoylation and S-nitrosylation of Synaptic Proteins* [S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1916-1938.	2.5	39
2055	Gene expression during the germination of coffee seed. <i>Journal of Seed Science</i> , 2019, 41, 168-179.	0.7	6
2056	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
2057	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
2058	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
2059	Diagnostic and prognostic value of mRNA expression of phospholipase C β family genes in hepatitis B virus-associated hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 41, 2855-2875.	1.2	10

#	ARTICLE	IF	CITATIONS
2060	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
2061	Transcriptomic and functional analyses of 3D placental extravillous trophoblast spheroids. <i>Scientific Reports</i> , 2019, 9, 12607.	1.6	18
2062	Illustrated guide to the classification of banana seeds and embryos. <i>Revista Brasileira De Fruticultura</i> , 2019, 41, .	0.2	1
2063	Integrative analysis of the contribution of mRNAs and long non-coding RNAs to the pathogenesis of asthma. <i>Molecular Medicine Reports</i> , 2019, 20, 2617-2624.	1.1	10
2064	Genome-wide mining of microsatellites in king cobra (<i>Ophiophagus hannah</i>) and cross-species development of tetranucleotide SSR markers in Chinese cobra (<i>Naja atra</i>). <i>Molecular Biology Reports</i> , 2019, 46, 6087-6098.	1.0	10
2065	Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994.	5.8	33
2066	The CRISPR-Cas9 crADSL HeLa transcriptome: A first step in establishing a model for ADSL deficiency and SAICAR accumulation. <i>Molecular Genetics and Metabolism Reports</i> , 2019, 21, 100512.	0.4	12
2067	Identification of differentially expressed genes between primary lung cancer and lymph node metastasis via bioinformatic analysis. <i>Oncology Letters</i> , 2019, 18, 3754-3768.	0.8	5
2068	VcFT-induced mobile florigenic signals in transgenic and transgrafted blueberries. <i>Horticulture Research</i> , 2019, 6, 105.	2.9	25
2069	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
2070	Weighted Gene Co-Expression Analyses Point to Long Non-Coding RNA Hub Genes at Different <i>Schistosoma mansoni</i> Life-Cycle Stages. <i>Frontiers in Genetics</i> , 2019, 10, 823.	1.1	22
2071	Influence Factors on the Hepatotoxicity of <i>Polygoni Multiflori Radix</i> . <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-12.	0.5	12
2072	Niche-Specific Factors Dynamically Regulate Sebaceous Gland Stem Cells in the Skin. <i>Developmental Cell</i> , 2019, 51, 326-340.e4.	3.1	32
2073	Accumulation mechanism of indigo and indirubin in <i>Polygonum tinctorium</i> revealed by metabolite and transcriptome analysis. <i>Industrial Crops and Products</i> , 2019, 141, 111783.	2.5	11
2074	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
2075	Intracellular changes of a swine tracheal cell line infected with a <i>Mycoplasma hyopneumoniae</i> pathogenic strain. <i>Microbial Pathogenesis</i> , 2019, 137, 103717.	1.3	8
2076	FunVar: A systematic pipeline to unravel the convergence patterns of genetic variants in ASD, a paradigmatic complex disease. <i>Journal of Biomedical Informatics</i> , 2019, 98, 103273.	2.5	2
2077	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

#	ARTICLE	IF	CITATIONS
2078	Mechanism of Brassica oleracea performance in bovine infectious mastitis by bioinformatic analysis. Microbial Pathogenesis, 2019, 129, 19-29.	1.3	13
2079	The CCR2+ Macrophage Subset Promotes Pathogenic Angiogenesis for Tumor Vascularization in Fibrotic Livers. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 371-390.	2.3	71
2080	Whole transcriptome expression profiling and biological network analysis of chickpea during heavy metal stress. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 345-352.	0.9	12
2081	Bladder cancer stage-associated hub genes revealed by WGCNA co-expression network analysis. Hereditas, 2019, 156, 7.	0.5	79
2082	Prediction of Plant miRNA Targets. Methods in Molecular Biology, 2019, 1932, 99-107.	0.4	18
2083	Identification of prognostic biomarkers for patients with hepatocellular carcinoma after hepatectomy. Oncology Reports, 2019, 41, 1586-1602.	1.2	26
2084	<p>Integrated analysis of lncRNA-associated ceRNA network reveals potential biomarkers for the prognosis of hepatitis B virus-related hepatocellular carcinoma</p>. Cancer Management and Research, 2019, Volume 11, 877-897.	0.9	24
2085	Network Analysis Reveals TNF as a Major Hub of Reactive Inflammation Following Spinal Cord Injury. Scientific Reports, 2019, 9, 928.	1.6	12
2086	Comprehensive bioinformation analysis of methylated and differentially expressed genes in esophageal squamous cell carcinoma. Molecular Omics, 2019, 15, 88-100.	1.4	9
2087	Phenotypic, Hormonal, and Genomic Variation Among Vitis vinifera Clones With Different Cluster Compactness and Reproductive Performance. Frontiers in Plant Science, 2018, 9, 1917.	1.7	18
2088	CMSENN: Computational Modification Sites with Ensemble Neural Network. Chemometrics and Intelligent Laboratory Systems, 2019, 185, 65-72.	1.8	20
2089	A Network Pharmacology Approach to Explore Mechanism of Action of Longzuan Tongbi Formula on Rheumatoid Arthritis. Evidence-based Complementary and Alternative Medicine, 2019, 2019, 1-13.	0.5	8
2090	The AP2/ERF Transcription Factor TINY Modulates Brassinosteroid-Regulated Plant Growth and Drought Responses in Arabidopsis. Plant Cell, 2019, 31, 1788-1806.	3.1	153
2091	Proteomics Profiling of Host Cell Response via Protein Expression and Phosphorylation upon Dengue Virus Infection. Virologica Sinica, 2019, 34, 549-562.	1.2	23
2092	Specific molecular interactions between Vitis vinifera and Botrytis cinerea are required for noble rot development in grape berries. Postharvest Biology and Technology, 2019, 156, 110924.	2.9	22
2093	Diagnostic and prognostic significance of mRNA expressions of apolipoprotein A and C family genes in hepatitis B virus-related hepatocellular carcinoma. Journal of Cellular Biochemistry, 2019, 120, 18246-18265.	1.2	25
2094	Neocarzinil A Is a Potent Inhibitor of Cancer Cell Motility Targeting VAT-1 Controlled Pathways. ACS Central Science, 2019, 5, 1170-1178.	5.3	12
2095	Investigation of Oligodendrocyte Precursor Cell Differentiation by Quantitative Proteomics. Proteomics, 2019, 19, e1900057.	1.3	14

#	ARTICLE	IF	CITATIONS
2096	A Novel Cys2His2 Zinc Finger Homolog of AZF1 Modulates Holocellulase Expression in <i>Trichoderma reesei</i> . <i>MSystems</i> , 2019, 4, .	1.7	32
2097	Genome-wide alternative splicing landscapes modulated by biotrophic sugarcane smut pathogen. <i>Scientific Reports</i> , 2019, 9, 8876.	1.6	24
2098	PUCHI regulates very long chain fatty acid biosynthesis during lateral root and callus formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14325-14330.	3.3	46
2099	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
2100	Distinct leaf transcriptomic response of water deficient <i>Eucalyptus grandis</i> submitted to potassium and sodium fertilization. <i>PLoS ONE</i> , 2019, 14, e0218528.	1.1	13
2101	Combination analysis of the physiology and transcriptome provides insights into the mechanism of silver nanoparticles phytotoxicity. <i>Environmental Pollution</i> , 2019, 252, 1539-1549.	3.7	40
2102	Exploring differentially expressed key genes related to development of follicle by RNA-seq in Peking ducks (<i>Anas Platyrhynchos</i>). <i>PLoS ONE</i> , 2019, 14, e0209061.	1.1	14
2103	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
2104	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
2105	Hippocampal sub-regional differences in the microRNA response to forebrain ischemia. <i>Molecular and Cellular Neurosciences</i> , 2019, 98, 164-178.	1.0	7
2106	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	1.1	20
2107	Estrogen receptor alpha activates MAPK signaling pathway to promote the development of endometrial cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 17593-17601.	1.2	19
2108	Global Proteome and Ubiquitinome Changes in the Soluble and Insoluble Fractions of Q175 Huntington Mice Brains. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1705-1720.	2.5	26
2109	Integrated analysis of competing endogenous RNA network revealing potential prognostic biomarkers of hepatocellular carcinoma. <i>Journal of Cancer</i> , 2019, 10, 3267-3283.	1.2	23
2110	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	4.7	61
2111	Novel transcriptional responses to heat revealed by turning up the heat at night. <i>Plant Molecular Biology</i> , 2019, 101, 1-19.	2.0	36
2112	Identification of cancer-related gene network in hepatocellular carcinoma by combined bioinformatic approach and experimental validation. <i>Pathology Research and Practice</i> , 2019, 215, 152428.	1.0	15
2113	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

#	ARTICLE	IF	CITATIONS
2114	Identification of timeâ€series differentially expressed genes and pathways associated with heart failure postâ€myocardial infarction using integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 5281-5290.	1.1	6
2115	Temporal patterning of apical progenitors and their daughter neurons in the developing neocortex. <i>Science</i> , 2019, 364, .	6.0	275
2116	Immunomodulation with Human Umbilical Cord Blood Stem Cells Ameliorates Ischemic Brain Injury â€“ A Brain Transcriptome Profiling Analysis. <i>Cell Transplantation</i> , 2019, 28, 864-873.	1.2	20
2117	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
2118	Genome and Ontogenetic-Based Transcriptomic Analyses of the Flesh Fly, <i>Sarcophaga bullata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1313-1320.	0.8	11
2119	<p>Identification of novel biomarkers and candidate small molecule drugs in non-small-cell lung cancer by integrated microarray analysis</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3545-3563.	1.0	32
2120	Identification of novel biomarkers and small molecule drugs in human colorectal cancer by microarray and bioinformatics analysis. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00713.	0.6	34
2121	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
2122	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
2123	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
2124	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
2125	Intravenous administration of cardiac progenitor cell-derived exosomes protects against doxorubicin/trastuzumab-induced cardiac toxicity. <i>Cardiovascular Research</i> , 2020, 116, 383-392.	1.8	91
2126	Bioinformatics Analysis of the Core Genes Related to Lupus Nephritis Through a Network and Pathway-Based Approach. <i>DNA and Cell Biology</i> , 2019, 38, 639-650.	0.9	4
2127	GSccluster: network-weighted gene-set clustering analysis. <i>BMC Genomics</i> , 2019, 20, 352.	1.2	12
2128	The promising novel biomarkers and candidate small molecule drugs in lowerâ€grade glioma: Evidence from bioinformatics analysis of highâ€throughput data. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15106-15118.	1.2	22
2129	Gene discovery informatics toolkit defines candidate genes for unexplained infertility and prenatal or infantile mortality. <i>Npj Genomic Medicine</i> , 2019, 4, 8.	1.7	31
2130	Integrative Differential Expression Analysis for Multiple EXperiments (IDEAMEX): A Web Server Tool for Integrated RNA-Seq Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 279.	1.1	60
2131	Genome analyses of the new model protist <i>Euplotes vannus</i> focusing on genome rearrangement and resistance to environmental stressors. <i>Molecular Ecology Resources</i> , 2019, 19, 1292-1308.	2.2	69

#	ARTICLE	IF	CITATIONS
2132	Competing endogenous RNA network of endometrial carcinoma: A comprehensive analysis. Journal of Cellular Biochemistry, 2019, 120, 15648-15660.	1.2	11
2133	A single-cell atlas of mouse brain macrophages reveals unique transcriptional identities shaped by ontogeny and tissue environment. Nature Neuroscience, 2019, 22, 1021-1035.	7.1	603
2134	Specific chromatin changes mark lateral organ founder cells in the Arabidopsis inflorescence meristem. Journal of Experimental Botany, 2019, 70, 3867-3879.	2.4	17
2135	Transcriptional alterations in <i>Caenorhabditis elegans</i> following exposure to an anthelmintic fraction of the plant <i>Picria fel-terrae</i> Lour.. Parasites and Vectors, 2019, 12, 181.	1.0	2
2136	Investigation of pesticide exposure by genotoxicological, biochemical, genetic polymorphic and in silico analysis. Ecotoxicology and Environmental Safety, 2019, 179, 135-142.	2.9	20
2137	The Transcriptomic Toolbox: Resources for Interpreting Large Gene Expression Data within a Precision Medicine Context for Metabolic Disease Atherosclerosis. Journal of Personalized Medicine, 2019, 9, 21.	1.1	6
2138	Integrative analyses of key genes and regulatory elements in fluoride-affected osteosarcoma. Journal of Cellular Biochemistry, 2019, 120, 15397-15409.	1.2	6
2139	Interaction network analysis of YBX1 for identification of therapeutic targets in adenocarcinomas. Journal of Biosciences, 2019, 44, 1.	0.5	3
2140	Current paradigms and new perspectives on fetal hypoxia: implications for fetal brain development in late gestation. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2019, 317, R1-R13.	0.9	17
2141	A systems biology view of wood formation in <i>Eucalyptus grandis</i> trees submitted to different potassium and water regimes. New Phytologist, 2019, 223, 766-782.	3.5	48
2142	Cytoscape: A Tool for Analyzing and Visualizing Network Data. , 2019, , 533-592.		0
2143	micro-RNAs dependent regulation of DNMT and HIF1 α gene expression in thrombotic disorders. Scientific Reports, 2019, 9, 4815.	1.6	6
2144	Salt-sensitive transcriptome of isolated kidney distal tubule cells. Physiological Genomics, 2019, 51, 125-135.	1.0	8
2145	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of Molecular Biology, 2019, 431, 1650-1670.	2.0	41
2146	Therapeutic targeting of macrophages enhances chemotherapy efficacy by unleashing type I interferon response. Nature Cell Biology, 2019, 21, 511-521.	4.6	121
2147	Integrated transcriptome and in vitro analysis revealed anti-proliferative effect of citral in human stomach cancer through apoptosis. Scientific Reports, 2019, 9, 4883.	1.6	12
2148	High density is a property of slow-cycling and treatment-resistant human glioblastoma cells. Experimental Cell Research, 2019, 378, 76-86.	1.2	14
2149	Genome-Wide Profiling of Circular RNAs in the Rapidly Growing Shoots of Moso Bamboo (<i>Phyllostachys edulis</i>). Plant and Cell Physiology, 2019, 60, 1354-1373.	1.5	56

#	ARTICLE	IF	CITATIONS
2150	Interaction of graphene oxide with cell culture medium: Evaluating the fetal bovine serum protein corona formation towards in vitro nanotoxicity assessment and nanobiointeractions. <i>Materials Science and Engineering C</i> , 2019, 100, 363-377.	3.8	52
2151	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
2152	Genome-scale integrated analysis to identify prospective molecular mechanisms and therapeutic targets in isocitrate dehydrogenase 2 R140Q-mutated acute myeloid leukemia. <i>Oncology Reports</i> , 2019, 41, 2876-2888.	1.2	4
2153	Female and male mouse lung group 2 innate lymphoid cells differ in gene expression profiles and cytokine production. <i>PLoS ONE</i> , 2019, 14, e0214286.	1.1	22
2154	Impact of RNA-Protein Interaction Modes on Translation Control: The Versatile Multidomain Protein Gemin5. <i>BioEssays</i> , 2019, 41, e1800241.	1.2	20
2155	Swift metabolite changes and leaf shedding are milestones in the acclimation process of grapevine under prolonged water stress. <i>BMC Plant Biology</i> , 2019, 19, 69.	1.6	30
2156	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	5.8	183
2157	Single-cell transcriptome analysis of <i>Physcomitrella</i> leaf cells during reprogramming using microcapillary manipulation. <i>Nucleic Acids Research</i> , 2019, 47, 4539-4553.	6.5	39
2158	Multimomics analysis profile acute liver injury module clusters to compare the therapeutic efficacy of bifendate and muaddil sapra. <i>Scientific Reports</i> , 2019, 9, 4335.	1.6	7
2159	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
2160	The Spinal Transcriptome after Cortical Stroke: In Search of Molecular Factors Regulating Spontaneous Recovery in the Spinal Cord. <i>Journal of Neuroscience</i> , 2019, 39, 4714-4726.	1.7	26
2161	Detection of protein complexes from multiple protein interaction networks using graph embedding. <i>Artificial Intelligence in Medicine</i> , 2019, 96, 107-115.	3.8	14
2162	Systems Biology Reveals NR2F6 and TGFBI as Key Regulators of Feed Efficiency in Beef Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 230.	1.1	41
2163	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
2164	Membrane Cholesterol Efflux Drives Tumor-Associated Macrophage Reprogramming and Tumor Progression. <i>Cell Metabolism</i> , 2019, 29, 1376-1389.e4.	7.2	261
2165	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
2166	Effective use of mesenchymal stem cells in human skin substitutes generated by tissue engineering. , 2019, 37, 233-249.		31
2167	Transcriptomics of the grape berry shrivel ripening disorder. <i>Plant Molecular Biology</i> , 2019, 100, 285-301.	2.0	19

#	ARTICLE	IF	CITATIONS
2168	Liraglutide alters hepatic metabolism in high-fat fed obese mice: A bioinformatic prediction and functional analysis. <i>Meta Gene</i> , 2019, 20, 100553.	0.3	2
2169	Transcriptomic profile of two developmental stages of the cestode parasite <i>Mesocostoides corti</i> . <i>Molecular and Biochemical Parasitology</i> , 2019, 229, 35-46.	0.5	15
2170	Transcriptomic analysis reveals protein homeostasis breakdown in the coral <i>Acropora millepora</i> during hypo-saline stress. <i>BMC Genomics</i> , 2019, 20, 148.	1.2	33
2171	Excessive backfat of sows at mating promotes oxidative stress and up-regulates mitochondrial-mediated apoptotic pathway in the full-term placenta. <i>Livestock Science</i> , 2019, 222, 71-82.	0.6	5
2172	Evolution and Identification of the WRKY Gene Family in Quinoa (<i>Chenopodium quinoa</i>). <i>Genes</i> , 2019, 10, 131.	1.0	22
2173	Genome-wide analysis and identification of the low potassium stress responsive gene SiMYB3 in foxtail millet (<i>Setaria italica</i> L.). <i>BMC Genomics</i> , 2019, 20, 136.	1.2	15
2174	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
2175	Conserved pathway activation following xenogeneic, heterotypic fusion. <i>FASEB Journal</i> , 2019, 33, 6767-6777.	0.2	1
2176	Cognition-Enhancing Vagus Nerve Stimulation Alters the Epigenetic Landscape. <i>Journal of Neuroscience</i> , 2019, 39, 2407-18.	1.7	27
2177	Identification of Potential Candidate Genes of Oral Cancer in Response to Chronic Infection With <i>Porphyromonas gingivalis</i> Using Bioinformatical Analyses. <i>Frontiers in Oncology</i> , 2019, 9, 91.	1.3	28
2178	Identifying hepatocellular carcinoma-related hub genes by bioinformatics analysis and CYP2C8 is a potential prognostic biomarker. <i>Gene</i> , 2019, 698, 9-18.	1.0	23
2179	Integrated bioinformatics analysis reveals novel key biomarkers and potential candidate small molecule drugs in gastric cancer. <i>Pathology Research and Practice</i> , 2019, 215, 1038-1048.	1.0	16
2180	The promising novel biomarkers and candidate small molecule drugs in kidney renal clear cell carcinoma: Evidence from bioinformatics analysis of high-throughput data. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e607.	0.6	44
2181	Evaluation of cardiovascular system state by urine proteome after manned space flight. <i>Acta Astronautica</i> , 2019, 160, 594-600.	1.7	4
2182	Network-based integrated analysis of omics data reveal novel players of TGF- β 1-induced EMT in human peritoneal mesothelial cells. <i>Scientific Reports</i> , 2019, 9, 1497.	1.6	10
2183	Multifaceted activity of cytokinin in leaf development shapes its size and structure in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 97, 805-824.	2.8	74
2184	Screening and authentication of molecular markers in malignant glioblastoma based on gene expression profiles. <i>Oncology Letters</i> , 2019, 18, 4593-4604.	0.8	11
2185	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

#	ARTICLE	IF	CITATIONS
2186	Transcriptomics analysis of Cabernet Sauvignon™ berry skins from Reno and Bordeaux in the late stages of ripening. <i>Acta Horticulturae</i> , 2019, , 353-360.	0.1	1
2187	Using Optimal F-Measure and Random Resampling in Gene Ontology Enrichment Calculations. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019, 5, .	0.7	3
2188	PECTIN ACETYLESTERASE9 Affects the Transcriptome and Metabolome and Delays Aphid Feeding. <i>Plant Physiology</i> , 2019, 181, 1704-1720.	2.3	27
2189	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	21
2190	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	4.7	250
2191	Diphenyl Ditelluride: Redox-Modulating and Antiproliferative Properties. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-14.	1.9	6
2192	Identification of key biomarkers associated with development and prognosis in patients with ovarian carcinoma: evidence from bioinformatic analysis. <i>Journal of Ovarian Research</i> , 2019, 12, 110.	1.3	23
2193	Integrative analysis of hexaploid wheat roots identifies signature components during iron starvation. <i>Journal of Experimental Botany</i> , 2019, 70, 6141-6161.	2.4	48
2194	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
2195	Bioinformatics analysis of key biomarkers and pathways in KSHV infected endothelial cells. <i>Medicine (United States)</i> , 2019, 98, e16277.	0.4	5
2196	Comparative Genomics Analysis of Ciliates Provides Insights on the Evolutionary History Within Nassophorea Synhymenia Phyllopharyngea Assemblage. <i>Frontiers in Microbiology</i> , 2019, 10, 2819.	1.5	31
2197	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
2198	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. <i>BMC Bioinformatics</i> , 2019, 20, 572.	1.2	7
2199	Microarray Gene Expression Dataset Re-analysis Reveals Variability in Influenza Infection and Vaccination. <i>Frontiers in Immunology</i> , 2019, 10, 2616.	2.2	24
2200	Organ transcriptomes of the lucinid clam <i>Loripes orbiculatus</i> (Poli, 1791) provide insights into their specialised roles in the biology of a chemosymbiotic bivalve. <i>BMC Genomics</i> , 2019, 20, 820.	1.2	13
2201	Metatranscriptomic Analysis of Multiple Environmental Stresses Identifies RAP2.4 Gene Associated with Arabidopsis Immunity to Botrytis cinerea. <i>Scientific Reports</i> , 2019, 9, 17010.	1.6	27
2202	Developmental hypomyelination in Wolfram syndrome: new insights from neuroimaging and gene expression analyses. <i>Orphanet Journal of Rare Diseases</i> , 2019, 14, 279.	1.2	22
2203	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

#	ARTICLE	IF	CITATIONS
2204	Temporal and Spatial Differential Expression of Glutamate Receptor Genes in the Brain of Down Syndrome. , 2019, , .		0
2205	Nuclear factor erythroid 2 â€ related factor 2 and its relationship with cellular response in nickel exposure: a systems biology analysis. BMC Pharmacology & Toxicology, 2019, 20, 78.	1.0	5
2206	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. Nature Communications, 2019, 10, 5731.	5.8	29
2207	GenFam: A web application and database for gene familyâ€based classification and functional enrichment analysis. Plant Direct, 2019, 3, e00191.	0.8	16
2208	Induction of an Alternative mRNA 5â€2 Leader Enhances Translation of the Ciliopathy Gene Inpp5e and Resistance to Oncolytic Virus Infection. Cell Reports, 2019, 29, 4010-4023.e5.	2.9	15
2209	Differential gene expression among three sex types reveals a MALE STERILITY 1 (CpMS1) for sex differentiation in papaya. BMC Plant Biology, 2019, 19, 545.	1.6	12
2210	Arabidopsis <i>UBC</i>13</i> differentially regulates two programmed cell death pathways in responses to pathogen and lowâ€temperature stress. New Phytologist, 2019, 221, 919-934.	3.5	56
2211	miR1432â€<i>Os</i>ACOT</i></i> (Acylâ€CoA thioesterase) module determines grain yield via enhancing grain filling rate in rice. Plant Biotechnology Journal, 2019, 17, 712-723.	4.1	68
2212	Differential secretome profiling of a swine tracheal cell line infected with mycoplasmas of the swine respiratory tract. Journal of Proteomics, 2019, 192, 147-159.	1.2	6
2213	Integrated proteomic analysis of tumor necrosis factor Î± and interleukin 1Î²-induced endothelial inflammation. Journal of Proteomics, 2019, 192, 89-101.	1.2	17
2214	Screening of a neuronal cell model of tau pathology for therapeutic compounds. Neurobiology of Aging, 2019, 76, 24-34.	1.5	12
2215	Proteomics turns functional. Journal of Proteomics, 2019, 198, 36-44.	1.2	74
2216	<i>PERPETUAL FLOWERING2</i> coordinates the vernalization response and perennial flowering in<i> Arabis alpina</i>. Journal of Experimental Botany, 2019, 70, 949-961.	2.4	17
2217	Portrait of blood-derived extracellular vesicles in patients with Parkinsonâ€™s disease. Neurobiology of Disease, 2019, 124, 163-175.	2.1	33
2218	CXCR6 protects from inflammation and fibrosis in NEMOLPC-KO mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 391-402.	1.8	14
2219	Identification of key biomarkers in diabetic nephropathy via bioinformatic analysis. Journal of Cellular Biochemistry, 2019, 120, 8676-8688.	1.2	18
2220	Pleiotropic effects of a cold shock protein homolog PprM on the proteome of Deinococcus radiodurans. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 98-106.	1.1	5
2221	Evaluating the evolution and function of the dynamic Venom Y protein in ectoparasitoid wasps. Insect Molecular Biology, 2019, 28, 499-508.	1.0	5

#	ARTICLE	IF	CITATIONS
2222	Transcriptome-wide effect of DE-ETIOLATED1 (DET1) suppression in embryogenic callus of <i>Carica papaya</i> . <i>Journal of Plant Research</i> , 2019, 132, 181-195.	1.2	6
2223	Evolution of embryonic cis-regulatory landscapes between divergent <i>Phallusia</i> and <i>Ciona</i> ascidians. <i>Developmental Biology</i> , 2019, 448, 71-87.	0.9	29
2224	Overexpression of the KNOX gene <i>Tkn4</i> affects pollen development and confers sensitivity to gibberellin and auxin in tomato. <i>Plant Science</i> , 2019, 281, 61-71.	1.7	12
2225	Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. <i>EBioMedicine</i> , 2019, 40, 471-487.	2.7	38
2226	Dysfunctional Mechanism of Liver Cancer Mediated by Transcription Factor and Non-coding RNA. <i>Current Bioinformatics</i> , 2019, 14, 100-107.	0.7	20
2227	Expression of the GAF Sensor, Carbohydrate-Active Enzymes, Elicitins, and RXLRs Differs Markedly Between Two <i>Phytophthora cactorum</i> Isolates. <i>Phytopathology</i> , 2019, 109, 726-735.	1.1	7
2228	Genome-wide identification, characterization and expression analysis of novel long non-coding RNAs that mediate IBA-induced adventitious root formation in apple rootstocks. <i>Plant Growth Regulation</i> , 2019, 87, 287-302.	1.8	21
2229	A gene expression map of shoot domains reveals regulatory mechanisms. <i>Nature Communications</i> , 2019, 10, 141.	5.8	96
2230	Macrophage Phosphoproteome Analysis Reveals MINCLE-dependent and -independent Mycobacterial Cord Factor Signaling. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 669-685.	2.5	20
2231	The genome-wide transcriptional consequences of the nullisomic-tetrasomic stocks for homoeologous group 7 in bread wheat. <i>BMC Genomics</i> , 2019, 20, 29.	1.2	3
2232	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
2233	Oxidative stress, apoptosis activation and symbiosis disruption in giant clam <i>Tridacna crocea</i> under high temperature. <i>Fish and Shellfish Immunology</i> , 2019, 84, 451-457.	1.6	40
2234	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
2235	Ectopic expression of <i>ARGOS8</i> reveals a role for ethylene in root lodging resistance in maize. <i>Plant Journal</i> , 2019, 97, 378-390.	2.8	35
2236	T cell dysfunction in chronic hepatitis B infection and liver cancer: evidence from transcriptome analysis. <i>Journal of Medical Genetics</i> , 2019, 56, 22-28.	1.5	12
2237	Proteomic Landscape of Cholangiocarcinomas Reveals Three Different Subgroups According to Their Localization and the Aspect of Non-Tumor Liver. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800128.	0.8	11
2238	Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	41
2239	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

#	ARTICLE	IF	CITATIONS
2240	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
2241	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
2242	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
2243	Simultaneous Transcriptome Analysis of Host and Pathogen Highlights the Interaction Between <i>Brassica oleracea</i> and <i>Sclerotinia sclerotiorum</i> . <i>Phytopathology</i> , 2019, 109, 542-550.	1.1	26
2244	<sc>EFFECTOR OF TRANSCRIPTION</sc> factors are novel plant-specific regulators associated with genomic <sc>DNA</sc> methylation in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2019, 221, 261-278.	3.5	20
2245	Antiviral compound screening, peptide designing, and protein network construction of influenza A virus (strain A/Puerto Rico/8/1934 H1N1). <i>Drug Development Research</i> , 2019, 80, 106-124.	1.4	6
2246	Potentially critical roles of TNPO1, RAP1B, ZDHHC17, and PPM1B in the progression of coronary atherosclerosis through microarray data analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 4301-4311.	1.2	22
2247	Discovering cooperative biomarkers for heterogeneous complex disease diagnoses. <i>Briefings in Bioinformatics</i> , 2019, 20, 89-101.	3.2	12
2248	Up-regulation of fibroblast growth factor receptor 1 due to prenatal tobacco exposure can lead to developmental defects in new born. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2020, 33, 1732-1743.	0.7	4
2249	When Correlation Filters Meet Siamese Networks for Real-Time Complementary Tracking. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2020, 30, 509-519.	5.6	26
2250	MicroRNA-301a promotes pancreatic cancer invasion and metastasis through the JAK/STAT3 signaling pathway by targeting SOCS5. <i>Carcinogenesis</i> , 2020, 41, 502-514.	1.3	46
2251	Gene set analysis methods for the functional interpretation of non-mRNA data—Genomic range and ncRNA data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1495-1508.	3.2	9
2252	Identification of distinctive long noncoding RNA competitive interactions and a six-methylated gene prognostic signature in acute myeloid leukemia with $\Delta 5/\text{del}(5q)$ or $\Delta 7/\text{del}(7q)$. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 1563-1574.	1.2	5
2253	Novel LRAP-binding partner revealing the plasminogen activation system as a regulator of cementoblast differentiation and mineral nodule formation in vitro. <i>Journal of Cellular Physiology</i> , 2020, 235, 4545-4558.	2.0	6
2254	Current Trends in Biomedical Engineering and Bioimages Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2020, , .	0.5	1
2255	Effects of temperature on the transcriptomes of pituitary and liver in Golden Pompano <i>Trachinotus blochii</i> . <i>Fish Physiology and Biochemistry</i> , 2020, 46, 63-73.	0.9	4
2256	Human chromatin remodeler cofactor, RNA interactor, eraser and writer sperm RNAs responding to obesity. <i>Epigenetics</i> , 2020, 15, 32-46.	1.3	15
2257	A Symbiotic Virus Facilitates Aphid Adaptation to Host Plants by Suppressing Jasmonic Acid Responses. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 55-65.	1.4	20

#	ARTICLE	IF	CITATIONS
2258	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. <i>Genomics</i> , 2020, 112, 820-830.	1.3	15
2259	Comparative transcriptome analysis of rhizome nodes and internodes in <i>Panax japonicus</i> var. major reveals candidate genes involved in the biosynthesis of triterpenoid saponins. <i>Genomics</i> , 2020, 112, 1112-1119.	1.3	7
2260	Transcriptomic analysis to affirm the regulatory role of long non-coding RNA in horn cancer of Indian zebu cattle breed Kankrej (<i>Bos indicus</i>). <i>Functional and Integrative Genomics</i> , 2020, 20, 75-87.	1.4	5
2261	Non-coding RNA regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194417.	0.9	262
2262	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
2263	Brain transcriptome profile after CRISPR-induced ghrelin mutations in zebrafish. <i>Fish Physiology and Biochemistry</i> , 2020, 46, 1-21.	0.9	5
2264	Integrated proteomic and metabolomic profiling the global response of rat glioma model by temozolomide treatment. <i>Journal of Proteomics</i> , 2020, 211, 103578.	1.2	11
2265	Mining TCGA database for screening and identification of hub genes in kidney renal clear cell carcinoma microenvironment. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3952-3960.	1.2	22
2266	Immune/Neural approach to characterize salivary gland neoplasms (SGN). <i>Applied Soft Computing Journal</i> , 2020, 88, 105877.	4.1	4
2267	Arabidopsis ZINC FINGER PROTEIN1 Acts Downstream of GL2 to Repress Root Hair Initiation and Elongation by Directly Suppressing bHLH Genes. <i>Plant Cell</i> , 2020, 32, 206-225.	3.1	67
2268	Transcriptome analysis defines myocardium gene signatures in children with ToF and ASD and reveals disease-specific molecular reprogramming in response to surgery with cardiopulmonary bypass. <i>Journal of Translational Medicine</i> , 2020, 18, 21.	1.8	11
2269	A Drug Repurposing and Protein-Protein Interaction Network Study of Ribosomopathies Using Yeast as a Model System. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 96-109.	1.0	4
2270	The complex response of free and bound amino acids to water stress during the seed setting stage in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 102, 838-855.	2.8	9
2271	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
2272	The diagnosis and prognosis values of WNT mRNA expression in colon adenocarcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3145-3161.	1.2	18
2273	Phosphoproteomic analysis reveals Akt isoform-specific regulation of cytoskeleton proteins in human temporal lobe epilepsy with hippocampal sclerosis. <i>Neurochemistry International</i> , 2020, 134, 104654.	1.9	7
2274	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
2275	Single-cell transcriptome sequencing of rumen ciliates provides insight into their molecular adaptations to the anaerobic and carbohydrate-rich rumen microenvironment. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106687.	1.2	14

#	ARTICLE	IF	CITATIONS
2276	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
2277	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
2278	Integrative network analysis identifies differential regulation of neuroimmune system in Schizophrenia and Bipolar disorder. <i>Brain, Behavior, & Immunity - Health</i> , 2020, 2, 100023.	1.3	9
2279	Transcriptional and biochemical analyses of gibberellin expression and content in germinated barley grain. <i>Journal of Experimental Botany</i> , 2020, 71, 1870-1884.	2.4	17
2280	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
2281	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
2282	PEATmoss (<i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	2.8	74
2283	Bioinformatics analysis reveals 6 key biomarkers associated with non-small-cell lung cancer. <i>Journal of International Medical Research</i> , 2020, 48, 030006051988763.	0.4	6
2284	Microplastic exposure represses the growth of endosymbiotic dinoflagellate <i>Cladocopium goreaui</i> in culture through affecting its apoptosis and metabolism. <i>Chemosphere</i> , 2020, 244, 125485.	4.2	73
2285	TCF19 Promotes Cell Proliferation through Binding to the Histone H3K4me3 Mark. <i>Biochemistry</i> , 2020, 59, 389-399.	1.2	20
2286	Functional Translatome Proteomics Reveal Converging and Dose-Dependent Regulation by mTORC1 and eIF2 β . <i>Molecular Cell</i> , 2020, 77, 913-925.e4.	4.5	81
2287	Comprehensive transcriptome analysis of faba bean in response to vernalization. <i>Planta</i> , 2020, 251, 22.	1.6	10
2288	Exploring the long noncoding RNAs-based biomarkers and pathogenesis of malignant transformation from dysplasia to oral squamous cell carcinoma by bioinformatics method. <i>European Journal of Cancer Prevention</i> , 2020, 29, 174-181.	0.6	9
2289	Molecular Signature of Subtypes of Non-Small-Cell Lung Cancer by Large-Scale Transcriptional Profiling: Identification of Key Modules and Genes by Weighted Gene Co-Expression Network Analysis (WGCNA). <i>Cancers</i> , 2020, 12, 37.	1.7	179
2290	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
2291	Coding transcriptome analyses reveal altered functions underlying immunotolerance of PEG-fused rat sciatic nerve allografts. <i>Journal of Neuroinflammation</i> , 2020, 17, 287.	3.1	2
2292	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
2293	Functional Transcription Factor Target Networks Illuminate Control of Epithelial Remodelling. <i>Cancers</i> , 2020, 12, 2823.	1.7	5

#	ARTICLE	IF	CITATIONS
2294	Ancestral gene duplications in mosses characterized by integrated phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2022, 60, 144-159.	1.6	19
2295	<p></p>The Perspective of Diagnostic and Prognostic Values of Lipoxygenases mRNA Expression in Colon Adenocarcinoma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 9389-9405.	1.0	11
2296	<p></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
2297	Analysis of autotrophic, mixotrophic and heterotrophic phenotypes in the microalgae <i>Chlorella vulgaris</i> using time-resolved proteomics and transcriptomics approaches. <i>Algal Research</i> , 2020, 51, 102060.	2.4	44
2298	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
2299	Transcriptomic Changes in Young Japanese Males After Exposure to Acute Hypobaric Hypoxia. <i>Frontiers in Genetics</i> , 2020, 11, 559074.	1.1	8
2300	EAT-UpTF: Enrichment Analysis Tool for Upstream Transcription Factors of a Group of Plant Genes. <i>Frontiers in Genetics</i> , 2020, 11, 566569.	1.1	5
2301	Comparative Study of Pine Reference Genomes Reveals Transposable Element Interconnected Gene Networks. <i>Genes</i> , 2020, 11, 1216.	1.0	11
2302	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
2303	DNA methylation microarrays identify epigenetically regulated lipid related genes in obese patients with hypercholesterolemia. <i>Molecular Medicine</i> , 2020, 26, 93.	1.9	12
2304	Cilia interactome with predicted proteinâ€“protein interactions reveals connections to Alzheimerâ€™s disease, aging and other neuropsychiatric processes. <i>Scientific Reports</i> , 2020, 10, 15629.	1.6	34
2305	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
2306	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
2307	<i>TYROBP</i> is a potential prognostic biomarker of clear cell renal cell carcinoma. <i>FEBS Open Bio</i> , 2020, 10, 2588-2604.	1.0	16
2308	Pancreatic Tissue Proteomics Unveils Key Proteins, Pathways, and Networks Associated with Type 1 Diabetes. <i>Proteomics - Clinical Applications</i> , 2020, 14, e2000053.	0.8	8
2309	PAFway: pairwise associations between functional annotations in biological networks and pathways. <i>Bioinformatics</i> , 2020, 36, 4963-4964.	1.8	2
2310	Annexin A2 depletion exacerbates the intracerebral microhemorrhage induced by acute rickettsia and Ebola virus infections. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007960.	1.3	9
2311	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

#	ARTICLE	IF	CITATIONS
2312	Genome-wide association of volatiles reveals candidate loci for blueberry flavor. <i>New Phytologist</i> , 2020, 226, 1725-1737.	3.5	84
2313	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	2.8	32
2314	Characterization of ASR gene and its role in drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2020, 15, e0234550.	1.1	18
2315	Comparative transcriptome and metabolomic profiling reveal the complex mechanisms underlying the developmental dynamics of tobacco leaves. <i>Genomics</i> , 2020, 112, 4009-4022.	1.3	15
2316	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
2317	Identification and Functional Annotation of Genes Related to Horses' Performance: From GWAS to Post-GWAS. <i>Animals</i> , 2020, 10, 1173.	1.0	9
2318	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
2319	Transcriptome-wide shift from photosynthesis and energy metabolism upon endogenous fluid protein depletion in young <i>Nepenthes ampullaria</i> pitchers. <i>Scientific Reports</i> , 2020, 10, 6575.	1.6	8
2320	Transcriptome analysis reveals key information on improving duck yolk lipid contents induced by dietary fish oil or flaxseed oil. <i>Journal of Applied Animal Research</i> , 2020, 48, 192-200.	0.4	0
2321	Tracing the footsteps of autophagy in computational biology. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
2322	Crosstalk between microglia and patient-derived glioblastoma cells inhibit invasion in a three-dimensional gelatin hydrogel model. <i>Journal of Neuroinflammation</i> , 2020, 17, 346.	3.1	21
2323	YODA Kinase Controls a Novel Immune Pathway of Tomato Conferring Enhanced Disease Resistance to the Bacterium <i>Pseudomonas syringae</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 584471.	1.7	9
2324	De novo RNA-Seq analysis in sensitive rice cultivar and comparative transcript profiling in contrasting genotypes reveal genetic biomarkers for fluoride-stress response. <i>Environmental Pollution</i> , 2020, 267, 115378.	3.7	8
2325	Precision medicine insight into primary prostate tumor through transcriptomic data and an integrated systems biology approach. <i>Meta Gene</i> , 2020, 26, 100787.	0.3	0
2326	A genome-wide association study for clinical mastitis in the dual-purpose German Black Pied cattle breed. <i>Journal of Dairy Science</i> , 2020, 103, 10289-10298.	1.4	14
2327	Flux variability analysis reveals a tragedy of commons in cancer cells. <i>SN Applied Sciences</i> , 2020, 2, 1.	1.5	2
2328	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
2329	Transcriptome Profiling Provides Insights Into Potential Antagonistic Mechanisms Involved in <i>Chaetomium globosum</i> Against <i>Bipolaris sorokiniana</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 578115.	1.5	19

#	ARTICLE	IF	CITATIONS
2330	Systematic expression analysis of EAF family reveals the importance of EAF2 in melanoma. <i>International Immunopharmacology</i> , 2020, 88, 106958.	1.7	2
2331	Genome-Wide Dynamic Evaluation of the UV-Induced DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2981-2988.	0.8	1
2332	GMP-compliant sponge-like dressing containing MSC lyo-secretome: Proteomic network of healing in a murine wound model. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2020, 155, 37-48.	2.0	34
2333	Identification of latent core genes and pathways associated with myelodysplastic syndromes based on integrated bioinformatics analysis. <i>Hematology</i> , 2020, 25, 299-308.	0.7	5
2334	Identification of Players Controlling Meristem Arrest Downstream of the FRUITFULL-APETALA2 Pathway. <i>Plant Physiology</i> , 2020, 184, 945-959.	2.3	16
2335	Physiological and transcriptomic analyses of brassinosteroid function in moso bamboo (<i>Phyllostachys edulis</i>) seedlings. <i>Planta</i> , 2020, 252, 27.	1.6	9
2336	Identifying the novel key genes in renal cell carcinoma by bioinformatics analysis and cell experiments. <i>Cancer Cell International</i> , 2020, 20, 331.	1.8	11
2337	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
2338	Integrated Bioinformatics Analysis Reveals Key Candidate Genes and Pathways Associated With Clinical Outcome in Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 814.	1.1	11
2339	Reckoning the Dearth of Bioinformatics in the Arena of Diabetic Nephropathy (DN)â€”Need to Improve. <i>Processes</i> , 2020, 8, 808.	1.3	4
2340	Profiling of circular RNA N ⁶ -methyladenosine in moso bamboo (<i>Phyllostachys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 1823-1838.	4.1	35
2341	Molecular memory of Flavescence dorée phytoplasma in recovering grapevines. <i>Horticulture Research</i> , 2020, 7, 126.	2.9	17
2342	Plant-specific Dof transcription factors VASCULAR-RELATED DOF1 and VASCULAR-RELATED DOF2 regulate vascular cell differentiation and lignin biosynthesis in Arabidopsis. <i>Plant Molecular Biology</i> , 2020, 104, 263-281.	2.0	14
2343	Identification of potential prognostic small nucleolar RNA biomarkers for predicting overall survival in patients with sarcoma. <i>Cancer Medicine</i> , 2020, 9, 7018-7033.	1.3	11
2344	Quantitative Proteomics Links the LRRC59 Interactome to mRNA Translation on the ER Membrane. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1826-1849.	2.5	15
2345	Chromatin-Level Differences Elucidate Potential Determinants of Contrasting Levels of Cold Sensitivity in Maize Lines. <i>Plant Molecular Biology Reporter</i> , 2021, 39, 335-350.	1.0	7
2346	System biological investigations of hydroxychloroquine and azithromycin targets and their implications in QT interval prolongation. <i>Chemico-Biological Interactions</i> , 2020, 332, 109299.	1.7	3
2347	Association between oxidative-stress-related markers and calcified femoral artery in type 2 diabetes patients. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 190, 113535.	1.4	7

#	ARTICLE	IF	CITATIONS
2348	Dynamics of protein synthesis in the initial steps of strobilation in the model cestode parasite <i>Mesosestoides corti</i> (syn. <i>vogae</i>). <i>Journal of Proteomics</i> , 2020, 228, 103939.	1.2	2
2349	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
2350	Evaluation of Cytotoxicity and α -Glucosidase Inhibitory Activity of Amide and Polyamino-Derivatives of Lupane Triterpenoids. <i>Molecules</i> , 2020, 25, 4833.	1.7	25
2351	Identification of epigenetic variation associated with synchronous pod maturity in mungbean (<i>Vigna</i>) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	2
2352	Dynamic transcriptional response of <i>Saccharomyces cerevisiae</i> cells to copper. <i>Scientific Reports</i> , 2020, 10, 18487.	1.6	8
2353	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
2354	Strict and Flexible Rule-Based Graph Repairing. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, , 1-1.	4.0	6
2355	Secretome Proteomic Approaches for Biomarker Discovery: An Update on Colorectal Cancer. <i>Medicina (Lithuania)</i> , 2020, 56, 443.	0.8	7
2356	Maleic hydrazide elicits global transcriptomic changes in chemically topped tobacco to influence shoot bud development. <i>Planta</i> , 2020, 252, 64.	1.6	3
2357	SUPER STARCHY1/ONAC025 participates in rice grain filling. <i>Plant Direct</i> , 2020, 4, e00249.	0.8	11
2358	Identification of hub genes and its correlation with the prognosis of acute myeloid leukemia based on high-throughput data analysis. <i>Precision Radiation Oncology</i> , 2020, 4, 49-56.	0.4	4
2359	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
2360	Multiplexed Proximity Biotinylation Coupled to Mass Spectrometry for Defining Integrin Adhesion Complexes. <i>Current Protocols in Cell Biology</i> , 2020, 88, e113.	2.3	4
2361	Identification of differentially expressed genes between mucinous adenocarcinoma and other adenocarcinoma of colorectal cancer using bioinformatics analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052094903.	0.4	5
2362	Systems Analysis of Biliary Atresia Through Integration of High-Throughput Biological Data. <i>Frontiers in Physiology</i> , 2020, 11, 966.	1.3	3
2363	Plant Immune System Activation Upon Citrus Leprosis Virus C Infection Is Mimicked by the Ectopic Expression of the P61 Viral Protein. <i>Frontiers in Plant Science</i> , 2020, 11, 1188.	1.7	15
2364	Genome-wide RNA-sequencing dataset reveals the prognostic value and potential molecular mechanisms of lncRNA in non-homologous end joining pathway 1 in early stage Pancreatic Ductal Adenocarcinoma. <i>Journal of Cancer</i> , 2020, 11, 5556-5567.	1.2	4
2365	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

#	ARTICLE	IF	CITATIONS
2366	The Molecular Priming of Defense Responses is Differently Regulated in Grapevine Genotypes Following Elicitor Application against Powdery Mildew. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6776.	1.8	15
2367	Bioinformatics analysis reveals novel hub gene pathways associated with IgA nephropathy. <i>European Journal of Medical Research</i> , 2020, 25, 40.	0.9	4
2368	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
2369	Adaptation by copy number variation increases insecticide resistance in the fall armyworm. <i>Communications Biology</i> , 2020, 3, 664.	2.0	41
2370	Using Alias Sampling Strategy Based on Network Embeddings to Detect Protein Complexes. <i>IEEE Access</i> , 2020, 8, 211773-211783.	2.6	0
2371	Screening of Key Proteins for Strontium Adsorption by Living Irradiated <i>Saccharomyces cerevisiae</i> Using Proteomics and Metalloproteomics Analysis. <i>Environmental Engineering Science</i> , 2020, 37, 803-814.	0.8	2
2372	Analysis of Hub Genes Involved in Distinction Between Aged and Fetal Bone Marrow Mesenchymal Stem Cells by Robust Rank Aggregation and Multiple Functional Annotation Methods. <i>Frontiers in Genetics</i> , 2020, 11, 573877.	1.1	6
2373	Prediction and analysis of human herpes simplex virus type 1 protein-protein interactions by integrating multiple methods. <i>Quantitative Biology</i> , 2020, 8, 312-324.	0.3	11
2374	Prognostic value of Glypican family genes in early-stage pancreatic ductal adenocarcinoma after pancreaticoduodenectomy and possible mechanisms. <i>BMC Gastroenterology</i> , 2020, 20, 415.	0.8	9
2375	Identification and Characterization of Serum microRNAs as Biomarkers for Human Disc Degeneration: An RNA Sequencing Analysis. <i>Diagnostics</i> , 2020, 10, 1063.	1.3	5
2376	TMEA: A Thermodynamically Motivated Framework for Functional Characterization of Biological Responses to System Acclimation. <i>Entropy</i> , 2020, 22, 1030.	1.1	5
2377	Role of AT1G72910, AT1G72940, and ADR1-LIKE 2 in Plant Immunity under Nonsense-Mediated mRNA Decay-Compromised Conditions at Low Temperatures. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7986.	1.8	8
2378	Comparative Transcriptome Analysis of Two Root-Feeding Grape Phylloxera (<i>D. vitifoliae</i>) Lineages Feeding on a Rootstock and <i>V. vinifera</i> . <i>Insects</i> , 2020, 11, 691.	1.0	5
2379	Extreme drought alters progeny dispersal unit properties of winter wild oat (<i>Avena sterilis</i> L.). <i>Planta</i> , 2020, 252, 77.	1.6	6
2380	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
2381	Dynamic Expression of Long Non-Coding RNAs Throughout Parasite Sexual and Neural Maturation in <i>Schistosoma japonicum</i> . <i>Non-coding RNA</i> , 2020, 6, 15.	1.3	7
2382	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
2383	Metabolomics and Multi-Omics Integration: A Survey of Computational Methods and Resources. <i>Metabolites</i> , 2020, 10, 202.	1.3	69

#	ARTICLE	IF	CITATIONS
2384	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
2385	Proteomic analysis of underlying apoptosis mechanisms of human retinal pigment epithelial ARPE-19 cells in response to mechanical stretch. <i>Journal of Cellular Physiology</i> , 2020, 235, 7604-7619.	2.0	5
2386	Transcriptomic Analysis of Pulmonary Microvascular Endothelial Cells with IQGAP1 Knockdown. <i>DNA and Cell Biology</i> , 2020, 39, 1127-1140.	0.9	6
2387	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
2388	Identification and Comparative Analysis of Long Non-Coding RNA in the Skeletal Muscle of Two Dezhou Donkey Strains. <i>Genes</i> , 2020, 11, 508.	1.0	18
2389	Comparative Analysis of Root Transcriptome Reveals Candidate Genes and Expression Divergence of Homoeologous Genes in Response to Water Stress in Wheat. <i>Plants</i> , 2020, 9, 596.	1.6	11
2390	Functional Divergence of the Arabidopsis Florigen-Interacting bZIP Transcription Factors FD and FDP. <i>Cell Reports</i> , 2020, 31, 107717.	2.9	49
2391	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
2392	Tissue-specific angiogenic and invasive properties of human neonatal thymus and bone MSCs: Role of SLIT3-ROBO1. <i>Stem Cells Translational Medicine</i> , 2020, 9, 1102-1113.	1.6	5
2393	Ocean acidification inhibits initial shell formation of oyster larvae by suppressing the biosynthesis of serotonin and dopamine. <i>Science of the Total Environment</i> , 2020, 735, 139469.	3.9	24
2394	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1281-1302.	2.5	53
2395	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
2396	Global responses to oxytetracycline treatment in tetracycline-resistant <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2020, 10, 8438.	1.6	7
2397	Loss of the Acetyltransferase NAA50 Induces Endoplasmic Reticulum Stress and Immune Responses and Suppresses Growth. <i>Plant Physiology</i> , 2020, 183, 1838-1854.	2.3	16
2398	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
2399	Temperature Dramatically Shapes Mosquito Gene Expression With Consequences for Mosquito-Zika Virus Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 901.	1.5	30
2400	Multidimensional gene regulatory landscape of a bacterial pathogen in plants. <i>Nature Plants</i> , 2020, 6, 883-896.	4.7	54
2401	Identification of genes and miRNA associated with idiopathic recurrent pregnancy loss: an exploratory data mining study. <i>BMC Medical Genomics</i> , 2020, 13, 75.	0.7	20

#	ARTICLE	IF	CITATIONS
2402	Differential gene expression of <i>Plasmodium homocircumflexum</i> (lineage pCOLL4) across two experimentally infected passerine bird species. <i>Genomics</i> , 2020, 112, 2857-2865.	1.3	14
2403	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
2404	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
2405	Integrated Analysis of a Gene Correlation Network Identifies Critical Regulation of Fibrosis by lncRNAs and TFs in Idiopathic Pulmonary Fibrosis. <i>BioMed Research International</i> , 2020, 2020, 1-14.	0.9	12
2406	Low-Phosphate Chromatin Dynamics Predict a Cell Wall Remodeling Network in Rice Shoots. <i>Plant Physiology</i> , 2020, 182, 1494-1509.	2.3	14
2407	Coordinating light responses between the nucleus and the chloroplast, a role for plant cryptochromes and phytochromes. <i>Physiologia Plantarum</i> , 2020, 169, 515-528.	2.6	16
2408	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
2409	Anti-infective nitazoxanide disrupts transcription of ribosome biogenesis-related genes in yeast. <i>Genes and Genomics</i> , 2020, 42, 915-926.	0.5	6
2410	Identification and profiling of microRNAs and differentially expressed genes during anther development between a genetic male-sterile mutant and its wildtype cotton via high-throughput RNA sequencing. <i>Molecular Genetics and Genomics</i> , 2020, 295, 645-660.	1.0	8
2411	CD163 expression defines specific, IRF8-dependent, immune-modulatory macrophages in the bone marrow. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1137-1151.	1.5	27
2412	Cardiopoietic stem cell therapy restores infarction-altered cardiac proteome. <i>Npj Regenerative Medicine</i> , 2020, 5, 5.	2.5	21
2413	Distinct epigenomic and transcriptomic modifications associated with <i>Wolbachia</i> -mediated asexuality. <i>PLoS Pathogens</i> , 2020, 16, e1008397.	2.1	18
2414	Distinctive Gene Expression Patterns Define Endodormancy to Ecodormancy Transition in Apricot and Peach. <i>Frontiers in Plant Science</i> , 2020, 11, 180.	1.7	37
2415	<i>Moniliophthora perniciosa</i> development: key genes involved in stress-mediated cell wall organization and autophagy. <i>International Journal of Biological Macromolecules</i> , 2020, 154, 1022-1035.	3.6	8
2416	Tumor endothelial cell up-regulation of IDO1 is an immunosuppressive feed-back mechanism that reduces the response to CD40-stimulating immunotherapy. <i>Oncolimmunology</i> , 2020, 9, 1730538.	2.1	23
2417	Functional analysis of the methyltransferase SMYD in the single-cell model organism <i>Tetrahymena thermophila</i> . <i>Marine Life Science and Technology</i> , 2020, 2, 109-122.	1.8	22
2418	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoe fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11
2419	The sexual cell cycle initiation is regulated by CDK19/CYC9 in <i>Tetrahymena thermophila</i> . <i>Journal of Cell Science</i> , 2020, 133, .	1.2	12

#	ARTICLE	IF	CITATIONS
2420	Associations between maternal body mass index and diet composition with placental DNA methylation at term. <i>Placenta</i> , 2020, 93, 74-82.	0.7	13
2421	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
2422	AT-Hook Transcription Factors Restrict Petiole Growth by Antagonizing PIFs. <i>Current Biology</i> , 2020, 30, 1454-1466.e6.	1.8	39
2423	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
2424	Specific expression and alternative splicing of mouse genes during spermatogenesis. <i>Molecular Omics</i> , 2020, 16, 258-267.	1.4	6
2425	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
2426	SSIF: Subsumption-based Sub-term Inference Framework to audit Gene Ontology. <i>Bioinformatics</i> , 2020, 36, 3207-3214.	1.8	7
2427	Proteomic identification and expression of oral apparatus constituents in cell regeneration of giant ciliate <i>Stentor coeruleus</i> (strain WHEL). <i>Gene</i> , 2020, 743, 144624.	1.0	7
2428	Potential therapeutic targets of the nuclear division cycle 80 (NDC80) complexes genes in lung adenocarcinoma. <i>Journal of Cancer</i> , 2020, 11, 2921-2934.	1.2	16
2429	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	4.7	225
2430	New genome assemblies reveal patterns of domestication and adaptation across <i>Brettanomyces</i> (Dekkera) species. <i>BMC Genomics</i> , 2020, 21, 194.	1.2	21
2431	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
2432	Small RNA technology for plant abiotic stress tolerance. , 2020, , 521-541.		2
2433	A temporal gene expression map of <i>Chrysanthemum</i> leaves infected with <i>Alternaria alternata</i> reveals different stages of defense mechanisms. <i>Horticulture Research</i> , 2020, 7, 23.	2.9	23
2434	<i>Pseudophoenix ekmanii</i> (Arecaceae) seeds at suboptimal temperature show reduced imbibition rates and enhanced expression of genes related to germination inhibition. <i>Plant Biology</i> , 2020, 22, 1041-1051.	1.8	4
2435	Shedding light on cashmere goat hair follicle biology: from morphology analyses to transcriptomic landscape. <i>BMC Genomics</i> , 2020, 21, 458.	1.2	8
2436	Identification and Verification of Biomarker in Clear Cell Renal Cell Carcinoma via Bioinformatics and Neural Network Model. <i>BioMed Research International</i> , 2020, 2020, 1-24.	0.9	6
2437	MMiRNA-Viewer2, a bioinformatics tool for visualizing functional annotation for MiRNA and MRNA pairs in a network. <i>BMC Bioinformatics</i> , 2020, 21, 247.	1.2	2

#	ARTICLE	IF	CITATIONS
2438	Proteomics of SARS-CoV-2-infected host cells reveals therapy targets. <i>Nature</i> , 2020, 583, 469-472.	13.7	841
2439	Bioinformatics analysis of high-throughput data to validate potential novel biomarkers and small molecule drugs for glioblastoma multiforme. <i>Journal of International Medical Research</i> , 2020, 48, 030006052092454.	0.4	2
2440	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
2441	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
2442	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
2443	Host Transcriptional Responses to High- and Low-Virulent Avian Malaria Parasites. <i>American Naturalist</i> , 2020, 195, 1070-1084.	1.0	19
2444	Mapping of quantitative trait loci for traits linked to fusarium head blight in barley. <i>PLoS ONE</i> , 2020, 15, e0222375.	1.1	15
2445	Toxicological response of the model fungus <i>Saccharomyces cerevisiae</i> to different concentrations of commercial graphene nanoplatelets. <i>Scientific Reports</i> , 2020, 10, 3232.	1.6	11
2446	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
2447	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
2448	Integrative Multi-omics Analyses of Barley Rootzones under Salinity Stress Reveal Two Distinctive Salt Tolerance Mechanisms. <i>Plant Communications</i> , 2020, 1, 100031.	3.6	26
2449	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
2450	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
2451	Oral gallic acid improve liver steatosis and metabolism modulating hepatic lipogenic markers in obese mice. <i>Experimental Gerontology</i> , 2020, 134, 110881.	1.2	35
2452	Physicochemical characterization of <i>Pseudomonas stutzeri</i> UFV5 and analysis of its transcriptome under heterotrophic nitrification/aerobic denitrification pathway induction condition. <i>Scientific Reports</i> , 2020, 10, 2215.	1.6	17
2453	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
2454	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
2455	Comparative analysis of the P-type ATPase gene family in seven Rosaceae species and an expression analysis in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genomics</i> , 2020, 112, 2550-2563.	1.3	14

#	ARTICLE	IF	CITATIONS
2456	Recent trends and advances in identification and functional characterization of plant miRNAs. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	22
2457	Transcriptome meta-analysis reveals differences of immune profile between eutopic endometrium from stage I-II and III-IV endometriosis independently of hormonal milieu. <i>Scientific Reports</i> , 2020, 10, 313.	1.6	54
2458	Placenta-Specific Genes, Their Regulation During Villous Trophoblast Differentiation and Dysregulation in Preterm Preeclampsia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 628.	1.8	30
2459	Histidine kinase MHZ1/OsHK1 interacts with ethylene receptors to regulate root growth in rice. <i>Nature Communications</i> , 2020, 11, 518.	5.8	37
2460	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. <i>Cells</i> , 2020, 9, 153.	1.8	19
2461	Integrative Transcriptomic and Proteomic Analyses of Molecular Mechanism Responding to Salt Stress during Seed Germination in Hulless Barley. <i>International Journal of Molecular Sciences</i> , 2020, 21, 359.	1.8	37
2462	Identify potential clinical significance of long noncoding RNA forkhead box P4 antisense RNA 1 in patients with early stage pancreatic ductal adenocarcinoma. <i>Cancer Medicine</i> , 2020, 9, 2062-2076.	1.3	12
2463	Key genes with prognostic values in suppression of osteosarcoma metastasis using comprehensive analysis. <i>BMC Cancer</i> , 2020, 20, 65.	1.1	19
2464	Comprehensive investigation of p53, p21, nm23, and VEGF expression in hepatitis B virus-related hepatocellular carcinoma overall survival after hepatectomy. <i>Journal of Cancer</i> , 2020, 11, 906-918.	1.2	4
2465	Open Data for Differential Network Analysis in Glioma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 547.	1.8	9
2466	Mechanism of adrenergic CaV1.2 stimulation revealed by proximity proteomics. <i>Nature</i> , 2020, 577, 695-700.	13.7	163
2467	Symbiont population control by host-symbiont metabolic interaction in Symbiodiniaceae-cnidarian associations. <i>Nature Communications</i> , 2020, 11, 108.	5.8	87
2468	Misconnecting the dots: altered mitochondrial protein-protein interactions and their role in neurodegenerative disorders. <i>Expert Review of Proteomics</i> , 2020, 17, 119-136.	1.3	6
2469	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
2470	A Guide to Conquer the Biological Network Era Using Graph Theory. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 34.	2.0	149
2471	Mechanism of tanshinones and phenolic acids from Danshen in the treatment of coronary heart disease based on co-expression network. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 28.	1.2	10
2472	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
2473	Identification of Hub Genes Related to Carcinogenesis and Prognosis in Colorectal Cancer Based on Integrated Bioinformatics. <i>Mediators of Inflammation</i> , 2020, 2020, 1-14.	1.4	30

#	ARTICLE	IF	CITATIONS
2474	Key genes of renal tubular necrosis: a bioinformatics analysis. Translational Andrology and Urology, 2020, 9, 654-664.	0.6	3
2475	Screening and Identification of Differentially Expressed Genes Expressed among Left and Right Colon Adenocarcinoma. BioMed Research International, 2020, 2020, 1-16.	0.9	4
2476	FBXW7 Triggers Degradation of KMT2D to Favor Growth of Diffuse Large B-cell Lymphoma Cells. Cancer Research, 2020, 80, 2498-2511.	0.4	19
2477	GOMCL: a toolkit to cluster, evaluate, and extract non-redundant associations of Gene Ontology-based functions. BMC Bioinformatics, 2020, 21, 139.	1.2	37
2478	SUPPRESSOR OF GAMMA RESPONSE 1 acts as a regulator coordinating crosstalk between DNA damage response and immune response in Arabidopsis thaliana. Plant Molecular Biology, 2020, 103, 321-340.	2.0	10
2479	Myeloid-specific IRE1alpha deletion reduces tumour development in a diabetic, non-alcoholic steatohepatitis-induced hepatocellular carcinoma mouse model. Metabolism: Clinical and Experimental, 2020, 107, 154220.	1.5	19
2480	Metabolomic and transcriptomic profiling reveals the alteration of energy metabolism in oyster larvae during initial shell formation and under experimental ocean acidification. Scientific Reports, 2020, 10, 6111.	1.6	34
2481	Viral Fitness Determines the Magnitude of Transcriptomic and Epigenomic Reprogramming of Defense Responses in Plants. Molecular Biology and Evolution, 2020, 37, 1866-1881.	3.5	27
2482	Cytosolic GLUTAMINE SYNTHETASE1;1 Modulates Metabolism and Chloroplast Development in Roots. Plant Physiology, 2020, 182, 1894-1909.	2.3	25
2483	Characterization of RNP Networks of PUM1 and PUM2 Post-Transcriptional Regulators in TCam-2 Cells, a Human Male Germ Cell Model. Cells, 2020, 9, 984.	1.8	3
2484	Systems Biology Analysis of the Antagonizing Effects of HIV-1 Tat Expression in the Brain over Transcriptional Changes Caused by Methamphetamine Sensitization. Viruses, 2020, 12, 426.	1.5	7
2485	Recapitulating kidney development in vitro by priming and differentiating mouse embryonic stem cells in monolayers. Npj Regenerative Medicine, 2020, 5, 7.	2.5	7
2486	Flow-induced Reorganization of Laminin-integrin Networks Within the Endothelial Basement Membrane Uncovered by Proteomics. Molecular and Cellular Proteomics, 2020, 19, 1179-1192.	2.5	14
2487	Intratumor β -catenin heterogeneity driven by genomic rearrangement dictates growth factor dependent prostate cancer progression. Oncogene, 2020, 39, 4358-4374.	2.6	5
2488	<i>Camellia</i> Plant Resistance and Susceptibility to Petal Blight Disease Are Defined by the Timing of Defense Responses. Molecular Plant-Microbe Interactions, 2020, 33, 982-995.	1.4	2
2489	ERdj3B-Mediated Quality Control Maintains Anther Development at High Temperatures. Plant Physiology, 2020, 182, 1979-1990.	2.3	19
2490	The circular RNA CDR1as regulate cell proliferation via TMED2 and TMED10. BMC Cancer, 2020, 20, 312.	1.1	14
2491	A genetic interaction map centered on cohesin reveals auxiliary factors in sister chromatid cohesion. Journal of Cell Science, 2020, 133, .	1.2	5

#	ARTICLE	IF	CITATIONS
2492	Genome-Wide Discovery of G-Quadruplexes in Wheat: Distribution and Putative Functional Roles. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2021-2032.	0.8	22
2493	Morpho-physiological integrators, transcriptome and coexpression network analyses signify the novel molecular signatures associated with axillary bud in chrysanthemum. <i>BMC Plant Biology</i> , 2020, 20, 145.	1.6	11
2494	Pro-opiomelanocortin (POMC) neuron translome signatures underlying obesogenic gestational malprogramming in mice. <i>Molecular Metabolism</i> , 2020, 36, 100963.	3.0	12
2495	Identification of Potential Hub Genes of Atherosclerosis Through Bioinformatic Analysis. <i>Journal of Computational Biology</i> , 2021, 28, 60-78.	0.8	4
2496	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
2497	Multi-Omics Analysis in a Network Context. , 2021, , 224-233.		1
2498	Endogenous indole-3-acetamide levels contribute to the crosstalk between auxin and abscisic acid, and trigger plant stress responses in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 459-475.	2.4	28
2499	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
2500	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
2501	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
2502	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
2503	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
2504	A photo-crosslinkable cartilage-derived extracellular matrix bioink for auricular cartilage tissue engineering. <i>Acta Biomaterialia</i> , 2021, 121, 193-203.	4.1	81
2505	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
2506	Comparative proteomic analysis of dental cementum from deciduous and permanent teeth. <i>Journal of Periodontal Research</i> , 2021, 56, 173-185.	1.4	9
2507	Mechanisms for the stimulatory effects of a five-component mixture of antibiotics in <i>Microcystis aeruginosa</i> at transcriptomic and proteomic levels. <i>Journal of Hazardous Materials</i> , 2021, 406, 124722.	6.5	41
2508	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
2509	Targeting immunosuppressive macrophages overcomes PARP inhibitor resistance in BRCA1-associated triple-negative breast cancer. <i>Nature Cancer</i> , 2021, 2, 66-82.	5.7	126

#	ARTICLE	IF	CITATIONS
2510	Proteomic analysis reveals the role of exogenous cysteine in alleviating chromium stress in maize seedlings. <i>Ecotoxicology and Environmental Safety</i> , 2021, 209, 111784.	2.9	22
2511	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
2512	Integrated Microarray to Identify the Hub miRNAs and Constructed miRNA-mRNA Network in Neuroblastoma Via Bioinformatics Analysis. <i>Neurochemical Research</i> , 2021, 46, 197-212.	1.6	12
2513	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
2514	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
2515	Study on the Prognostic Values of Dynactin Genes in Low-Grade Glioma. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110101.	0.8	5
2516	Exosomes as an emerging nanoplatform for functional therapeutics. , 2021, , 483-498.		3
2517	Protein Interaction Studies for Understanding the Tremor Pathway in Parkinson's Disease. <i>CNS and Neurological Disorders - Drug Targets</i> , 2021, 19, 780-790.	0.8	1
2518	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
2519	Databases and Bioinformatics Tools for Data Mining. , 2021, , 103-128.		0
2520	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
2521	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
2522	HBFP: a new repository for human body fluid proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	17
2523	Screening and identification of hub genes in bladder cancer by bioinformatics analysis and KIF11 is a potential prognostic biomarker. <i>Oncology Letters</i> , 2021, 21, 205.	0.8	9
2524	Transcriptome profiling of <i>Stevia rebaudiana</i> MS007 revealed genes involved in flower development. <i>Turkish Journal of Biology</i> , 2021, 45, 314-322.	2.1	2
2525	Co-expression Networks in Predicting Transcriptional Gene Regulation. <i>Methods in Molecular Biology</i> , 2021, 2328, 1-11.	0.4	5
2526	Relevance of Bioinformatics and Database in Omics Study. , 2021, , 19-39.		0
2527	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0

#	ARTICLE	IF	CITATIONS
2528	Proteomic and Functional Studies Reveal Detyrosinated Tubulin as Treatment Target in Sarcomere Mutation-Induced Hypertrophic Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2021, 14, e007022.	1.6	58
2529	Aberrant splicing isoforms detected by full-length transcriptome sequencing as transcripts of potential neoantigens in non-small cell lung cancer. <i>Genome Biology</i> , 2021, 22, 9.	3.8	58
2530	Identification of novel biomarkers and candidate small-molecule drugs in cutaneous melanoma by comprehensive gene microarrays analysis. <i>Journal of Cancer</i> , 2021, 12, 1307-1317.	1.2	6
2531	Escalation in the host-pathogen arms race: A host resistance response corresponds to a heightened bacterial virulence response. <i>PLoS Pathogens</i> , 2021, 17, e1009175.	2.1	5
2533	Transfer of oral bacteria to the fetus during late gestation. <i>Scientific Reports</i> , 2021, 11, 708.	1.6	4
2535	Co-expression for Genotype-Phenotype Function Annotation in Potato Research. <i>Methods in Molecular Biology</i> , 2021, 2354, 261-272.	0.4	0
2536	Gene signature of children with severe respiratory syncytial virus infection. <i>Pediatric Research</i> , 2021, 89, 1664-1672.	1.1	13
2537	Comprehensive investigation of the clinical significance of long non-coding RNA HOXA-AS2 in acute myeloid leukemia using genome-wide RNA sequencing dataset. <i>Journal of Cancer</i> , 2021, 12, 2151-2164.	1.2	4
2538	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
2539	Studies on the Mechanism of Gegen Qinlian Decoction in Treating Diabetes Mellitus Based on Network Pharmacology. <i>Natural Product Communications</i> , 2021, 16, 1934578X2098213.	0.2	2
2540	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
2541	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
2542	Sex-biased DNA methylation in papillary thyroid cancer. <i>Biomarkers in Medicine</i> , 2021, 15, 109-121.	0.6	9
2544	Proteomic Analysis of Caspofungin-Induced Responses in Planktonic Cells and Biofilms of <i>Candida albicans</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 639123.	1.5	5
2545	Network Topological Analysis for the Identification of Novel Hubs in Plant Nutrition. <i>Frontiers in Plant Science</i> , 2021, 12, 629013.	1.7	14
2546	<i>In silico</i> 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
2547	Plant virus evolution under strong drought conditions results in a transition from parasitism to mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	58
2548	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

#	ARTICLE	IF	CITATIONS
2549	Caloric Restriction Promotes Immunometabolic Reprogramming Leading to Protection from Tuberculosis. <i>Cell Metabolism</i> , 2021, 33, 300-318.e12.	7.2	35
2550	Oleic Acid and Eicosapentaenoic Acid Reverse Palmitic Acid-induced Insulin Resistance in Human HepG2 Cells via the Reactive Oxygen Species/JUN Pathway. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 754-771.	3.0	8
2551	Identification of microRNAs and their gene targets in cytoplasmic male sterile and fertile maintainer lines of pigeonpea. <i>Planta</i> , 2021, 253, 59.	1.6	10
2552	Epigenetic Regulation of Processes Related to High Level of Fibroblast Growth Factor 21 in Obese Subjects. <i>Genes</i> , 2021, 12, 307.	1.0	8
2553	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
2554	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
2556	A snapshot of translation in <i>Mycobacterium tuberculosis</i> during exponential growth and nutrient starvation revealed by ribosome profiling. <i>Cell Reports</i> , 2021, 34, 108695.	2.9	16
2557	Novel Insights into Quantitative Proteomics from an Innovative Bottom-Up Simple Light Isotope Metabolic (bSLIM) Labeling Data Processing Strategy. <i>Journal of Proteome Research</i> , 2021, 20, 1476-1487.	1.8	7
2558	Integrated metabolic profiling and transcriptome analysis of pigment accumulation in <i>Lonicera japonica</i> flower petals during colour-transition. <i>BMC Plant Biology</i> , 2021, 21, 98.	1.6	36
2559	High expression of MCM10 is predictive of poor outcomes in lung adenocarcinoma. <i>PeerJ</i> , 2021, 9, e10560.	0.9	2
2560	Screening of Hub Gene Targets for Lung Cancer via Microarray Data. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 269-285.	0.6	8
2562	Shotgun Proteomics of Isolated Urinary Extracellular Vesicles for Investigating Respiratory Impedance in Healthy Preschoolers. <i>Molecules</i> , 2021, 26, 1258.	1.7	2
2563	Identifying Breast Cancer-induced Gene Perturbations and its Application in Guiding Drug Repurposing. <i>Current Bioinformatics</i> , 2021, 15, 1075-1089.	0.7	12
2564	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
2565	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
2566	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
2567	Computational Analysis of Rice Transcriptomic and Genomic Datasets in Search for SNPs Involved in Flavonoid Biosynthesis. , 0, , .		0
2568	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

#	ARTICLE	IF	CITATIONS
2569	Sex-Related Differences in Protein Expression in Sarcomere Mutation-Positive Hypertrophic Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 612215.	1.1	11
2570	Secondary Metabolism and Defense Responses Are Differently Regulated in Two Grapevine Cultivars during Ripening. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3045.	1.8	9
2571	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
2572	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
2573	Activation of Toll-Like Receptor 7 Signaling Pathway in Primary Sjögren's Syndrome-Associated Thrombocytopenia. <i>Frontiers in Immunology</i> , 2021, 12, 637659.	2.2	10
2574	HiC2Vec: hierarchical representations of Gene Ontology and genes in the Poincaré ball. <i>Bioinformatics</i> , 2021, 37, 2971-2980.	1.8	10
2575	Transcriptional profiling reveals the transcription factor networks regulating the survival of striatal neurons. <i>Cell Death and Disease</i> , 2021, 12, 262.	2.7	17
2576	Comparison of Brassica Genomes reveals asymmetrical gene retention between functional groups of genes in recurrent polyploidizations. <i>Plant Molecular Biology</i> , 2021, 106, 193-206.	2.0	6
2577	Genome-wide regulation of CpG methylation by ecCEBP1 in acute myeloid leukemia. <i>F1000Research</i> , 2021, 10, 204.	0.8	1
2578	N ⁶ -methyladenosine modification of lncRNA <i>Pvt1</i> governs epidermal stemness. <i>EMBO Journal</i> , 2021, 40, e106276.	3.5	30
2579	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
2580	Genome-wide profiling of miRNAs during seed development reveals their functional relevance in seed size/weight determination in chickpea. <i>Plant Direct</i> , 2021, 5, e00299.	0.8	13
2581	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
2582	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
2583	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. <i>ELife</i> , 2021, 10, .	2.8	43
2585	A Tale of Two Transcriptomic Responses in Agricultural Pests via Host Defenses and Viral Replication. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3568.	1.8	8
2586	MMP7 as a potential biomarker of colon cancer and its prognostic value by bioinformatics analysis. <i>Medicine (United States)</i> , 2021, 100, e24953.	0.4	13
2587	Characterization of Biological Pathways Regulating Acute Cold Resistance of Zebrafish. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3028.	1.8	28

#	ARTICLE	IF	CITATIONS
2589	DGCR8 deficiency impairs macrophage growth and unleashes the interferon response to mycobacteria. Life Science Alliance, 2021, 4, e202000810.	1.3	0
2591	Cross species multi-omics reveals cell wall sequestration and elevated global transcript abundance as mechanisms of boron tolerance in plants. New Phytologist, 2021, 230, 1985-2000.	3.5	25
2592	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. Plant Cell, 2021, 33, 1863-1887.	3.1	27
2593	Metallothioneins alter macrophage phenotype and represent novel therapeutic targets for acetaminophen-induced liver injury. Journal of Leukocyte Biology, 2021, 111, 123-133.	1.5	8
2597	Expression level of long non-coding RNA colon adenocarcinoma hypermethylated serves as a novel prognostic biomarker in patients with thyroid carcinoma. Bioscience Reports, 2021, 41, .	1.1	5
2598	The Na/K-ATPase β 1/Src interaction regulates metabolic reserve and Western diet intolerance. Acta Physiologica, 2021, 232, e13652.	1.8	12
2599	Varied clinical significance of ATP-binding cassette C sub-family members for lung adenocarcinoma. Medicine (United States), 2021, 100, e25246.	0.4	3
2600	Genome-wide discovery of G-quadruplexes in barley. Scientific Reports, 2021, 11, 7876.	1.6	16
2602	Transcriptome Analysis of Seed Weight Plasticity in Brassica napus. International Journal of Molecular Sciences, 2021, 22, 4449.	1.8	6
2603	Pinpointing cysteine oxidation sites by high-resolution proteomics reveals a mechanism of redox-dependent inhibition of human STING. Science Signaling, 2021, 14, .	1.6	15
2604	Combining Mass Spectrometry-Based Phosphoproteomics with a Network-Based Approach to Reveal FLT3-Dependent Mechanisms of Chemoresistance. Proteomes, 2021, 9, 19.	1.7	4
2605	Circulating inflammatory cytokines alter transcriptional activity within fibrotic tissue of Dupuytren's disease patients. Journal of Orthopaedic Research, 2021, , .	1.2	2
2607	Transcriptome analysis of the liver of <i>Eospalax fontanierii</i> under hypoxia. PeerJ, 2021, 9, e11166.	0.9	3
2608	Changes in the gene expression profile during spontaneous migraine attacks. Scientific Reports, 2021, 11, 8294.	1.6	10
2609	Induced Torpor as a Countermeasure for Low Dose Radiation Exposure in a Zebrafish Model. Cells, 2021, 10, 906.	1.8	8
2610	Similarity Calculation, Enrichment Analysis, and Ontology Visualization of Biomedical Ontologies using UFO. Current Protocols, 2021, 1, e115.	1.3	1
2611	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
2612	Genome-wide association study and transcriptome comparison reveal novel QTL and candidate genes that control petal size in rapeseed. Journal of Experimental Botany, 2021, 72, 3597-3610.	2.4	7

#	ARTICLE	IF	CITATIONS
2613	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
2614	<u>C</u>YTO<u>K</u>ININ-RESPONSIVE <u>G</u>ROWTH REGULATOR regulates cell expansion and cytokinin-mediated cell cycle progression. <i>Plant Physiology</i> , 2021, 186, 1734-1746.	2.3	22
2615	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
2616	Investigation and verification of the clinical significance and perspective of natural killer group 2 member D ligands in colon adenocarcinoma. <i>Aging</i> , 2021, 13, 12565-12586.	1.4	4
2617	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
2618	Prion protein is associated with a worse prognosis of head and neck squamous cell carcinoma. <i>Journal of Oral Pathology and Medicine</i> , 2021, 50, 985-994.	1.4	10
2619	Global Transcriptional Response of <i>Aspergillus niger</i> to Blocked Active Citrate Export through Deletion of the Exporter Gene. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 409.	1.5	7
2620	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
2621	Disentangling the aging gene expression network of termite queens. <i>BMC Genomics</i> , 2021, 22, 339.	1.2	10
2622	Understanding the differences in 2G ethanol fermentative scales through omics data integration. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	6
2624	Genetic interaction network has a very limited impact on the evolutionary trajectories in continuous culture-grown populations of yeast. <i>Bmc Ecology and Evolution</i> , 2021, 21, 99.	0.7	1
2626	Cellular and transcriptomic analyses reveal two-staged chloroplast biogenesis underpinning photosynthesis build-up in the wheat leaf. <i>Genome Biology</i> , 2021, 22, 151.	3.8	28
2627	ADAMTS12 acts as a tumor microenvironment related cancer promoter in gastric cancer. <i>Scientific Reports</i> , 2021, 11, 10996.	1.6	13
2629	Fusion protein EWS-FLI1 is incorporated into a protein granule in cells. <i>Rna</i> , 2021, 27, 920-932.	1.6	14
2630	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
2631	Characterization of Alternative Splicing (AS) Events during Chicken (<i>Gallus gallus</i>) Male Germ-Line Stem Cell Differentiation with Single-Cell RNA-seq. <i>Animals</i> , 2021, 11, 1469.	1.0	4
2632	Secretome signature of cardiopoietic cells echoed in rescued infarcted heart proteome. <i>Stem Cells Translational Medicine</i> , 2021, 10, 1320-1328.	1.6	2
2633	Screening and identification of LMNB1 and DLGAP5, two key biomarkers in gliomas. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7

#	ARTICLE	IF	CITATIONS
2634	Identification of viral-mediated pathogenic mechanisms in neurodegenerative diseases using network-based approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
2635	RNA-Seq Analysis of Gene Expression Changes Related to Delay of Flowering Time under Drought Stress in Tropical Maize. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 4273.	1.3	6
2637	Identification of Key Biomarkers and Immune Infiltration in Sciatic Nerve of Diabetic Neuropathy BKS-db/db Mice by Bioinformatics Analysis. <i>Frontiers in Pharmacology</i> , 2021, 12, 682005.	1.6	2
2638	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
2639	Revisiting <i>Ehrlichia ruminantium</i> Replication Cycle Using Proteomics: The Host and the Bacterium Perspectives. <i>Microorganisms</i> , 2021, 9, 1144.	1.6	2
2640	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
2641	Nitrogen availability improves the physiological resilience of coral endosymbiont <i>Cladocopium goreaui</i> to high temperature. <i>Journal of Phycology</i> , 2021, 57, 1187-1198.	1.0	6
2642	Chromosome-Level Reference Genome Assembly for the American Pika (<i>Ochotona princeps</i>). <i>Journal of Heredity</i> , 2021, 112, 549-557.	1.0	10
2643	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
2644	The USP7-TRIM27 axis mediates non-canonical PRC1.1 function and is a druggable target in leukemia. <i>IScience</i> , 2021, 24, 102435.	1.9	19
2645	Altered MicroRNA Expression in Intracranial Aneurysmal Tissues: Possible Role in TGF- β 2 Signaling Pathway. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 2393-2405.	1.7	8
2646	Gene Expression Response to Stony Coral Tissue Loss Disease Transmission in <i>M. cavernosa</i> and <i>O. faveolata</i> From Florida. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	25
2647	Single-cell RNA sequencing of human femoral head in vivo. <i>Aging</i> , 2021, 13, 15595-15619.	1.4	13
2649	<i>slim shady</i> is a novel allele of <i>PHYTOCHROME B</i> present in the Tâ€DNA line SALK_015201. <i>Plant Direct</i> , 2021, 5, e00326.	0.8	6
2651	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. <i>Communications Biology</i> , 2021, 4, 655.	2.0	12
2652	Integrative proteomic network analyses support depotâ€specific roles for leucine rich repeat LGI family member 3 in adipose tissues. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 837.	0.8	3
2654	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
2655	Transcriptional drug repositioning and cheminformatics approach for differentiation therapy of leukaemia cells. <i>Scientific Reports</i> , 2021, 11, 12537.	1.6	6

#	ARTICLE	IF	CITATIONS
2657	Jak-STAT Inhibition Mediates Romidepsin and Mechlorethamine Synergism in Cutaneous T-Cell Lymphoma. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2908-2920.e7.	0.3	12
2658	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
2659	Adaptive evolution of sulfite tolerance in <i>Brettanomyces bruxellensis</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	6
2660	Identification and function analysis of fasciclin-like arabinogalactan protein family genes in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	3
2662	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
2663	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
2664	A novel method to identify gene interaction patterns. <i>BMC Genomics</i> , 2021, 22, 436.	1.2	5
2665	Eutopic endometrium from women with endometriosis and chlamydial endometritis share immunological cell types and DNA repair imbalance: A transcriptome meta-analytical perspective. <i>Journal of Reproductive Immunology</i> , 2021, 145, 103307.	0.8	8
2666	Insights Into the Mechanisms Implicated in <i>Pinus pinaster</i> Resistance to Pinewood Nematode. <i>Frontiers in Plant Science</i> , 2021, 12, 690857.	1.7	15
2667	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
2668	Transcriptional Responses of <i>Sclerotinia sclerotiorum</i> to the Infection by SsHADV-1. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 493.	1.5	20
2669	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
2670	Effects of Cancer Presence and Therapy on the Platelet Proteome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8236.	1.8	8
2673	Exogenous cysteine alleviates chromium stress via reducing its uptake and regulating proteome in roots of <i>Brassica napus</i> L. seedlings. <i>South African Journal of Botany</i> , 2021, 139, 114-121.	1.2	15
2674	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
2675	The methylome of the model arbuscular mycorrhizal fungus, <i>Rhizophagus irregularis</i> , shares characteristics with early diverging fungi and <i>Dikarya</i> . <i>Communications Biology</i> , 2021, 4, 901.	2.0	17
2676	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
2677	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. <i>Journal of Proteome Research</i> , 2021, 20, 3840-3852.	1.8	17

#	ARTICLE	IF	CITATIONS
2678	Identification of endometriosis-associated genes and pathways based on bioinformatic analysis. <i>Medicine (United States)</i> , 2021, 100, e26530.	0.4	7
2679	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
2680	Oxidative Posttranslational Modifications of Blood Plasma Proteins of Cosmonauts after a Long-Term Flight: Part II. <i>Human Physiology</i> , 2021, 47, 438-447.	0.1	1
2681	Multiple G-quadruplex binding ligand induced transcriptomic map of cancer cell lines. <i>Journal of Cell Communication and Signaling</i> , 2022, 16, 129-135.	1.8	5
2682	Genetic Exchange of Lung-Derived Exosome to Brain Causing Neuronal Changes on COVID-19 Infection. <i>Molecular Neurobiology</i> , 2021, 58, 5356-5368.	1.9	17
2683	A near-complete genome sequence of mungbean (<i>Vigna radiata</i> L.) provides key insights into the modern breeding program. <i>Plant Genome</i> , 2021, 14, e20121.	1.6	27
2684	Comparative Transcriptional Analysis of Pulmonary Arterial Hypertension Associated With Three Different Diseases. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 672159.	1.8	6
2685	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
2686	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
2687	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
2690	Malpigmentation of Common Sole (<i>Solea solea</i>) during Metamorphosis Is Associated with Differential Synaptic-Related Gene Expression. <i>Animals</i> , 2021, 11, 2273.	1.0	2
2691	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
2692	Comprehensive transcriptome mining identified the gene expression signature and differentially regulated pathways of the late-onset preeclampsia. <i>Pregnancy Hypertension</i> , 2021, 25, 91-102.	0.6	6
2693	In silico comparative analysis of LRRK2 interactomes from brain, kidney and lung. <i>Brain Research</i> , 2021, 1765, 147503.	1.1	6
2694	G6pd-Deficient Mice Are Protected From Experimental Cerebral Malaria and Liver Injury by Suppressing Proinflammatory Response in the Early Stage of <i>Plasmodium berghei</i> Infection. <i>Frontiers in Immunology</i> , 2021, 12, 719189.	2.2	4
2695	Genome-wide regulation of CpG methylation by ecCEBP1 in acute myeloid leukemia. <i>F1000Research</i> , 2021, 10, 204.	0.8	2
2696	Nitrate triggered phosphoproteome changes and a PIN2 phosphosite modulating root system architecture. <i>EMBO Reports</i> , 2021, 22, e51813.	2.0	22
2697	Transcriptome Analysis of <i>Melocactus glaucescens</i> (Cactaceae) Reveals Metabolic Changes During in vitro Shoot Organogenesis Induction. <i>Frontiers in Plant Science</i> , 2021, 12, 697556.	1.7	1

#	ARTICLE	IF	CITATIONS
2698	KLF10 integrates circadian timing and sugar signaling to coordinate hepatic metabolism. <i>ELife</i> , 2021, 10, .	2.8	18
2699	TCF19 and p53 regulate transcription of <i>TIGAR</i> and <i>SCO2</i> in HCC for mitochondrial energy metabolism and stress adaptation. <i>FASEB Journal</i> , 2021, 35, e21814.	0.2	11
2700	Comparative analyses of extreme dry seed thermotolerance in five Cactaceae species. <i>Environmental and Experimental Botany</i> , 2021, 188, 104514.	2.0	4
2701	Restructuring of the male mice peripheral circadian network after bariatric surgery. <i>Journal of Endocrinology</i> , 2021, 250, 67-79.	1.2	4
2702	First transcriptome profiling of <i>D. melanogaster</i> after development in a deep underground low radiation background laboratory. <i>PLoS ONE</i> , 2021, 16, e0255066.	1.1	11
2703	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
2704	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , 2021, 8, 170.	2.9	12
2705	Longitudinal stability of urinary extracellular vesicle protein patterns within and between individuals. <i>Scientific Reports</i> , 2021, 11, 15629.	1.6	6
2708	iRegNet: an integrative regulatory network analysis tool for <i>Arabidopsis thaliana</i> . <i>Plant Physiology</i> , 2021, 187, 1292-1309.	2.3	6
2709	Mitochondrial Fragmentation Triggers Ineffective Hematopoiesis in Myelodysplastic Syndromes. <i>Cancer Discovery</i> , 2022, 12, 250-269.	7.7	14
2710	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
2711	Landscape genomics and selection signatures of local adaptation of Eritrean indigenous cattle along environmental gradients. <i>Tropical Animal Health and Production</i> , 2021, 53, 423.	0.5	2
2712	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
2713	Mechanisms of Paeoniflorin against myocardial ischemia reperfusion injury based on network pharmacology. <i>Materials Express</i> , 2021, 11, 1505-1515.	0.2	3
2714	NRF2 as a therapeutic opportunity to impact in the molecular roadmap of ALS. <i>Free Radical Biology and Medicine</i> , 2021, 173, 125-141.	1.3	21
2716	Tissue-specific gene expression shows a cynipid wasp repurposes oak host gene networks to create a complex and novel parasite-specific organ. <i>Molecular Ecology</i> , 2022, 31, 3228-3240.	2.0	20
2717	Dramatic transcriptomic differences in <i>Macaca mulatta</i> and <i>Macaca fascicularis</i> with <i>Plasmodium knowlesi</i> infections. <i>Scientific Reports</i> , 2021, 11, 19519.	1.6	5
2718	Overexpression of DEFECTIVE IN ANTHAR DEHISCENCE 1 increases rapeseed silique length through crosstalk between JA and auxin signaling. <i>Industrial Crops and Products</i> , 2021, 168, 113576.	2.5	8

#	ARTICLE	IF	CITATIONS
2719	Elucidation of the Algicidal Mechanism of the Marine Bacterium <i>Pseudoruegeria</i> sp. M32A2M Against the Harmful Alga <i>Alexandrium catenella</i> Based on Time-Course Transcriptome Analysis. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
2720	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. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-7.	2.0	1
2721	Complement-containing small extracellular vesicles from adventitial fibroblasts induce proinflammatory and metabolic reprogramming in macrophages. <i>JCI Insight</i> , 2021, 6, .	2.3	13
2722	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
2724	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
2725	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
2726	Genome-wide high-resolution mapping of DNA methylation reveals epigenetic variation in the offspring of sexual and asexual propagation in <i>Robinia pseudoacacia</i> . <i>Plant Cell Reports</i> , 2021, 40, 2435-2447.	2.8	4
2727	Computational analysis of human host binding partners of chikungunya and dengue viruses during coinfection. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	2
2728	Results of the Seventh Scientific Workshop of ECCO: Precision Medicine in IBDâ€”What, Why, and How. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 1410-1430.	0.6	28
2729	New insights into the dynamic development of the cerebral cortex in childhood and adolescence: Integrating macro- and microstructural MRI findings. <i>Progress in Neurobiology</i> , 2021, 204, 102109.	2.8	54
2730	Beyond phosphorylation: Putative roles of post-translational modifications in <i>Plasmodium</i> sexual stages. <i>Molecular and Biochemical Parasitology</i> , 2021, 245, 111406.	0.5	1
2731	Global gene expression analysis of pigeonpea with male sterility conditioned by A 2 cytoplasm. <i>Plant Genome</i> , 2021, 14, e20132.	1.6	7
2732	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
2733	Quantitative proteomics analysis reveals novel insights into mechanisms of action of disulfiram (DSF). <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100031.	0.8	0
2734	Evaluation of protein extraction methods for in-depth proteome analysis of narrow-leafed lupin (<i>Lupinus angustifolius</i>) seeds. <i>Food Chemistry</i> , 2022, 367, 130722.	4.2	10
2735	Network Analysis Reveals Proteins Associated with Aortic Dilatation in Mucopolysaccharidoses. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 34-43.	2.2	3
2736	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
2737	Transcriptome analysis and postharvest behavior of the kiwifruit â€” <i>Actinidia deliciosa</i> â€” reveal the role of ethylene-related phytohormones during fruit ripening. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	15

#	ARTICLE	IF	CITATIONS
2738	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
2739	Improving Nitrogen Use Efficiency Through Overexpression of Alanine Aminotransferase in Rice, Wheat, and Barley. <i>Frontiers in Plant Science</i> , 2021, 12, 628521.	1.7	27
2740	Bioinformatics Approaches for Interpreting Metabolomics Datasets. , 2021, , 370-384.		0
2741	RNA-Seq in Nonmodel Organisms. <i>Methods in Molecular Biology</i> , 2021, 2243, 143-167.	0.4	4
2742	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
2743	Transcriptome Based System Biology Exploration Reveals Homogeneous Tumorigenicity of Alimentary Tract Malignancy. <i>Frontiers in Oncology</i> , 2020, 10, 580276.	1.3	2
2744	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
2745	Disease-Based Network Pharmacology PracticeÂProcess. , 2021, , 395-429.		1
2746	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
2747	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
2748	Analysis of Proteomic Data for Toxicological Applications. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 257-284.	0.1	1
2749	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
2750	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. <i>Methods in Molecular Biology</i> , 2017, 1558, 395-413.	0.4	7
2751	Learning Differential Module Networks Across Multiple Experimental Conditions. <i>Methods in Molecular Biology</i> , 2019, 1883, 303-321.	0.4	6
2752	Metaanalysis of ChIP-chip Data. <i>Methods in Molecular Biology</i> , 2010, 631, 185-207.	0.4	2
2753	The Use of Open Source Bioinformatics Tools to Dissect Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2012, 835, 311-331.	0.4	9
2754	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2012, 850, 483-494.	0.4	14
2755	BioTest - Remote Platform for Hypothesis Testing and Analysis of Biomedical Data. <i>Advances in Intelligent Systems and Computing</i> , 2020, , 152-165.	0.5	1

#	ARTICLE	IF	CITATIONS
2757	Bottom-Up Proteomics. , 2016, , 155-185.		1
2758	Constructing Treatment Portfolios Using Affinity Propagation. Lecture Notes in Computer Science, 2008, , 360-371.	1.0	25
2759	Semi-bipartite Graph Visualization for Gene Ontology Networks. Lecture Notes in Computer Science, 2010, , 244-255.	1.0	9
2760	Visualizing Multivariate Hierarchic Data Using Enhanced Radial Space-Filling Layout. Lecture Notes in Computer Science, 2010, , 350-360.	1.0	2
2761	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. Lecture Notes in Computer Science, 2012, , 287-301.	1.0	7
2762	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. , 2007, 97, 277-307.		7
2763	Transcriptomics Analysis Methods: Microarray Data Processing, Analysis and Visualization Using the Affymetrix Genechip® Vitis Vinifera Genome Array. , 2010, , 317-334.		4
2764	Processing of Mass Spectrometry Data in Clinical Applications. Translational Bioinformatics, 2013, , 207-233.	0.0	1
2765	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2013, 5, 59.	4.8	3
2766	The Penium margaritaceum Genome: Hallmarks of the Origins of Land Plants. Cell, 2020, 181, 1097-1111.e12.	13.5	153
2767	CLIP and Massively Parallel Functional Analysis of CELF6 Reveal a Role in Destabilizing Synaptic Gene mRNAs through Interaction with 3' UTR Elements. Cell Reports, 2020, 33, 108531.	2.9	14
2768	How tryptophan levels in plant-based aquafeeds affect fish physiology, metabolism and proteome. Journal of Proteomics, 2020, 221, 103782.	1.2	30
2769	Distinct genetic architectures for phenotype means and plasticities in Zea mays. Nature Plants, 2017, 3, 715-723.	4.7	98
2770	Building an octaploid genome and transcriptome of the medicinal plant Pogostemon cablin from Lamiales. Scientific Data, 2018, 5, 180274.	2.4	17
2771	Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. New Developments in Mass Spectrometry, 2014, , 185-210.	0.2	3
2772	Bioinformatics-based analysis of the lncRNA-miRNA-mRNA and TF regulatory networks reveals functional genes in esophageal squamous cell carcinoma. Bioscience Reports, 2020, 40, .	1.1	7
2773	Functional genomics: applications to production agriculture.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , 1-21.	0.6	2
2774	The protein interaction network of the inherited central nervous system diseases reveals new gene candidates for molecularly unclassified myelin disorders. Journal of Complex Networks, 2020, 8, .	1.1	1

#	ARTICLE	IF	CITATIONS
2775	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
2776	The Full-Length Transcriptome of <i>Spartina alterniflora</i> Reveals the Complexity of High Salt Tolerance in Monocotyledonous Halophyte. <i>Plant and Cell Physiology</i> , 2020, 61, 882-896.	1.5	25
2777	Screening and identification of key biomarkers for retinoblastoma. <i>Medicine (United States)</i> , 2020, 99, e19952.	0.4	3
2806	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
2807	Virulence of the Pathogen <i>Porphyromonas gingivalis</i> Is Controlled by the CRISPR-Cas Protein Cas3. <i>MSystems</i> , 2020, 5, .	1.7	19
2808	Post-Translational Oxidation Modifications of Blood Plasma Proteins of Cosmonauts after a Long-term Flight: Part I. <i>Human Physiology</i> , 2020, 46, 531-539.	0.1	5
2809	Placental proteome abnormalities in women with gestational diabetes and large-for-gestational-age newborns. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001586.	1.2	13
2810	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
2811	Bioinformatic Tools for Inferring Functional Information from Plant Microarray Data II: Analysis Beyond Single Gene. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-13.	2.2	12
2812	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
2814	Personalized Identification of Differentially Expressed Modules in Osteosarcoma. <i>Medical Science Monitor</i> , 2017, 23, 774-779.	0.5	4
2815	eXamine: Visualizing annotated networks in Cytoscape. <i>F1000Research</i> , 2018, 7, 519.	0.8	3
2816	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. <i>F1000Research</i> , 2015, 4, 103.	0.8	32
2817	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. <i>F1000Research</i> , 2015, 4, 103.	0.8	29
2818	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015, 4, 485.	0.8	11
2819	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015, 4, 485.	0.8	8
2820	Predicted protein interactions of IFITMs which inhibit Zika virus infection. <i>F1000Research</i> , 2016, 5, 1919.	0.8	7
2821	Predicted protein interactions of IFITMs may shed light on mechanisms of Zika virus-induced microcephaly and host invasion. <i>F1000Research</i> , 2016, 5, 1919.	0.8	7

#	ARTICLE	IF	CITATIONS
2822	Repair mechanism of astrocytes and non-astrocytes in spinal cord injury. World Journal of Clinical Cases, 2020, 8, 854-863.	0.3	5
2823	Disease-Aging Network Reveals Significant Roles of Aging Genes in Connecting Genetic Diseases. PLoS Computational Biology, 2009, 5, e1000521.	1.5	74
2824	Transcriptional Orchestration of the Global Cellular Response of a Model Pennate Diatom to Diel Light Cycling under Iron Limitation. PLoS Genetics, 2016, 12, e1006490.	1.5	129
2825	Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial. PLoS Medicine, 2020, 17, e1003229.	3.9	60
2826	Linking Gene Expression and Functional Network Data in Human Heart Failure. PLoS ONE, 2007, 2, e1347.	1.1	40
2827	Genome Wide Identification of Recessive Cancer Genes by Combinatorial Mutation Analysis. PLoS ONE, 2008, 3, e3380.	1.1	12
2828	An Attempt to Understand Kidney's Protein Handling Function by Comparing Plasma and Urine Proteomes. PLoS ONE, 2009, 4, e5146.	1.1	60
2829	Inferring the Transcriptional Landscape of Bovine Skeletal Muscle by Integrating Co-Expression Networks. PLoS ONE, 2009, 4, e7249.	1.1	63
2830	Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands. PLoS ONE, 2009, 4, e7448.	1.1	33
2831	ESNOQ, Proteomic Quantification of Endogenous S-Nitrosation. PLoS ONE, 2010, 5, e10015.	1.1	32
2832	Dynamic Zebrafish Interactome Reveals Transcriptional Mechanisms of Dioxin Toxicity. PLoS ONE, 2010, 5, e10465.	1.1	47
2833	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
2834	Changes in Hepatic Gene Expression upon Oral Administration of Taurine-Conjugated Ursodeoxycholic Acid in ob/ob Mice. PLoS ONE, 2010, 5, e13858.	1.1	47
2835	Integrative Identification of Arabidopsis Mitochondrial Proteome and Its Function Exploitation through Protein Interaction Network. PLoS ONE, 2011, 6, e16022.	1.1	33
2836	Identification of Lactoferricin B Intracellular Targets Using an Escherichia coli Proteome Chip. PLoS ONE, 2011, 6, e28197.	1.1	33
2837	Transcriptome Analysis of the Model Protozoan, Tetrahymena thermophila, Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
2838	De-Novo Transcriptome Sequencing of a Normalized cDNA Pool from Influenza Infected Ferrets. PLoS ONE, 2012, 7, e37104.	1.1	13
2839	Transcriptome Kinetics of Circulating Neutrophils during Human Experimental Endotoxemia. PLoS ONE, 2012, 7, e38255.	1.1	38

#	ARTICLE	IF	CITATIONS
2840	Modulation of <i>Lactobacillus plantarum</i> Gastrointestinal Robustness by Fermentation Conditions Enables Identification of Bacterial Robustness Markers. PLoS ONE, 2012, 7, e39053.	1.1	56
2841	Cross-Species Functional Genomic Analysis Identifies Resistance Genes of the Histone Deacetylase Inhibitor Valproic Acid. PLoS ONE, 2012, 7, e48992.	1.1	17
2842	Bioinformatic Inference of Specific and General Transcription Factor Binding Sites in the Plant Pathogen <i>Phytophthora infestans</i> . PLoS ONE, 2012, 7, e51295.	1.1	13
2843	The Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> : New Assembly, Reannotation and Analysis of the Genome and Characterization of Tissue Transcriptomes. PLoS ONE, 2013, 8, e54732.	1.1	77
2844	Transcriptome Analysis of Tomato Flower Pedicel Tissues Reveals Abscission Zone-Specific Modulation of Key Meristem Activity Genes. PLoS ONE, 2013, 8, e55238.	1.1	48
2845	Human 14-3-3 Paralogs Differences Uncovered by Cross-Talk of Phosphorylation and Lysine Acetylation. PLoS ONE, 2013, 8, e55703.	1.1	45
2846	Medullospheres from DAOY, UW228 and ONS-76 Cells: Increased Stem Cell Population and Proteomic Modifications. PLoS ONE, 2013, 8, e63748.	1.1	35
2847	Nodes Having a Major Influence to Break Cooperation Define a Novel Centrality Measure: Game Centrality. PLoS ONE, 2013, 8, e67159.	1.1	18
2848	The Cardiac Acetyl-Lysine Proteome. PLoS ONE, 2013, 8, e67513.	1.1	86
2849	PhenoTimer: Software for the Visual Mapping of Time-Resolved Phenotypic Landscapes. PLoS ONE, 2013, 8, e72361.	1.1	2
2850	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. PLoS ONE, 2013, 8, e74074.	1.1	36
2851	Cathepsin B Gene Disruption Induced <i>Leishmania donovani</i> Proteome Remodeling Implies Cathepsin B Role in Secretome Regulation. PLoS ONE, 2013, 8, e79951.	1.1	17
2852	Molecular and Cellular Features of Murine Craniofacial and Trunk Neural Crest Cells as Stem Cell-Like Cells. PLoS ONE, 2014, 9, e84072.	1.1	15
2853	Transcriptomic Analysis of Carboxylic Acid Challenge in <i>Escherichia coli</i> : Beyond Membrane Damage. PLoS ONE, 2014, 9, e89580.	1.1	28
2854	Modulation of Neuronal Proteome Profile in Response to Japanese Encephalitis Virus Infection. PLoS ONE, 2014, 9, e90211.	1.1	27
2855	RNA-Seq and Microarrays Analyses Reveal Global Differential Transcriptomes of <i>Mesorhizobium huakuii</i> 7653R between Bacteroids and Free-Living Cells. PLoS ONE, 2014, 9, e93626.	1.1	24
2856	Systematic Identification of Cell-Wall Related Genes in <i>Populus</i> Based on Analysis of Functional Modules in Co-Expression Network. PLoS ONE, 2014, 9, e95176.	1.1	26
2857	Transcriptional Evidence for Inferred Pattern of Pollen Tube-Stigma Metabolic Coupling during Pollination. PLoS ONE, 2014, 9, e107046.	1.1	23

#	ARTICLE	IF	CITATIONS
2858	Genes Expressed in Grapevine Leaves Reveal Latent Wood Infection by the Fungal Pathogen <i>Neofusicoccum parvum</i> . PLoS ONE, 2015, 10, e0121828.	1.1	44
2859	Gene Profiling Characteristics of Radioadaptive Response in AG01522 Normal Human Fibroblasts. PLoS ONE, 2015, 10, e0123316.	1.1	20
2860	Integrated RNA-Seq and sRNA-Seq Analysis Identifies Chilling and Freezing Responsive Key Molecular Players and Pathways in Tea Plant (<i>Camellia sinensis</i>). PLoS ONE, 2015, 10, e0125031.	1.1	104
2861	Coupling of Cellular Processes and Their Coordinated Oscillations under Continuous Light in <i>Cyanothece</i> sp. ATCC 51142, a Diazotrophic Unicellular Cyanobacterium. PLoS ONE, 2015, 10, e0125148.	1.1	7
2862	High-Throughput Sequencing and De Novo Assembly of Red and Green Forms of the <i>Perilla frutescens</i> var. <i>crispa</i> Transcriptome. PLoS ONE, 2015, 10, e0129154.	1.1	40
2863	Transcriptome Response Signatures Associated with the Overexpression of a Mitochondrial Uncoupling Protein (AtUCP1) in Tobacco. PLoS ONE, 2015, 10, e0130744.	1.1	11
2864	Metatranscriptome Analysis of Fig Flowers Provides Insights into Potential Mechanisms for Mutualism Stability and Gall Induction. PLoS ONE, 2015, 10, e0130745.	1.1	24
2865	Systematic Analysis of the Molecular Mechanism Underlying Decidualization Using a Text Mining Approach. PLoS ONE, 2015, 10, e0134585.	1.1	15
2866	Deep Sequencing of the <i>Scutellaria baicalensis</i> Georgi Transcriptome Reveals Flavonoid Biosynthetic Profiling and Organ-Specific Gene Expression. PLoS ONE, 2015, 10, e0136397.	1.1	23
2867	Intermediate Tyrosyl Radical and Amyloid Structure in Peroxide-Activated Cytochrome c. PLoS ONE, 2015, 10, e0136554.	1.1	9
2868	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
2869	Plastid Proteomic Analysis in Tomato Fruit Development. PLoS ONE, 2015, 10, e0137266.	1.1	48
2870	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
2871	Predicting Abdominal Aortic Aneurysm Target Genes by Level-2 Protein-Protein Interaction. PLoS ONE, 2015, 10, e0140888.	1.1	2
2872	A Genome-Wide mRNA Expression Profile in <i>Caenorhabditis elegans</i> under Prolonged Exposure to 1750MHz Radiofrequency Fields. PLoS ONE, 2016, 11, e0147273.	1.1	7
2873	Transcriptomic Analysis of Tea Plant Responding to Drought Stress and Recovery. PLoS ONE, 2016, 11, e0147306.	1.1	67
2874	Transcriptomics Modeling of the Late-Gestation Fetal Pituitary Response to Transient Hypoxia. PLoS ONE, 2016, 11, e0148465.	1.1	6
2875	Time-Course Transcriptome Analysis Reveals Resistance Genes of <i>Panax ginseng</i> Induced by <i>Cylindrocarpum destructans</i> Infection Using RNA-Seq. PLoS ONE, 2016, 11, e0149408.	1.1	20

#	ARTICLE	IF	CITATIONS
2876	The Arabidopsis Domain of Unknown Function 1218 (DUF1218) Containing Proteins, MODIFYING WALL LIGNIN-1 and 2 (At1g31720/MWL-1 and At4g19370/MWL-2) Function Redundantly to Alter Secondary Cell Wall Lignin Content. PLoS ONE, 2016, 11, e0150254.	1.1	14
2877	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
2878	Proteomic Profiling of Mouse Liver following Acute Toxoplasma gondii Infection. PLoS ONE, 2016, 11, e0152022.	1.1	66
2879	Computational Identification of Novel Stage-Specific Biomarkers in Colorectal Cancer Progression. PLoS ONE, 2016, 11, e0156665.	1.1	60
2880	Dissecting the Root Nodule Transcriptome of Chickpea (Cicer arietinum L.). PLoS ONE, 2016, 11, e0157908.	1.1	20
2881	Reprogramming of Strawberry (Fragaria vesca) Root Transcriptome in Response to Phytophthora cactorum. PLoS ONE, 2016, 11, e0161078.	1.1	58
2882	Dietary Intake Influences Adult Fertility and Offspring Fitness in Zebrafish. PLoS ONE, 2016, 11, e0166394.	1.1	17
2883	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
2884	Mapping the Interactome of a Major Mammalian Endoplasmic Reticulum Heat Shock Protein 90. PLoS ONE, 2017, 12, e0169260.	1.1	20
2885	Splicing-related genes are alternatively spliced upon changes in ambient temperatures in plants. PLoS ONE, 2017, 12, e0172950.	1.1	75
2886	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
2887	Integrated network analysis reveals potentially novel molecular mechanisms and therapeutic targets of refractory epilepsies. PLoS ONE, 2017, 12, e0174964.	1.1	13
2888	Different adaptation strategies of two citrus scion/rootstock combinations in response to drought stress. PLoS ONE, 2017, 12, e0177993.	1.1	28
2889	Protein complex prediction via dense subgraphs and false positive analysis. PLoS ONE, 2017, 12, e0183460.	1.1	10
2890	Predicting protein complexes using a supervised learning method combined with local structural information. PLoS ONE, 2018, 13, e0194124.	1.1	12
2891	Innate immune gene expression in Acropora palmata is consistent despite variance in yearly disease events. PLoS ONE, 2020, 15, e0228514.	1.1	12
2892	Enhanced in planta Fitness through Adaptive Mutations in EfpR, a Dual Regulator of Virulence and Metabolic Functions in the Plant Pathogen Ralstonia solanacearum. PLoS Pathogens, 2016, 12, e1006044.	2.1	37
2894	The Differences in Local Translatome across Distinct Neuron Types Is Mediated by Both Baseline Cellular Differences and Post-transcriptional Mechanisms. ENeuro, 2018, 5, ENEURO.0320-18.2018.	0.9	15

#	ARTICLE	IF	CITATIONS
2895	Systems understanding of plant–pathogen interactions through genome-wide protein–protein interaction networks. <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 102.	0.9	23
2896	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
2897	Gene Ontology: A Resource for Analysis and Interpretation of Alzheimerâ€™s Disease Data. , 0, , 23-36.		9
2898	Sulforaphane alters the acidification of the yeast vacuole. <i>Microbial Cell</i> , 2020, 7, 129-138.	1.4	2
2899	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
2900	Protein Function Easily Investigated by Genomics Data Mining Using the ProteINSIDE Online Tool. <i>Genomics and Computational Biology</i> , 2015, 1, 16.	0.7	12
2901	The acute transcriptional response to resistance exercise: impact of age and contraction mode. <i>Aging</i> , 2019, 11, 2111-2126.	1.4	14
2902	Genetic polymorphisms and transcription profiles associated with intracranial aneurysm: a key role for NOTCH3. <i>Aging</i> , 2019, 11, 5173-5191.	1.4	3
2903	Co-expression network analysis identified hub genes critical to triglyceride and free fatty acid metabolism as key regulators of age-related vascular dysfunction in mice. <i>Aging</i> , 2019, 11, 7620-7638.	1.4	56
2904	Identification of frailty-associated genes by coordination analysis of gene expression. <i>Aging</i> , 2020, 12, 4222-4229.	1.4	9
2905	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
2906	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
2907	Therapeutic potential of targeting HSPA5 through dual regulation of two candidate prognostic biomarkers ANXA1 and PSAT1 in osteosarcoma. <i>Aging</i> , 2021, 13, 1212-1235.	1.4	6
2908	Pan-organ transcriptome variation across 21 cancer types. <i>Oncotarget</i> , 2017, 8, 6809-6818.	0.8	6
2909	Accumulation of prohibitin is a common cellular response to different stressing stimuli and protects melanoma cells from ER stress and chemotherapy-induced cell death. <i>Oncotarget</i> , 2017, 8, 43114-43129.	0.8	19
2910	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
2911	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
2912	MicroRNA-23a promotes pancreatic cancer metastasis by targeting epithelial splicing regulator protein 1. <i>Oncotarget</i> , 2017, 8, 82854-82871.	0.8	28

#	ARTICLE	IF	CITATIONS
2913	Proteomics and metabolomics analysis of hepatic mitochondrial metabolism in alcohol-preferring and non-preferring rats. <i>Oncotarget</i> , 2017, 8, 102020-102032.	0.8	6
2914	2D-DIGE proteomic analysis identifies new potential therapeutic targets for adrenocortical carcinoma. <i>Oncotarget</i> , 2015, 6, 5695-5706.	0.8	28
2915	Investigating the dysfunctional pathogenesis of Wilms's tumor through a multidimensional integration strategy. <i>Annals of Translational Medicine</i> , 2019, 7, 136-136.	0.7	7
2916	Data mining approaches highlighted transcription factors that play role in thermo-priming. <i>Plant OMICS</i> , 2017, 10, 139-145.	0.4	7
2917	Mapping of Protein-Protein Interactions: Web-Based Resources for Revealing Interactomes. <i>Current Medicinal Chemistry</i> , 2019, 26, 3890-3910.	1.2	11
2918	Comparative Analysis of RNAi Screening Technologies at Genome-Scale Reveals an Inherent Processing Inefficiency of the Plasmid-Based shRNA Hairpin. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2014, 17, 98-113.	0.6	6
2919	Bioinformatics Tools for the Functional Interpretation of Quantitative Proteomics Results. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 435-449.	1.0	14
2920	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
2921	Protein-Protein Interaction Network Analysis of Salivary Proteomic Data in Oral Cancer Cases. <i>Asian Pacific Journal of Cancer Prevention</i> , 2018, 19, 1639-1645.	0.5	9
2922	miR-190, CDK1, MCM10 and NDC80 predict the prognosis of the patients with lung cancer. <i>Romanian Journal of Laboratory Medicine</i> , 2019, 27, 15-24.	0.1	3
2923	Rab1b and ARF5 are novel RNA-binding proteins involved in FMDV IRES-driven RNA localization. <i>Life Science Alliance</i> , 2019, 2, e201800131.	1.3	14
2924	The function of histamine receptor H4R in the brain revealed by interaction partners. <i>Frontiers in Bioscience - Scholar</i> , 2011, S3, 1058.	0.8	6
2925	Transcriptome Reprogramming of <i>Symbiodiniaceae</i> <i>Breviolum minutum</i> in Response to Casein Amino Acids Supplementation. <i>Frontiers in Physiology</i> , 2020, 11, 574654.	1.3	5
2926	The Interactome of Cancer-Related Lysyl Oxidase and Lysyl Oxidase-Like Proteins. <i>Cancers</i> , 2021, 13, 71.	1.7	20
2927	A Reference Genome of <i>Bursaphelenchus mucronatus</i> Provides New Resources for Revealing Its Displacement by Pinewood Nematode. <i>Genes</i> , 2020, 11, 570.	1.0	10
2929	Genome-wide Analysis of μDR-related Transposable Elements Insertion Population in Maize. <i>Acta Agronomica Sinica(China)</i> , 2011, 37, 772-777.	0.1	1
2930	Predicting Disease Genes of Coronary Artery Disease Based on Functional Consistency and Network Topological Features*. <i>Progress in Biochemistry and Biophysics</i> , 2009, 2009, 781-786.	0.3	1
2931	Discovering Active Subnetwork in Protein Interaction Network*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 208-217.	0.3	2

#	ARTICLE	IF	CITATIONS
2932	Natural taurine promotes apoptosis of human hepatic stellate cells in proteomics analysis. World Journal of Gastroenterology, 2010, 16, 1916.	1.4	18
2933	The role of myoglobin in epithelial cancers: Insights from transcriptomics. International Journal of Molecular Medicine, 2020, 45, 385-400.	1.8	13
2934	Identification of key genes and evaluation of clinical outcomes in lung squamous cell carcinoma using integrated bioinformatics analysis. Oncology Letters, 2019, 18, 5859-5870.	0.8	13
2935	Identification of key candidate genes and pathways in endometrial cancer: Evidence from bioinformatics analysis. Oncology Letters, 2019, 18, 6679-6689.	0.8	5
2936	Distinct diagnostic and prognostic values of Î³-aminobutyric acid type A receptor family genes in patients with colon adenocarcinoma. Oncology Letters, 2020, 20, 275-291.	0.8	25
2937	Identification of lung adenocarcinoma biomarkers based on bioinformatic analysis and human samples. Oncology Reports, 2020, 43, 1437-1450.	1.2	18
2938	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
2939	Characterization of Clostridium acetobutylicum Protein Interaction Network from Butanol Fermentation. Journal of Analytical & Bioanalytical Techniques, 2013, 04, .	0.6	1
2940	Adult and neonatal astrocytes exhibit diverse gene expression profiles in response to beta amyloid <i>in vivo</i>. World Journal of Neuroscience, 2012, 02, 57-67.	0.1	5
2941	Identification of marker genes in diabetic wounds by DNA microarray study. Genetics and Molecular Research, 2013, 12, 5348-5355.	0.3	3
2942	Transcriptome network-based method to identify genes associated with unruptured intracranial aneurysms. Genetics and Molecular Research, 2013, 12, 3263-3273.	0.3	4
2943	From proteomics toward systems biology: integration of different types of proteomics data into network models. BMB Reports, 2008, 41, 184-193.	1.1	25
2944	Characterizing gene coexpression modules in Oryza sativa based on a graph-clustering approach. Plant Biotechnology, 2009, 26, 485-493.	0.5	12
2946	Transcriptional regulatory networks in response to salt and drought stress in Arabidopsis thaliana. Journal of Medicinal Plants Research, 2012, 6, .	0.2	26
2947	OntoVisT: A general purpose Ontological Visualization Tool. Bioinformation, 2011, 6, 288-290.	0.2	3
2948	Network biology approach for identifying key regulatory genes by expression based study of breast cancer. Bioinformation, 2012, 8, 1132-1138.	0.2	14
2949	A manually curated network of the PML nuclear body interactome reveals an important role for PML-NBs in SUMOylation dynamics. International Journal of Biological Sciences, 2010, 6, 51-67.	2.6	175
2950	Transcriptome Network Analysis Reveals Potential Candidate Genes for Esophageal Squamous Cell Carcinoma. Asian Pacific Journal of Cancer Prevention, 2012, 13, 767-773.	0.5	4

#	ARTICLE	IF	CITATIONS
2951	Bicluster and Pathway Enrichment Analysis of HCV-induced Cirrhosis and Hepatocellular Carcinoma. Asian Pacific Journal of Cancer Prevention, 2012, 13, 3741-3745.	0.5	17
2952	Meta-analysis of Gene Expression Data Identifies Causal Genes for Prostate Cancer. Asian Pacific Journal of Cancer Prevention, 2013, 14, 457-461.	0.5	11
2954	Human Nup98 regulates the localization and activity of DExH/D-box helicase DHX9. ELife, 2017, 6, .	2.8	33
2955	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. ELife, 2017, 6, .	2.8	51
2956	Emergence of trait variability through the lens of nitrogen assimilation in Prochlorococcus. ELife, 2019, 8, .	2.8	57
2957	Protein quality control in the nucleolus safeguards recovery of epigenetic regulators after heat shock. ELife, 2019, 8, .	2.8	46
2958	Cell-type diversity and regionalized gene expression in the planarian intestine. ELife, 2020, 9, .	2.8	35
2959	Expression of collagen type 1 alpha 1 indicates lymph node metastasis and poor outcomes in squamous cell carcinomas of the lung. PeerJ, 2020, 8, e10089.	0.9	17
2960	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
2961	A candidate multimodal functional genetic network for thermal adaptation. PeerJ, 2014, 2, e578.	0.9	24
2962	Exploring regulatory networks in plants: transcription factors of starch metabolism. PeerJ, 2019, 7, e6841.	0.9	31
2963	Identification of significant gene and pathways involved in HBV-related hepatocellular carcinoma by bioinformatics analysis. PeerJ, 2019, 7, e7408.	0.9	64
2964	Expression of Heat Shock Proteins by Heat Stress in Soybean. Plant Breeding and Biotechnology, 2017, 5, 344-353.	0.3	8
2965	Gene Expression Analysis and Polymorphism Discovery to Investigate Drought Responsive System in Tropical Maize. Plant Breeding and Biotechnology, 2018, 6, 354-362.	0.3	1
2966	Chemical proteomic profiling reveals protein interactors of the alarmones diadenosine triphosphate and tetraphosphate. Nature Communications, 2021, 12, 5808.	5.8	14
2968	Isobaric tags for relative and absolute quantification (<scp>iTRAQ</scp>)â€based quantitative analysis of the salivary proteome during healthy pregnancy and pregnancy gingivitis. Journal of Clinical Periodontology, 2021, 48, 1559-1569.	2.3	4
2969	Identification and Characterization of Downy Mildew-Responsive microRNAs in Indian Vitis vinifera by High-Throughput Sequencing. Journal of Fungi (Basel, Switzerland), 2021, 7, 899.	1.5	1
2971	Application of Bioinformatics Analysis to Identify Important Pathways and Hub Genes in Ovarian Cancer Affected by WT1. Frontiers in Bioengineering and Biotechnology, 2021, 9, 741051.	2.0	4

#	ARTICLE	IF	CITATIONS
2972	Arabidopsis bioinformatics: tools and strategies. Plant Journal, 2021, 108, 1585-1596.	2.8	9
2973	Transcriptome profiling of pepper leaves by RNA-Seq during an incompatible and a compatible pepper-tobamovirus interaction. Scientific Reports, 2021, 11, 20680.	1.6	10
2974	Gene Ontology curation of the bloodâ€“brain barrier to improve the analysis of Alzheimerâ€™s and other neurological diseases. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	6
2975	Identification of C3 and FN1 as potential biomarkers associated with progression and prognosis for clear cell renal cell carcinoma. BMC Cancer, 2021, 21, 1135.	1.1	8
2976	Identification of a key protein set involved in Moniliophthora perniciosa necrotrophic mycelium and basidiocarp development. Fungal Genetics and Biology, 2021, 157, 103635.	0.9	3
2977	Identification of the key miRNA; hsa-miR-1269a targeting TP53, Caspase-9 and FOXO3a in breast cancer cells under hypoxia by integrated bioinformatics analysis. Gene Reports, 2021, 25, 101408.	0.4	2
2978	Rhesus macaques self-curing from a schistosome infection can display complete immunity to challenge. Nature Communications, 2021, 12, 6181.	5.8	10
2979	Integrated in silico analysis for the identification of key genes and signaling pathways in copper oxide nanoparticles toxicity. Toxicology, 2021, 463, 152984.	2.0	5
2980	Aggregation of Bioinformatics Data Using Semantic Web Technology. SSRN Electronic Journal, 0, , .	0.4	1
2981	Detecting and Characterizing the Modular Structure of the Yeast Transcription Network. Studies in Computational Intelligence, 2009, , 35-46.	0.7	0
2982	Graphical Analysis and Visualization Tools for Protein Interaction Networks. , 2009, , 286-311.		0
2983	3-Phosphoinositide-Dependent Protein Kinase is a Switchboard from Signaling Lipids to Protein Phosphorylation Cascades. Plant Cell Monographs, 2010, , 243-259.	0.4	0
2984	PNmerger: a Cytoscape Plugin to Merge Biological Pathways and Protein Interaction Networks*. Progress in Biochemistry and Biophysics, 2010, 2009, 1613-1616.	0.3	0
2985	Systems Biology: A Promising Tool to Study Abiotic Stress Responses. , 2011, , 163-172.		6
2986	Dynamic Bayesian Network Modeling of Cyanobacterial Biological Processes via Gene Clustering. Lecture Notes in Computer Science, 2011, , 97-106.	1.0	0
2987	Filtering and Interpreting Large-Scale Experimental Proteinâ€“Protein Interaction Data. Methods in Molecular Biology, 2011, 781, 295-309.	0.4	0
2988	On-Chip Living-Cell Microarrays for Network Biology. , 0, , .		0
2989	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

#	ARTICLE	IF	CITATIONS
2990	Identifying Disease-Related Genes by Topological Features of Protein-Protein Interaction Network. Journal of Convergence Information Technology, 2011, 6, 283-292.	0.1	1
2991	Analysis and visualization of gene expression data using biclustering: A comparative study. African Journal of Biotechnology, 2012, 11, .	0.3	1
2993	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
2994	A regulatory network for human adenocarcinoma. African Journal of Biotechnology, 2012, 11, .	0.3	0
2995	Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30.	0.8	0
2996	Ontology Analysis of Biological Networks. , 2013, , 1561-1562.		0
2997	Biología de Sistemas de Pectinases do Fungo Moniliophthora perniciosa. Diálogos & Ciência, 2013, 11, 27-30.	0.1	0
2998	A Module Searching Method in Protein-protein Interaction Networks with Gene Expression Profile. Journal of Information and Computational Science, 2013, 10, 1541-1549.	0.1	0
2999	Network Topology and Functional Analysis of Genes in Ocular Disorders. Journal of Applied Bioinformatics & Computational Biology, 2014, 3, .	0.2	0
3000	Modeling Structural Protein Interaction Networks for Betweenness Analysis. , 2014, , 367-376.		1
3002	Subspace Clustering of DNA Microarray Data. International Journal of Computational Models and Algorithms in Medicine, 2014, 4, 1-52.	0.4	1
3004	Identification of Gene Markers for Aggressive Forms of Low-Grade Glioma Using TCGA Expression Data. Mathematical Biology and Bioinformatics, 2014, 9, 527-533.	0.1	0
3006	Computational Data Integration in Toxicogenomics. Methods in Pharmacology and Toxicology, 2015, , 371-392.	0.1	0
3007	Epitope specificity and protein signaling interactions driving epidemic occurrences of Ebola disease. F1000Research, 0, 4, 166.	0.8	2
3009	Protein disorder reduced in Saccharomyces cerevisiae to survive heat shock. F1000Research, 2015, 4, 1222.	0.8	2
3015	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
3019	Role of Bioinformatics in Nanotechnology. Advances in Medical Technologies and Clinical Practice Book Series, 2017, , 293-317.	0.3	0
3020	Network Pharmacology of JinChaiKangBingDu Capsule Against Influenza A (H1N1) Virus Infection. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
3022	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
3032	Macromolecular Connectivity Landscape of Mammalian Brain. SSRN Electronic Journal, 0, , .	0.4	1
3033	Network Analysis Reveals Heterogeneous Response of Redox Metabolism in Hepatocellular Carcinoma Patients. SSRN Electronic Journal, 0, , .	0.4	0
3034	Tumor-Induced Cholesterol Efflux from Macrophages Drives IL-4 Mediated Reprogramming and Tumor Progression. SSRN Electronic Journal, 0, , .	0.4	1
3035	Novel Genetic Loci Affecting Facial Shape Variation in Humans. SSRN Electronic Journal, 0, , .	0.4	0
3039	Evaluation of the Proteome Profile Changes of Canola Leaf Inoculated With Pseudomonas Florescence FY32 under Salinity Stress. Journal of Crop Breeding, 2018, 9, 40-49.	0.4	0
3041	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	0.8	2
3046	Biomarker identification of thyroid associated ophthalmopathy using microarray data. International Journal of Ophthalmology, 2018, 11, 1482-1488.	0.5	5
3052	The Detection of Gene Modules with Overlapping Characteristic via Integrating Multi-omics Data in Six Cancers. Lecture Notes in Computer Science, 2019, , 394-405.	1.0	1
3053	Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.		0
3055	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
3056	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
3059	Evaluation and Interpretation of Transcriptome Data Underlying Heterogeneous Chronic Obstructive Pulmonary Disease. Genomics and Informatics, 2019, 17, e2.	0.4	6
3065	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
3068	Identification of prognostic biomarkers for malignant melanoma using microarray datasets. Oncology Letters, 2019, 18, 5243-5254.	0.8	3
3071	Networks of Function and Shared Ancestry Provide Insights into Diversification of Histone Fold Domain in the Plant Kingdom. Studies in Computational Intelligence, 2020, , 789-801.	0.7	0
3077	Expression characteristics of peripheral blood genes reveal potential biomarkers and candidate therapeutic targets for Parkinson's disease. Cellular and Molecular Biology, 2020, 66, 118.	0.3	1
3080	Comprehensive multi-factors reveal the pathogenesis of degenerative intervertebral disc. Cellular and Molecular Biology, 2020, 66, 65-71.	0.3	1

#	ARTICLE	IF	CITATIONS
3081	Bioinformatic screening and identification of downregulated hub genes in adrenocortical carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 2730-2742.	0.8	2
3082	Comprehensive multi-factor analysis and exploration for the pathogenesis of non-ischemic cardiomyopathy and ischemic cardiomyopathy. <i>Cellular and Molecular Biology</i> , 2020, 66, 66.	0.3	2
3086	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
3087	Oxidative stress response and programmed cell death guided by NAC013 modulate pithiness in radish taproots. <i>Plant Journal</i> , 2021, , .	2.8	2
3089	Epigenetic and Transcriptional Regulation of the Reproductive Hypothalamus. <i>Masterclass in Neuroendocrinology</i> , 2020, , 207-235.	0.1	0
3090	DNAJB4 identified as a potential breast cancer marker: evidence from bioinformatics analysis and basic experiments. <i>Gland Surgery</i> , 2020, 9, 1955-1972.	0.5	9
3092	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
3093	Stat3 oxidation-dependent regulation of gene expression impacts on developmental processes and involves cooperation with Hif-1 α . <i>PLoS ONE</i> , 2020, 15, e0244255.	1.1	11
3097	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
3098	Deciphering the network of interconnected pathways of <i>Chaetomium globosum</i> antagonistic related genes against <i>Bipolaris sorokiniana</i> using RNA seq approach. <i>Journal of Biological Control</i> , 2020, 34, 258-269.	0.2	5
3100	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
3101	Variation of biomolecules in plant species. , 2022, , 81-99.		2
3103	Role of Bioinformatics in Nanotechnology. , 2020, , 1875-1894.		1
3105	Leaf Curing Practices Alter Gene Expression and the Chemical Constituents of Tobacco Leaves. <i>Compendium of Plant Genomes</i> , 2020, , 73-83.	0.3	1
3111	Candidate genes of SARS-CoV-2 gender susceptibility. <i>Scientific Reports</i> , 2021, 11, 21968.	1.6	14
3112	Potential role of nitrogen in spore dispersal and infection of <i>Paraphysoderma sedebokerense</i> , a fungal parasite of <i>Haematococcus pluvialis</i> . <i>Algal Research</i> , 2021, 60, 102552.	2.4	3
3115	Identification of UBE2T as an independent prognostic biomarker for gallbladder cancer. <i>Oncology Letters</i> , 2020, 20, 44.	0.8	12
3116	Biclustering of DNA Microarray Data. , 0, , 513-551.		3

#	ARTICLE	IF	CITATIONS
3117	Handling and Interpreting Gene Groups. , 2007, , 69-84.		0
3118	Gene Arrays for Gene Discovery. , 2008, , 23-36.		0
3119	Network-Based Inference of Cancer Progression from Microarray Data. , 2008, , 268-279.		1
3126	Construction of Protein Expression Network. Methods in Molecular Biology, 2021, 2189, 119-132.	0.4	1
3127	Comprehensive analysis and identification of key genes and signaling pathways in the occurrence and metastasis of cutaneous melanoma. PeerJ, 2020, 8, e10265.	0.9	6
3128	Gene module identification from microarray data using nonnegative independent component analysis. Gene Regulation and Systems Biology, 2008, 1, 349-63.	2.3	9
3129	Acid stress response of a mycobacterial proteome: insight from a gene ontology analysis. International Journal of Clinical and Experimental Medicine, 2009, 2, 309-28.	1.3	10
3130	Biomarkers of the Hedgehog/Smoothed pathway in healthy volunteers. American Journal of Translational Research (discontinued), 2012, 4, 229-39.	0.0	2
3131	Module cover - a new approach to genotype-phenotype studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 135-46.	0.7	14
3135	Screening feature genes of osteosarcoma with DNA microarray: a bioinformatic analysis. International Journal of Clinical and Experimental Medicine, 2015, 8, 7134-42.	1.3	2
3136	Proteomics and bioinformatics analysis of mouse hypothalamic neurogenesis with or without EPHX2 gene deletion. International Journal of Clinical and Experimental Pathology, 2015, 8, 12634-45.	0.5	3
3138	Discovering regulated networks during HIV-1 latency and reactivation. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 354-66.	0.7	13
3139	Integrated mRNA and lncRNA expression profiling for exploring metastatic biomarkers of human intrahepatic cholangiocarcinoma. American Journal of Cancer Research, 2017, 7, 688-699.	1.4	18
3140	Exploring conserved mRNA-miRNA interactions in colon and lung cancers. Gastroenterology and Hepatology From Bed To Bench, 2017, 10, 184-193.	0.6	5
3141	Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 536-547.	0.7	7
3142	Exploring Potential Biomarkers Underlying Pathogenesis of Alzheimer's Disease by Differential Co-expression Analysis. Avicenna Journal of Medical Biotechnology, 2018, 10, 233-241.	0.2	2
3144	Serum proteomics study reveals candidate biomarkers for systemic lupus erythematosus. International Journal of Clinical and Experimental Pathology, 2017, 10, 10681-10694.	0.5	2
3145	Tumor necrosis factor α promotes HEp-2 cell proliferation via toll-like receptor 4 and NF- κ B signaling pathways. International Journal of Clinical and Experimental Pathology, 2017, 10, 11666-11672.	0.5	0

#	ARTICLE	IF	CITATIONS
3146	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
3147	Diagnostic and prognostic values of forkhead box D4 gene in colonic adenocarcinoma. International Journal of Clinical and Experimental Pathology, 2020, 13, 2615-2627.	0.5	0
3148	Differences in key genes in human alveolar macrophages between phenotypically normal smokers and nonsmokers: diagnostic and prognostic value in lung cancer. International Journal of Clinical and Experimental Pathology, 2020, 13, 2788-2805.	0.5	0
3149	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
3150	Proteome Analysis of the Hypothalamic Arcuate Nucleus in Chronic High-Fat Diet-Induced Obesity. BioMed Research International, 2021, 2021, 1-11.	0.9	1
3151	STMN1 is highly expressed and contributes to clonogenicity in acute promyelocytic leukemia cells. Investigational New Drugs, 2022, 40, 438-452.	1.2	6
3152	A Colorectal Cancer 3D Bioprinting Workflow as a Platform for Disease Modeling and Chemotherapeutic Screening. Frontiers in Bioengineering and Biotechnology, 2021, 9, 755563.	2.0	17
3154	Chikungunya Virus Infects the Heart and Induces Heart-Specific Transcriptional Changes in an Immunodeficient Mouse Model of Infection. American Journal of Tropical Medicine and Hygiene, 2022, 106, 99-104.	0.6	6
3155	Novel genome characteristics contribute to the invasiveness of <i>Phragmites australis</i> (common) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.0	10
3156	Targeted re-sequencing and genome-wide association analysis for wood property traits in breeding population of Eucalyptus tereticornis Å— E. grandis. Genomics, 2021, 113, 4276-4292.	1.3	7
3157	In silico Methods for Identification of Potential Therapeutic Targets. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 285-310.	2.2	17
3158	Microglial PDâ€1 stimulation by astrocytic PDâ€1 suppresses neuroinflammation and Alzheimerâ€™s disease pathology. EMBO Journal, 2021, 40, e108662.	3.5	41
3159	Identification of Potential Genes in Pathogenesis and Diagnostic Value Analysis of Partial Androgen Insensitivity Syndrome Using Bioinformatics Analysis. Frontiers in Endocrinology, 2021, 12, 731107.	1.5	1
3160	CTRP3 exacerbates tendinopathy by dysregulating tendon stem cell differentiation and altering extracellular matrix composition. Science Advances, 2021, 7, eabg6069.	4.7	18
3161	Investigation of the Proteomes of the Truffles Tuber albidum pico, T. aestivum, T. indicum, T. magnatum, and T. melanosporum. International Journal of Molecular Sciences, 2021, 22, 12999.	1.8	8
3162	Targeting Bone Metastases Signaling Pathway Using<i>Moringa oleifera</i> Seed Nutri-miRs: A Cross Kingdom Approach. Nutrition and Cancer, 2022, 74, 2522-2539.	0.9	5
3164	Targeting the spliceosome through RBM39 degradation results in exceptional responses in high-risk neuroblastoma models. Science Advances, 2021, 7, eabj5405.	4.7	32
3165	Transcripts associated with chronic lung allograft dysfunction in transbronchial biopsies of lung transplants. American Journal of Transplantation, 2021, , .	2.6	10

#	ARTICLE	IF	CITATIONS
3166	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
3167	Comprehensive Transcriptome and Metabolic Profiling of Petal Color Development in <i>Lycoris sprengeri</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 747131.	1.7	7
3168	Epigenome-wide association study of sarcopenia: findings from the Hertfordshire Sarcopenia Study (HSS). <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2022, 13, 240-253.	2.9	13
3169	Gene regulatory network analysis defines transcriptome landscape with alternative splicing of human umbilical vein endothelial cells during replicative senescence. <i>BMC Genomics</i> , 2021, 22, 869.	1.2	4
3170	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
3171	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
3172	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
3173	Manufacturing T cells in hollow fiber membrane bioreactors changes their programming and enhances their potency. <i>Oncotarget</i> , 2021, 10, 1995168.	2.1	2
3174	Neuronetworks: Analysis of brain pathology in Mucopolysaccharidoses – A systems biology approach. <i>Neuroscience Informatics</i> , 2022, 2, 100036.	2.8	1
3175	Data Integration Challenges for Machine Learning in Precision Medicine. <i>Frontiers in Medicine</i> , 2021, 8, 784455.	1.2	18
3177	Physiological and transcriptomic analyses reveal the threat of herbicides glufosinate and glyphosate to the scleractinian coral <i>Pocillopora damicornis</i> . <i>Ecotoxicology and Environmental Safety</i> , 2022, 229, 113074.	2.9	8
3178	Sequential lipidomic, metabolomic, and proteomic analyses of serum, liver, and heart tissue specimens from peroxisomal biogenesis factor 11 β knockout mice. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 2235-2250.	1.9	13
3179	MOET: a web-based gene set enrichment tool at the Rat Genome Database for multiontology and multispecies analyses. <i>Genetics</i> , 2022, 220, .	1.2	7
3180	Deciphering the Genome-Wide Transcriptomic Changes during Interactions of Resistant and Susceptible Genotypes of American Elm with <i>Ophiostoma novo-ulmi</i> . <i>Journal of Fungi (Basel)</i> , 2022, 9, 10784314.	1.7	10
3181	Bacterial volatile organic compounds induce adverse ultrastructural changes and DNA damage to the sugarcane pathogenic fungus <i>Thielaviopsis ethacetica</i> . <i>Environmental Microbiology</i> , 2022, 24, 1430-1453.	1.8	15
3182	Aligned Poly-L-lactic Acid Nanofibers Induce Self-Assembly of Primary Cortical Neurons into 3D Cell Clusters. <i>ACS Biomaterials Science and Engineering</i> , 2022, 8, 765-776.	2.6	5
3184	Exploring the Multi-Tissue Crosstalk Relevant to Insulin Resistance Through Network-Based Analysis. <i>Frontiers in Endocrinology</i> , 2021, 12, 756785.	1.5	1
3185	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

#	ARTICLE	IF	CITATIONS
3186	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
3187	The hidden world within plants: metatranscriptomics unveils the complexity of wood microbiomes. <i>Journal of Experimental Botany</i> , 2022, 73, 2682-2697.	2.4	24
3188	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
3189	Elevated mutation rates underlie the evolution of the aquatic plant family Podostemaceae. <i>Communications Biology</i> , 2022, 5, 75.	2.0	6
3190	A comparative genomics examination of desiccation tolerance and sensitivity in two sister grass species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
3191	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
3192	The Role of miR-4256/HOXC8 Signaling Axis in the Gastric Cancer Progression: Evidence From lncRNA-miRNA-mRNA Network Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 793678.	1.3	6
3193	Over-Expression and Prognostic Significance of FATP5, as a New Biomarker, in Colorectal Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 770624.	1.6	4
3194	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
3195	Checking gene expression profile associated with IRF7 and UNC93B deficient patient peripheral blood mononuclear cells infected with pH1N1 influenza virus. <i>AIP Conference Proceedings</i> , 2022, , .	0.3	0
3196	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
3197	Alpha B-Crystallin in Muscle Disease Prevention: The Role of Physical Activity. <i>Molecules</i> , 2022, 27, 1147.	1.7	10
3198	Molecular basis of the association between transcription regulators nuclear respiratory factor 1 and inhibitor of DNA binding protein 3 and the development of microvascular lesions. <i>Microvascular Research</i> , 2022, 141, 104337.	1.1	2
3199	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
3200	Gene expression profiling of coronary artery disease and its relation with different severities. <i>Journal of Genetics</i> , 2018, 97, 853-867.	0.4	2
3201	Interaction network analysis of YBX1 for identification of therapeutic targets in adenocarcinomas. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	1
3202	Analysis of chickpea gene co-expression networks and pathways during heavy metal stress. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	0
3203	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

#	ARTICLE	IF	CITATIONS
3204	Platforms for Analyzing Networks of Neurodegenerative and Psychiatric Diseases. , 2022, , 1-36.		0
3205	Computational approaches to identify biomarkers, enzymes, and pathways of hepatocellular carcinoma. , 2022, , 21-34.		0
3207	Identification of hub genes and molecular pathways in human T-lymphotropic virus type 1 associated diseases using protein-protein interactions networks. Iranian Journal of Microbiology, 0, , .	0.8	0
3208	Identification of Potential Genes Encoding Protein Transporters in Arabidopsis thaliana Glucosinolate (GSL) Metabolism. Life, 2022, 12, 326.	1.1	2
3209	â€”Nebbioloâ€” genome assembly allows surveying the occurrence and functional implications of genomic structural variations in grapevines (Vitis vinifera L.). BMC Genomics, 2022, 23, 159.	1.2	11
3211	MonaGO: a novel gene ontology enrichment analysis visualisation system. BMC Bioinformatics, 2022, 23, 69.	1.2	12
3212	Commensal Pseudomonas strains facilitate protective response against pathogens in the host plant. Nature Ecology and Evolution, 2022, 6, 383-396.	3.4	44
3213	System-Level Analysis of Transcriptional and Translational Regulatory Elements in Streptomyces griseus. Frontiers in Bioengineering and Biotechnology, 2022, 10, 844200.	2.0	1
3214	Proteomic profiling of hydatid fluid from pulmonary cystic echinococcosis. Parasites and Vectors, 2022, 15, 99.	1.0	3
3215	Microvesicles released from activated CD4 ⁺ T cells alter microvascular endothelial cell function. European Journal of Clinical Investigation, 2022, , e13769.	1.7	3
3217	Comparative transcriptome analysis of cold-tolerant and -sensitive asparagus bean under chilling stress and recovery. PeerJ, 2022, 10, e13167.	0.9	7
3219	Clinical Significance and Potential Mechanisms of ATP Binding Cassette Subfamily C Genes in Hepatocellular Carcinoma. Frontiers in Genetics, 2022, 13, 805961.	1.1	5
3220	Mechanosensory trichome cells evoke a mechanical stimuliâ€”induced immune response in Arabidopsis thaliana. Nature Communications, 2022, 13, 1216.	5.8	43
3222	MicroRNA-mediated post-transcriptional regulation of Pinus pinaster response and resistance to pinewood nematode. Scientific Reports, 2022, 12, 5160.	1.6	7
3223	Screening of Potential Key Biomarkers for Ewing Sarcoma: Evidence from Gene Array Analysis. International Journal of General Medicine, 2022, Volume 15, 2575-2588.	0.8	1
3224	Context dependent isoform specific PI3K inhibition confers drug resistance in hepatocellular carcinoma cells. BMC Cancer, 2022, 22, 320.	1.1	3
3225	Global chromosome rearrangement induced by CRISPR-Cas9 reshapes the genome and transcriptome of human cells. Nucleic Acids Research, 2022, 50, 3456-3474.	6.5	8
3226	Application of Transcriptomics for Predicting Protein Interaction Networks, Drug Targets and Drug Candidates. Frontiers in Medical Technology, 2022, 4, 693148.	1.3	1

#	ARTICLE	IF	CITATIONS
3227	Zfp1, a Cys2His2 zinc finger protein is required for meiosis initiation in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2022, , 1-12.	1.3	1
3228	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
3229	Transcription factor protein interactomes reveal genetic determinants in heart disease. <i>Cell</i> , 2022, 185, 794-814.e30.	13.5	39
3230	Defense response-like reaction associated with an anomaly in <i>Eucalyptus grandis</i> . <i>Trees - Structure and Function</i> , 0, , 1.	0.9	0
3231	Transcriptome and Small RNA Sequencing Reveal the Mechanisms Regulating Harvest Index in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 855486.	1.7	2
3232	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
3233	Functional and structural deficiencies of Gemin5 variants associated with neurological disorders. <i>Life Science Alliance</i> , 2022, 5, e202201403.	1.3	7
3234	Transcriptomic Analysis of Sex-Associated DEGs in Female and Male Flowers of Kiwifruit (<i>Actinidia</i>) Tj ETQq1 1 0.784314 rgBT ₀ /Overlook	1.2	0
3235	Targeting CK2 mediated signaling to impair/tackle SARS-CoV-2 infection: a computational biology approach. <i>Molecular Medicine</i> , 2021, 27, 161.	1.9	9
3236	Identification of Potential Genetic Biomarkers and Target Genes of Peri-Implantitis Using Bioinformatics Tools. <i>BioMed Research International</i> , 2021, 2021, 1-16.	0.9	12
3237	GeneTonic: an R/Bioconductor package for streamlining the interpretation of RNA-seq data. <i>BMC Bioinformatics</i> , 2021, 22, 610.	1.2	21
3238	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
3239	Different Regulatory Modes of <i>Synechocystis</i> sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. <i>MSystems</i> , 2021, 6, e0094321.	1.7	7
3241	Promising novel biomarkers and candidate small-molecule drugs for lung adenocarcinoma: Evidence from bioinformatics analysis of high-throughput data. <i>Open Medicine (Poland)</i> , 2021, 17, 96-112.	0.6	1
3242	Genetic insights into the regulatory pathways for continuous flowering in a unique orchid <i>Arundina graminifolia</i> . <i>BMC Plant Biology</i> , 2021, 21, 587.	1.6	11
3243	Transcriptomic, proteomic, and phosphoproteomic analyses reveal dynamic signaling networks influencing long-grain rice development. <i>Crop Journal</i> , 2021, , .	2.3	1
3245	The Identification of Small RNAs Differentially Expressed in Apple Buds Reveals a Potential Role of the Mir159-MYB Regulatory Module during Dormancy. <i>Plants</i> , 2021, 10, 2665.	1.6	9
3247	Integration of transcriptomic and proteomic analyses reveals several levels of metabolic regulation in the excess starch and early senescent leaf mutant <i>Ises1</i> in rice. <i>BMC Plant Biology</i> , 2022, 22, 137.	1.6	3

#	ARTICLE	IF	CITATIONS
3248	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
3249	Sulfur signaling and starvation response in <i>Arabidopsis</i> . <i>IScience</i> , 2022, 25, 104242.	1.9	16
3250	Inhibitor of DNA binding 2 (ID2) regulates the expression of developmental genes and tumorigenesis in ewing sarcoma. <i>Oncogene</i> , 2022, 41, 2873-2884.	2.6	2
3251	Jasmonates and Histone deacetylase 6 activate <i>Arabidopsis</i> genome-wide histone acetylation and methylation during the early acute stress response. <i>BMC Biology</i> , 2022, 20, 83.	1.7	5
3535	Software Tools for Systems Biology: Visualizing the Outcomes of N Experiments on M Entities. , 0, , 167-195.		0
3536	Gene evolutionary trajectories in <i>Mycobacterium tuberculosis</i> reveal temporal signs of selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113600119.	3.3	13
3537	Integrated analysis of 14 lymphoma datasets revealed high expression of CXCL14 promotes cell migration in mantle cell lymphoma. <i>Aging</i> , 2022, 14, 3446-3463.	1.4	0
3538	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
3539	Exploring Diverse Coagulation Factor XIII Subunit Expression Datasets: A Bioinformatic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4725.	1.8	5
3540	Protein-Protein Interaction (PPI) Network of Zebrafish Oestrogen Receptors: A Bioinformatics Workflow. <i>Life</i> , 2022, 12, 650.	1.1	1
3541	<i>Quercus suber</i> Transcriptome Analyses: Identification of Genes and SNPs Related to Cork Quality. , 2022, 11, .		2
3542	Effective high-throughput isolation of enriched platelets and circulating pro-angiogenic cells to accelerate skin-wound healing. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 259.	2.4	3
3543	Proteomic Perspective of Cadmium Tolerance in Providencia rettgeri Strain KDM3 and Its In-situ Bioremediation Potential in Rice Ecosystem. <i>Frontiers in Microbiology</i> , 2022, 13, 852697.	1.5	0
3544	KATP channel dependent heart multiome atlas. <i>Scientific Reports</i> , 2022, 12, 7314.	1.6	1
3545	Divergence in the ABA gene regulatory network underlies differential growth control. <i>Nature Plants</i> , 2022, 8, 549-560.	4.7	19
3546	Brain-specific deletion of GIT1 impairs cognition and alters phosphorylation of synaptic protein networks implicated in schizophrenia susceptibility. <i>Molecular Psychiatry</i> , 2022, 27, 3272-3285.	4.1	5
3547	Exploration of Potential Biomarker Genes and Pathways in Kawasaki Disease: An Integrated in-Silico Approach. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	6
3548	Inferring the Significance of the Polyamine Metabolism in the Phytopathogenic Bacteria <i>Pseudomonas syringae</i> : A Meta-Analysis Approach. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5

#	ARTICLE	IF	CITATIONS
3549	The glycosaminoglycan interactome 2.0. American Journal of Physiology - Cell Physiology, 2022, 322, C1271-C1278.	2.1	29
3550	Transcriptome Characterization of Different Tissues of Stone Pine (<i>Pinus pinea</i> L.): De Novo Assembly. , 2021, 11, .		0
3551	Hearing Impairment in Mucopolysaccharidosis: A Systems Biology Approach. Journal of Inborn Errors of Metabolism and Screening, 0, 10, .	0.3	0
3552	OsOSCA1.1 Mediates Hyperosmolality and Salt Stress Sensing in <i>Oryza sativa</i> . Biology, 2022, 11, 678.	1.3	6
3553	NUF2 Is a Potential Immunological and Prognostic Marker for Non-Small-Cell Lung Cancer. Journal of Immunology Research, 2022, 2022, 1-22.	0.9	2
3554	Modelling liver cancer microenvironment using a novel 3D culture system. Scientific Reports, 2022, 12, 8003.	1.6	24
3555	A Structural Characterisation of the Mitogen-Activated Protein Kinase Network in Cancer. Symmetry, 2022, 14, 1009.	1.1	2
3556	Revealing the novel complexity of plant long non-coding RNA by strand-specific and whole transcriptome sequencing for evolutionarily representative plant species. BMC Genomics, 2022, 23, 381.	1.2	3
3558	Salivary Proteomics Markers for Preclinical Sjögren's Syndrome: A Pilot Study. Biomolecules, 2022, 12, 738.	1.8	5
3559	Yield-associated putative gene regulatory networks in <i>Oryza sativa</i> L. subsp. indica and their association with high-yielding genotypes. Molecular Biology Reports, 2022, 49, 7649-7663.	1.0	1
3560	A novel and diverse set of SNP markers for rangewide genetic studies in <i>Picea abies</i> . Conservation Genetics Resources, 2022, 14, 267-270.	0.4	1
3561	Competition for dominance within replicating quasispecies during prolonged SARS-CoV-2 infection in an immunocompromised host. Virus Evolution, 2022, 8, .	2.2	21
3562	Deciphering miR-520c-3p as a probable target for immunometabolism in non-small cell lung cancer using systems biology approach. Oncotarget, 2022, 13, 725-746.	0.8	4
3563	Transcriptome analysis reveals dysregulation of inflammatory and neuronal function in dorsal root ganglion of paclitaxel-induced peripheral neuropathy rats. Molecular Pain, 2023, 19, 174480692211061.	1.0	9
3564	Host-dependent impairment of parasite development and reproduction in the acanthocephalan model. Cell and Bioscience, 2022, 12, .	2.1	3
3565	High-energy-level metabolism and transport occur at the transition from closed to open flowers. Plant Physiology, 2022, 190, 319-339.	2.3	2
3567	Soluble factors secreted by human Wharton's jelly mesenchymal stromal/stem cells exhibit therapeutic radioprotection: A mechanistic study with integrating network biology. World Journal of Stem Cells, 2022, 14, 347-361.	1.3	1
3568	Genome-wide identification of Aux/IAA and ARF gene families in bread wheat (<i>Triticum aestivum</i> L.). Protoplasma, 2023, 260, 257-270.	1.0	7

#	ARTICLE	IF	CITATIONS
3569	Fish Hydrolysate Supplementation Prevents Stress-Induced Dysregulation of Hippocampal Proteins Relative to Mitochondrial Metabolism and the Neuronal Network in Mice. <i>Foods</i> , 2022, 11, 1591.	1.9	2
3570	<i>ARID</i> 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
3571	Transcriptomic analysis provides insights into molecular mechanisms of thermal physiology. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
3574	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
3576	Comprehensive Effects of Flowering Locus T-Mediated Stem Growth in Tobacco. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3577	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
3578	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
3579	<i>Bcl11a</i> and the Correlated Key Genes Ascribable to Globin Switching: An In-silico Study. <i>Cardiovascular & Hematological Disorders Drug Targets</i> , 2022, 22, 128-142.	0.2	1
3580	A prominent gene activation role for C-terminal binding protein in mediating PcG/trxG proteins through Hox gene regulation. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
3581	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
3582	Immune Cell Networks Uncover Candidate Biomarkers of Melanoma Immunotherapy Response. <i>Journal of Personalized Medicine</i> , 2022, 12, 958.	1.1	0
3583	Immunoregulation of Ghrelin in neurocognitive sequelae associated with COVID-19: an in silico investigation. <i>Gene</i> , 2022, 834, 146647.	1.0	5
3584	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
3585	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
3586	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
3587	SERPINE1 Gene Is a Reliable Molecular Marker for the Early Diagnosis of Aortic Dissection. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	2
3588	The <i>pho1;2a</i> allele of <i>Phosphate1</i> conditions misregulation of the phosphorus starvation response in maize (<i>Zea mays</i> ssp. <i>mays</i> L.). <i>Plant Direct</i> , 2022, 6, .	0.8	0
3589	Characterization of the Nuclear Proteome of <i>Chlamydomonas</i> in Response to Salt Stress. <i>Phycology</i> , 2022, 2, 280-296.	1.7	2

#	ARTICLE	IF	CITATIONS
3590	Effective Mechanisms for Improving Seed Oil Production in Pennycress (<i>Thlaspi arvense</i> L.) Highlighted by Integration of Comparative Metabolomics and Transcriptomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
3591	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
3592	Intestine-enriched apolipoprotein b orthologs are required for stem cell progeny differentiation and regeneration in planarians. <i>Nature Communications</i> , 2022, 13, .	5.8	8
3593	Towards Cohesive Anomaly Mining. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2013, 27, 984-990.	3.6	4
3594	Proteomic and physiological analyses to elucidate nitric oxide-mediated adaptive responses of barley under cadmium stress. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1467-1476.	1.4	8
3595	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
3596	Sustainable environmental remediation via biomimetic multifunctional lignocellulosic nano-framework. <i>Nature Communications</i> , 2022, 13, .	5.8	26
3597	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
3598	Proteomic and phosphoproteomic measurements enhance ability to predict ex vivo drug response in AML. <i>Clinical Proteomics</i> , 2022, 19, .	1.1	9
3599	Microgel culture and spatial identity mapping elucidate the signalling requirements for primate epiblast and amnion formation. <i>Development (Cambridge)</i> , 0, , .	1.2	6
3600	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
3601	Local burn wound environment versus systemic response: Comparison of proteins and metabolites. <i>Wound Repair and Regeneration</i> , 2022, 30, 560-572.	1.5	3
3602	Glioblastoma hijacks neuronal mechanisms for brain invasion. <i>Cell</i> , 2022, 185, 2899-2917.e31.	13.5	168
3603	Genome of <i>Pythium myriotylum</i> Uncovers an Extensive Arsenal of Virulence-Related Genes among the Broad-Host-Range Necrotrophic <i>Pythium</i> Plant Pathogens. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
3604	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
3605	Differentiallyâ€reset transcriptomes and genome bias response orchestrate wheat response to phosphate deficiency. <i>Physiologia Plantarum</i> , 0, , .	2.6	2
3606	Integration of miRNA:mRNA Co-Expression Revealed Crucial Mechanisms Modulated in Immunogenic Cancer Cell Death. <i>Biomedicines</i> , 2022, 10, 1896.	1.4	2
3607	Network analysis and ligand-based pharmacophore modeling for discovery of small molecule against glioblastoma multiforme. <i>Future Medicinal Chemistry</i> , 2022, 14, 1203-1218.	1.1	2

#	ARTICLE	IF	CITATIONS
3608	Lysophosphatidic acid acyltransferase 2 and 5 commonly, but differently, promote seed oil accumulation in <i>Brassica napus</i> . , 2022, 15, .		6
3609	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
3610	A novel age-related gene expression signature associates with proliferation and disease progression in breast cancer. <i>British Journal of Cancer</i> , 2022, 127, 1865-1875.	2.9	5
3612	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
3613	DDX5 mRNA-targeting antisense oligonucleotide as a new promising therapeutic in combating castration-resistant prostate cancer. <i>Molecular Therapy</i> , 2023, 31, 471-486.	3.7	12
3614	Metabolic engineering to enhance the accumulation of bioactive flavonoids licochalcone A and echinatin in <i>Glycyrrhiza inflata</i> (Licorice) hairy roots. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3617	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
3618	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
3619	SUPPRESSOR OF PHYTOCHROME B-4#3 reduces the expression of PIF-activated genes and increases expression of growth repressors to regulate hypocotyl elongation in short days. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
3620	Comparative genomics analysis of drought response between obligate CAM and C3 photosynthesis plants. <i>Journal of Plant Physiology</i> , 2022, 277, 153791.	1.6	3
3621	Glucose-driven TOR#x201c;FIE#x201c;PRC2 signalling controls plant development. <i>Nature</i> , 2022, 609, 986-993.	13.7	47
3622	Ubiquitination regulates cytoophidium assembly in <i>Schizosaccharomyces pombe</i> . <i>Experimental Cell Research</i> , 2022, 420, 113337.	1.2	2
3623	GOMpare: An R Package to Compare Functional Enrichment Analysis between Two Species. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3624	Analysis of the Human Pineal Proteome by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2022, , 123-132.	0.4	0
3625	<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
3626	Adaptations in Nucleus Accumbens Neuron Subtypes Mediate Negative Affective Behaviors in Fentanyl Abstinence. <i>Biological Psychiatry</i> , 2023, 93, 489-501.	0.7	8
3627	Lactic acid from vaginal microbiota enhances cervicovaginal epithelial barrier integrity by promoting tight junction protein expression. <i>Microbiome</i> , 2022, 10, .	4.9	25
3628	Integrated Microarray Analysis to Identify Genes and Small-Molecule Drugs Associated with Stroke Progression. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	2

#	ARTICLE	IF	CITATIONS
3629	<i>SRPK1 Regulates Asexual Blood Stage Schizogony and Is Essential for Male Gamete Formation. Microbiology Spectrum</i> , 2022, 10, .	1.2	4
3630	Comparative genomics reveals putative evidence for high-elevation adaptation in the American pika (<i>Ochotona princeps</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
3633	Overview of methods for characterization and visualization of a protein–protein interaction network in a multi-omics integration context. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
3634	Anti-proliferative and pro-apoptotic effects of curcumin on skin cutaneous melanoma: Bioinformatics analysis and in vitro experimental studies. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
3635	CRHR1 mediates the transcriptional expression of pituitary hormones and their receptors under hypoxia. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	0
3636	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
3637	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
3638	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
3639	Genome-wide analysis suggests the potential role of lncRNAs during seed development and seed size/weight determination in chickpea. <i>Planta</i> , 2022, 256, .	1.6	3
3640	Accurate detection of benign and malignant renal tumor subtypes with MethylBoostER: An epigenetic marker–driven learning framework. <i>Science Advances</i> , 2022, 8, .	4.7	1
3641	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
3642	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
3643	Culturomic-, metagenomic-, and transcriptomic-based characterization of commensal lactic acid bacteria isolated from domestic dogs using <i>Caenorhabditis elegans</i> as a model for aging. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	6
3645	Functional analysis of litter size and number of teats in pigs: From GWAS to post-GWAS. <i>Theriogenology</i> , 2022, 193, 157-166.	0.9	4
3646	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
3647	Ag NCs as a potent antibiofilm agent against pathogenic <i>Pseudomonas aeruginosa</i> and <i>Acinetobacter baumannii</i> and drug-resistant <i>Bacillus subtilis</i> by affecting chemotaxis and flagellar assembly pathway genes. <i>Biomaterials Science</i> , 2022, 10, 6778-6790.	2.6	6
3648	Activity-dependent translation dynamically alters the proteome of the perisynaptic astrocyte process. <i>Cell Reports</i> , 2022, 41, 111474.	2.9	17
3649	Metabolomic and transcriptomic changes in mungbean (<i>Vigna radiata</i> (L.) R. Wilczek) sprouts under salinity stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4

#	ARTICLE	IF	CITATIONS
3652	Rhizobium etli CFN42 proteomes showed isoenzymes in free-living and symbiosis with a different transcriptional regulation inferred from a transcriptional regulatory network. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3653	Histone methyltransferases SDG33 and SDG34 regulate organ-specific nitrogen responses in tomato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3654	Dissecting the cotranscriptome landscape of plants and their microbiota. <i>EMBO Reports</i> , 2022, 23, .	2.0	13
3655	Transcriptome Analysis Reveals Putative Genes Involved in the Lipid Metabolism of Chaulmoogra Oil Biosynthesis in <i>Carpotroche brasiliensis</i> (Raddi) A.Gray, a Tropical Tree Species. <i>Forests</i> , 2022, 13, 1806.	0.9	0
3657	Inflammatory priming with IL-1 β promotes the immunomodulatory behavior of adipose derived stem cells. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	4
3658	Systematic molecular profiling of acute leukemia cancer stem cells allows identification of druggable targets. <i>Heliyon</i> , 2022, 8, e11093.	1.4	0
3659	Proteomic Analysis of Decellularized Extracellular Matrix: Achieving a Competent Biomaterial for Osteogenesis. <i>BioMed Research International</i> , 2022, 2022, 1-18.	0.9	1
3660	Chemical proteomics reveals interactors of the alarmone diadenosine triphosphate in the cancer cell line H1299. <i>Journal of Peptide Science</i> , 2023, 29, .	0.8	1
3661	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
3664	Phenotypically abnormal cotyledonary <i>Vitis vinifera</i> embryos differ in anatomy, endogenous hormone levels and transcriptome profiles. <i>Tree Physiology</i> , 2023, 43, 467-485.	1.4	4
3665	DNA repair-related genes and adipogenesis: Lessons from congenital lipodystrophies. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	1
3666	Transcriptome Profiling of Stem-Differentiating Xylem in Response to Abiotic Stresses Based on Hybrid Sequencing in <i>Cunninghamia lanceolata</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13986.	1.8	1
3668	Identification of the common neurobiological process disturbed in genetic and non-genetic models for autism spectrum disorders. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	0
3669	Genome-scale signatures of adaptive gene expression changes in an invasive seaweed <i>Gracilaria vermiculophylla</i> . <i>Molecular Ecology</i> , 2023, 32, 613-627.	2.0	3
3670	YMLA: A comparative platform to carry out functional enrichment analysis for multiple gene lists in yeast. <i>Computers in Biology and Medicine</i> , 2022, , 106314.	3.9	0
3671	An integrated gene network analysis to decode the multi-drug resistance mechanism in <i>Klebsiella pneumoniae</i> . <i>Microbial Pathogenesis</i> , 2022, 173, 105878.	1.3	3
3672	Genome-wide dissection of changes in maize root system architecture during modern breeding. <i>Nature Plants</i> , 2022, 8, 1408-1422.	4.7	32
3673	Altering the balance between AOX1A and NDB2 expression affects a common set of transcripts in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1

#	ARTICLE	IF	CITATIONS
3674	Elucidating the mechanism of antimicrobial resistance in <i>Mycobacterium tuberculosis</i> using gene interaction networks. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , .	1.0	1
3675	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
3676	GOMcompare: An R package to compare functional enrichment analysis between two species. <i>Genomics</i> , 2023, 115, 110528.	1.3	0
3677	Nuclear access of DNlg3 c-terminal fragment and its function in regulating innate immune response genes. <i>Biochemical and Biophysical Research Communications</i> , 2023, 641, 93-101.	1.0	0
3678	Genome-wide identification and characterization of SPX domain-containing proteins and their responses to phosphorus and/or nitrogen deficiency in apple (<i>Malus domestica</i> Borkh.). <i>Scientia Horticulturae</i> , 2023, 310, 111767.	1.7	2
3679	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
3680	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
3681	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
3682	Antennal Transcriptome of the Fruit-Sucking Moth <i>Eudocima materna</i> : Identification of Olfactory Genes and Preliminary Evidence for RNA-Editing Events in Odorant Receptors. <i>Genes</i> , 2022, 13, 1207.	1.0	1
3683	Molecular, Circuit, and Stress Response Characterization of Ventral Pallidum Npas1-Neurons. <i>Journal of Neuroscience</i> , 2023, 43, 405-418.	1.7	15
3684	Genes Associated with Biological Nitrogen Fixation Efficiency Identified Using RNA Sequencing in Red Clover (<i>Trifolium pratense</i> L.). <i>Life</i> , 2022, 12, 1975.	1.1	5
3685	Bioinformatic Tools for Exploring the SUMO Gene Network: An Update. <i>Methods in Molecular Biology</i> , 2023, , 367-383.	0.4	1
3686	IL1RN and PRRX1 as a Prognostic Biomarker Correlated with Immune Infiltrates in Colorectal Cancer: Evidence from Bioinformatic Analysis. <i>International Journal of Genomics</i> , 2022, 2022, 1-24.	0.8	6
3687	Transcriptome Analysis Reveals Immunomodulatory Effect of Spore-Displayed p75 on Human Intestinal Epithelial Caco-2 Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14519.	1.8	2
3688	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
3689	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
3690	A strategy can be used to analyze intracellular interaction proteomics of cell-surface receptors. <i>Amino Acids</i> , 2023, 55, 263-273.	1.2	2
3691	Two vacuolar invertase inhibitors PpINH _a and PpINH ₃ display opposite effects on fruit sugar accumulation in peach. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2

#	ARTICLE	IF	CITATIONS
3692	Bioinformatics analysis of key biomarkers for bladder cancer. Biomedical Reports, 2022, 18, .	0.9	2
3693	Co-expression pan-network reveals genes involved in complex traits within maize pan-genome. BMC Plant Biology, 2022, 22, .	1.6	0
3694	Toxicity assessment of hexafluoropropylene oxide-dimer acid on morphology, heart physiology, and gene expression during zebrafish (<i>Danio rerio</i>) development. Environmental Science and Pollution Research, 2023, 30, 32320-32336.	2.7	4
3695	Studies on biotransformation mechanism of <i>Fusarium</i> sp. C39 to enhance saponin content of <i>Paridis Rhizoma</i> . Frontiers in Microbiology, 0, 13, .	1.5	2
3697	Living with high potassium: Balance between nutrient acquisition and K-induced salt stress signaling. Plant Physiology, 2023, 191, 1102-1121.	2.3	6
3698	Identification of molecular network of gut-brain axis associated with neuroprotective effects of PPAR γ -ligand erucic acid in rotenone-induced Parkinson's disease model in zebrafish. European Journal of Neuroscience, 2023, 57, 585-606.	1.2	8
3699	Transcriptional responses of human intestinal epithelial HT-29 cells to spore-displayed p40 derived from <i>Lactocaseibacillus rhamnosus</i> GG. BMC Microbiology, 2022, 22, .	1.3	0
3700	Leaves and stolons transcriptomic analysis provide insight into the role of <i>phytochrome F</i> in potato flowering and tuberization. Plant Journal, 2023, 113, 402-415.	2.8	4
3701	ENO2 affects the EMT process of renal cell carcinoma and participates in the regulation of the immune microenvironment. Oncology Reports, 2022, 49, .	1.2	0
3702	Evolutionary analysis of endogenous intronic retroviruses in primates reveals an enrichment in transcription binding sites associated with key regulatory processes. PeerJ, 0, 10, e14431.	0.9	0
3704	Network Analysis of Anti-inflammatory Phytochemicals and Omics Data for Rheumatoid Arthritis. Current Computer-Aided Drug Design, 2023, 19, 356-366.	0.8	0
3705	Signaling landscape of mitochondrial non-coding RNAs. Journal of Biomolecular Structure and Dynamics, 0, , 1-10.	2.0	0
3706	Transcriptomic Signature of the Simulated Microgravity Response in <i>Caenorhabditis elegans</i> and Comparison to Spaceflight Experiments. Cells, 2023, 12, 270.	1.8	2
3707	MAGNET: A web-based application for gene set enrichment analysis using macrophage data sets. PLoS ONE, 2023, 18, e0272166.	1.1	0
3708	Stem transcriptome screen for selection in wild and cultivated pitahaya (<i>Selenicereus</i>) Tj ETQq0 0 0 rgBT /Overlook 10 Tf 50 182 Td (0.9	1
3709	<scp>PRpnp</scp>, a novel dual activity <scp>PNP</scp> family protein improves plant vigour and confers multiple stress tolerance in <i>Citrus aurantifolia</i> . Plant Biotechnology Journal, 2023, 21, 726-741.	4.1	2
3710	Anti-obesity effect of vegetable juice fermented with lactic acid bacteria isolated from kimchi in C57BL/6J mice and human mesenchymal stem cells. Food and Function, 2023, 14, 1349-1356.	2.1	11
3712	The Integrated mRNA and miRNA Approach Reveals Potential Regulators of Flowering Time in <i>Arundina graminifolia</i> . International Journal of Molecular Sciences, 2023, 24, 1699.	1.8	3

#	ARTICLE	IF	CITATIONS
3713	Understanding of molecular basis of histological graded horn cancer by transcriptome profiling. <i>Gene</i> , 2023, 857, 147196.	1.0	0
3714	Comparative transcriptome analysis provides insight into the important pathways and key genes related to the pollen abortion in the thermo-sensitive genic male sterile line 373S in <i>Brassica napus</i> L.. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
3715	Genome-wide identification of the MATE gene family and functional characterization of PbrMATE9 related to anthocyanin in pear. <i>Horticultural Plant Journal</i> , 2023, 9, 1079-1094.	2.3	3
3716	RSL24D1 sustains steady-state ribosome biogenesis and pluripotency translational programs in embryonic stem cells. <i>Nature Communications</i> , 2023, 14, .	5.8	4
3717	Building, Visualizing, and Analyzing Glycosaminoglycan-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2023, , 211-224.	0.4	1
3718	Chromosome-level wild <i>Hevea brasiliensis</i> genome provides new tools for genomic-assisted breeding and valuable loci to elevate rubber yield. <i>Plant Biotechnology Journal</i> , 2023, 21, 1058-1072.	4.1	10
3719	Unraveling the Relevance of Tissue-Specific Decellularized Extracellular Matrix Hydrogels for Vocal Fold Regenerative Biomaterials: A Comprehensive Proteomic and In-Vitro Study. <i>Advanced NanoBiomed Research</i> , 2023, 3, .	1.7	0
3720	Alternative 5'-untranslated regions regulate high-salt tolerance of <i>Spartina alterniflora</i> . <i>Plant Physiology</i> , 2023, 191, 2570-2587.	2.3	4
3721	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
3722	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
3723	Sweetener System Intervention Shifted Neutrophils from Homeostasis to Priming. <i>Nutrients</i> , 2023, 15, 1260.	1.7	2
3724	Translating desktop success to the web in the cytoscape project. <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	0
3725	Identification of key modules and candidate genes associated with endometriosis based on transcriptome data via bioinformatics analysis. <i>Pathology Research and Practice</i> , 2023, 244, 154404.	1.0	1
3726	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
3727	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
3728	Acute hypoxia induces reduction of algal symbiont density and suppression of energy metabolism in the scleractinian coral <i>Pocillopora damicornis</i> . <i>Marine Pollution Bulletin</i> , 2023, 191, 114897.	2.3	0
3729	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
3730	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

#	ARTICLE	IF	CITATIONS
3731	Gene expression changes in Tayâ€“Sachs disease begin early in fetal brain development. Journal of Inherited Metabolic Disease, 2023, 46, 687-694.	1.7	1
3733	Transcriptome Analysis of Heat Shock Factor C2a Over-Expressing Wheat Roots Reveals Ferroptosis-like Cell Death in Heat Stress Recovery. International Journal of Molecular Sciences, 2023, 24, 3099.	1.8	3
3734	Volatile Organic Compounds from <i>Pythium oligandrum</i> Play a Role in Its Parasitism on Plant-Pathogenic <i>Pythium myriotylum</i> . Applied and Environmental Microbiology, 2023, 89, .	1.4	3
3735	Toxicoproteomics of Mono(2-ethylhexyl) phthalate and Perfluorooctanesulfonic Acid in Models of Prostatic Diseases. Chemical Research in Toxicology, 2023, 36, 251-259.	1.7	3
3736	Targeting Glutaminolysis Shows Efficacy in Both Prednisolone-Sensitive and in Metabolically Rewired Prednisolone-Resistant B-Cell Childhood Acute Lymphoblastic Leukaemia Cells. International Journal of Molecular Sciences, 2023, 24, 3378.	1.8	2
3737	Identification of lncRNAs associated with the progression of acute lymphoblastic leukemia using a competing endogenous RNAs network. Oncology Research, 2022, 30, 259-268.	0.6	2
3739	Multi-Omics of Circular RNAs and Their Responses to Hormones in Moso Bamboo (<i>Phyllostachys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.0	1
3740	The SAGA histone acetyltransferase module targets SMC5/6 to specific genes. Epigenetics and Chromatin, 2023, 16, .	1.8	4
3742	Feasibility of detecting snake envenomation biomarkers from dried blood spots. Analytical Science Advances, 2023, 4, 26-36.	1.2	0
3743	The Protein Network in Subcutaneous Fat Biopsies from Patients with AL Amyloidosis: More Than Diagnosis?. Cells, 2023, 12, 699.	1.8	1
3744	circRNAs deregulation in exosomes derived from BEAS-2B cells is associated with vascular stiffness induced by PM2.5. Journal of Environmental Sciences, 2024, 137, 527-539.	3.2	0
3745	The Pleiotropic Effects of Carbohydrate-Mediated Growth Rate Modifications in <i>Bifidobacterium longum</i> NCC 2705. Microorganisms, 2023, 11, 588.	1.6	0
3746	Elucidation of the GAUT gene family in eight Rosaceae species and function analysis of PbrGAUT22 in pear pollen tube growth. Planta, 2023, 257, .	1.6	1
3747	Potato tonoplast sugar transporter 1 controls tuber sugar accumulation during postharvest cold storage. Horticulture Research, 2023, 10, .	2.9	2
3748	Integrative transcriptomic and proteomic analyses reveal a positive role of BES1 in salt tolerance in Arabidopsis. Frontiers in Plant Science, 0, 14, .	1.7	6
3749	Chromosome-level genome assembly of <i>Phrynocephalus forsythii</i> using third-generation DNA sequencing and Hi-C analysis. DNA Research, 2023, 30, .	1.5	0
3750	Platelet-Derived MicroRNAs Regulate Cardiac Remodeling After Myocardial Ischemia. Circulation Research, 2023, 132, .	2.0	8
3751	Conditional expression of endorepellin in the tumor vasculature attenuates breast cancer growth, angiogenesis and hyaluronan deposition. Matrix Biology, 2023, 118, 92-109.	1.5	2

#	ARTICLE	IF	CITATIONS
3752	Screening and identification of key biomarkers of depression using bioinformatics. Scientific Reports, 2023, 13, .	1.6	1
3753	Engineered Mesenchymal Stem Cells Over-Expressing BDNF Protect the Brain from Traumatic Brain Injury-Induced Neuronal Death, Neurological Deficits, and Cognitive Impairments. Pharmaceuticals, 2023, 16, 436.	1.7	5
3754	The Molecular Mechanism of the TEAD1 Gene and miR-410-5p Affect Embryonic Skeletal Muscle Development: A miRNA-Mediated ceRNA Network Analysis. Cells, 2023, 12, 943.	1.8	2
3755	Discovery of the relationship between bitter taste and bitter flavor (efficacy) based on hTAS2Rs. Journal of Traditional Chinese Medical Sciences, 2023, , .	0.1	0
3756	First-in-human clinical trial of the NKT cell-stimulatory glycolipid OCH in multiple sclerosis. Therapeutic Advances in Neurological Disorders, 2023, 16, 175628642311621.	1.5	6
3757	Multi-Targeted Prediction of the Antiviral Effect of <i>Momordica charantia</i> extract based on Network Pharmacology. Journal of Natural Remedies, 0, , 169-183.	0.1	0
3758	The 2020 derecho revealed limited overlap between maize genes associated with root lodging and root system architecture. Plant Physiology, 2023, 192, 2394-2403.	2.3	2
3759	Functional Annotation Routines Used by ABRF Bioinformatics Core Facilities - Observations, Comparisons, and Considerations. Journal of Biomolecular Techniques, 2023, 34, 3fc1f5fe.0b74b9db.	0.8	0
3761	EBV-Upregulated B7-H3 Inhibits NK cell-Mediated Antitumor Function and Contributes to Nasopharyngeal Carcinoma Progression. Cancer Immunology Research, 2023, 11, 830-846.	1.6	4
3762	Runs of homozygosity and signatures of selection for number of oocytes and embryos in the Gir Indicine cattle. Mammalian Genome, 2023, 34, 482-496.	1.0	2
3763	Human Adult Astrocyte Extracellular Vesicle Transcriptomics Study Identifies Specific RNAs Which Are Preferentially Secreted as EV Luminal Cargo. Genes, 2023, 14, 853.	1.0	0
3764	Nuclear translocation of cGAS orchestrates VEGF-A-mediated angiogenesis. Cell Reports, 2023, 42, 112328.	2.9	4
3765	The effect of temperature and invasive alien predator on genetic and phenotypic variation in the damselfly <i>Ischnura elegans</i> : cross-latitude comparison. Frontiers in Zoology, 2023, 20, .	0.9	1
3767	Cytological, transcriptome and miRNome temporal landscapes decode enhancement of rice grain size. BMC Biology, 2023, 21, .	1.7	0
3768	The miR167-OsARF12 module regulates rice grain filling and grain size downstream of miR159. Plant Communications, 2023, 4, 100604.	3.6	5
3769	Screening of feature genes related to immune and inflammatory responses in periodontitis. BMC Oral Health, 2023, 23, .	0.8	1
3771	Systems biology tools for the identification of potential drug targets and biological markers effective for cancer therapeutics. , 2023, , 259-292.		0
3780	Isolation and whole genome sequencing of <i>Pseudomonas aeruginosa</i> strain RK1 and its biocontrol potential against phytopathogens of rice. , 0, , .		0

#	ARTICLE	IF	CITATIONS
3788	Structure-based virtual screening. , 2023, , 239-262.		0
3815	Platforms for Analyzing Networks of Neurodegenerative and Psychiatric Diseases. , 2023, , 503-538.		0
3892	Biological interaction networks and their application for microbial pathogenesis. , 2024, , 131-143.		0
3893	In Silico Models to Validate Novel Blood-Based Biomarkers. Methods in Molecular Biology, 2024, , 321-344.	0.4	0